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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein · protein database search, using Smith-Waterman algorithm Wed Sep 1 16:16:39 1999; MasPar time 6.77 Seconds 550.316 Million cell updates/sec MPsrch_pp Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-93) from PCTUS9913024.pep (6 of 12) 634 1 MEKFWAEFGQGVVQTPPLSE.......DSKSYAFSTSNDTTSAAFVS 93 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

122810 seqs, 40068593 residues

Searched:

Database:

Mean 38.761; Variance 72.705; scale 0.533 Statistics:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Pred. No.	1 996-01	10-900-1	5 258-01	1.356+00	1.35e+00	1.35e+00	1.35e+00	1.35e+00	1.85e+00	1.85e+00	1.85e+00	2.52e+00	2.52e+00	3.42e+00	3.42e+00	3.42e+00	3.42e+00	4.63e+00	4.63e+00	4.63e+00	4.63e+00	6.25e+00	6.25e+00
70	Description	hypothetical protein				neutral proteinase (E		NADH dehydrogenase (u	genome polyprotein -	licheninase (EC 3.2.1	ecdysone-induced memb	cfac protein precurso	licheninase (EC 3.2.1	parasporal crystal pr		hypothetical protein	hypothetical protein	ethylene response sen	tyrosine kinase - hum	hypothetical protein	transporter homolog y	tyrosine kinase - hum	flagellar L-ring prot	probable GTP cyclohyd
SUMMARIES	ID	S61248	HYBSN	G71525	A29091	139956	S28275	A45456	MNWWHE	LXBS	A61046	C56617	S15388	S17402	D70961	538913	D70928	T00758	138375	S55092	F69762	184483	G70447	S45767
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аÞ	Query Match	14.5	14.5	14.0	13.6	13.6	13.6	13.6	13.6	13.4	13.4	13.4	13.2	13.2	13.1	13.1	13.1	13.1		12.9			12.8	
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Vasantha, N.; Thompson, L.D.; Rhodes, C.; Banner, C.; Nagle, J.; Filpula, D.
J. Bacteriol. (1984) 159:811-819
Genes for alkaline protease and neutral protease from

HYBSN *type complete
bacillolysin (EC 3.4.24.28) precursor - Bacillus
amploliquefaciens
amploliquefaciens
Bacillus metalloendopeptidase; microbial metalloproteinase;
neutral proteinase
*formal_name Bacillus amyloliquefaciens
30-Jun-1988 *sequence_revision 30-Jun-1988 *text_change
A25415

ALTERNATE_NAMES

RESULT ENTRY TITLE

ORGANISM

ACCESSIONS REFERENCE #authors

#journal #title

- AF CEV 1	hypothetical protein 6.2 enolase (eno) homolog 6.2 Txk - mouse 6.2 protein tyrosine kina 6.2 polyprotein protein 8 dypothetical protein 8 dypothetical protein 8 dypothetial protein 8 dypothetial protein 9 dypothetial 9 dypotheti	Avaidades - Frevoteila a NABJ protein - yeast glucan 1,4-alpha-gluc B vitellogenin precurso genome polyprotein - hypothetical protein paracystalline surfa vitamin D-binding pro methylmalonyl.CoA mut parasporal crystal pr NADH dehydrogenase (u	ALIGNMENTS. S61248	ary label VLC 248053; ND:9971311; PID:9971327 varicella-zoster virus gene 53 protein #molecular-weight 32379 #checksum 1192 ; Score 92; DB 2; Length 299; pred. No. 1.99e-01; 9; Mismatches 6; Indels 4; Gaps 4; SITHLRV-EPSTGALL 79 :: : ;
- AF CEV 1	H71282 H70141 149133 A55631 S40770 B38162 I39495 S14200	S48529 S461029 S461029 JC4956 GNWVC3 S69718 S337810 S337810 S337810 S359926 S17664 S71000	ALIGNMENTS pe complete rotein - bo ovine herpe equence_rev es, V.; Lu, tk, G.J.; S he EMBL Dat. uence analy 1 genome wh #ith the UL	abel VLC 18053; N aricella moleculai Score Pred. D 9; M ITHLRV-EL
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calcium; extracellular protein; hydrolase; metalloproteinase;
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licheninase (EC 3.2.1.73) beta - Bacillus amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, Q.; Koonin, E.V.; Davis, R.W. Science (1998) 282:754-759 the Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G71525 #type complete
probable OMP [leader (19) peptide] - Chlamydia trachomatis
(serotype D, strain UW3/Cx)
#formal_mame Chlamydia trachomatis
13.5ep-1998 #sequence_revision 13.5ep-1998 #text_change
21-Nov-1998
                                                                                                                                                                                                                                                              *domain signal sequence *status predicted *label SIGN *domain propeptide *status predicted *label PRON *product bacillolysin *status predicted *label MATN *binding_site zinc (His, His, Glu) *status predicted *active_zite Glu, His *status predicted yth 521 *molecular-weight 56840 *checksum 7195
Bacillus amyloliquefaciens contain a large open reading frame between the regions coding for signal sequence and
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Pred. No. 5.25e-01;
25; Mismatches 18; Indels
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                                 mature protein.
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ilarity 27.8%;
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Best Local Similarity 26.2%;
Matches 17; Conservative
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#authors Hofemeister, J.; Kurtz, A.; Borriss, R.; Knowles, J.
#journal Gene (1986) 49:177-187
#fitle The beta-glucanase gene from Bacillus amyloliquefaciens shows
#cross-references MUID:87192007
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Manabe, K.; Furutani, Y.
J. Biotechnol. (1985) 2:75-85
The nucleotide sequence and some properties of the neutral
1,3-1,4-beta-D-glucan 4-glucanohydrolase; beta-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139956 #type complete
neutral proteinase (EC 3.4.24..) - Bacillus amyloliquefa
#formal_name Bacillus amyloliquefaciens
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
00-sep-1997
S28275
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glycosidase; hydrolase; polysaccharide degradation
#length 239 #molecular-weight 26928 #checksum 1611
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hydrolase; metalloproteinase
#length 521 #molecular-weight 56725 #checksum 6816
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Pred. No. 1.35e+00;
18; Mismatches 19; Indels
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##cross-references GB:M15674; NID:q143009; PID:q143010
##experimental_source strain BE20/78
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                                  #formal_name Bacillus amyloliquefaciens
16-Aug-1988 #sequence_revision 16-Aug-1988
20-Mar-1998
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Pred. No. 1.35e+00;
20; Mismatches 18;
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Best Local Similarity 27.8%;
Matches 15; Conservative
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Best Local Similarity 25.5%;
Matches 14; Conservative
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                            lichenase
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Blochemistry (1993) 32:968-981
DNA sequencing of the seven remaining structural genes of the gene cluster encoding the energy-transducing NADH-quinone oxidoreductase of Paracoccus denitrificans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence extracted from NCBI backbone (NCBIN:123409, NCBIP:123410) *superfamily NADH dehydrogenase (ubiquinone) chain 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 VRFTTEVAGITQMGQTGRG-EDSEITSYLNQTLESNMQGNIIDLCPVGALV-SKPYAFTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO3 Paracoccus denitrificans
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                                                                                                                                                                                                                                                                                                                                                                    #formal_name Paracoccus denitrificans
24-Feb-1994 #sequence_revision 12-Apr-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD: oxidoreductase
#length 673 #molecular-weight 73159 #checksum 4307
                                                                                                        14/3; 51/2; 98/3; 213/2; 266/3; 294/3; 336/2; 381/2
         submitted to the EMBL Data Library, December 1992 S28275
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                                                                                                                                                                     Length 574
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:219155; NID:96712; PID:96715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 86; DB 2; L 28.3%; Pred. No. 1.35e+00; vative 19; Mismatches 21
                                                                                                                                                                  Score 86; DB 2; L
Pred. No. 1.35e+00;
9; Mismatches 10
                                                                                                                                                                                                                                 282 TFTEGLEYLRNFQPDADELFNRK-LRFSAGDDAA 314
                                                                                                                                                                                                                                                  nucleus
#length 574 #checksum 3597
                                                                                                                                                                                                                                                                                                                           #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658-673 ##label XU1
                                 ##molecule_type DNA ##label SUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
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                                                                                                                                                                    Query Match 13.6%;
Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   04-Sep-1998
S23948; A45456
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Sulston, J.
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##residues 1-67
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nes 17; Conserv
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                 #submission
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#title
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SUMMARY
                                                                                                                      KEYWORDS
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Broulllet, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                       sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, J.P.; Luk, K.C.;
Young, L.M.; Platak, M.; Feldman, R.A.; Yun, K.Y.; Purdy,
M.A.; McCaustland, K.A.; Bradley, D.W.; Reyes, G.R.
M.A.; McCaustland, K.A.; Bradley, D.W.; Reyes, G.R.
#title Hepatitis E virus (HEV): strain variation in the
nonstructural gene region encoding consensus motifs for ar
#cross-references MUID:92271462
#accession A48547
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Microbiology (1995) 141:281-290
Genes encoding xylan and beta-glucan hydrolysing enzymes in
Bacillus subtilis: characterization, mapping and
construction of strains deficient in lichenase, cellulase
                                                                                      *authors Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.R.

† Journal Virology (1991) 185:120-131

*title Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.

*teross-references MuID:92024067

*accession A40778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##modecule_type genomic RNA
##residues 967-1693 ##label FRY
##cross-references GB:M32400; NID:g330021; PID:g330022
##note extracted from NCBI backbone (NCBIN:104572,
NCBIP:104573)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 FRISFVDGAVLEINGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LXBS #type complete
licheninase (EC 3.2.1.73) precursor - Bacillus subtilis
1,3-1,4-beta-D-glucan 4-gluconohydrolase; beta-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              licheninase E-1; licheninase E-2
#formal_name Bacillus subtilis
30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change
24-Sep-1998
140370; B69594; A22914; A90026; A90027; JU0110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily hepatitis E virus nonstructural protein ATP; nonstructural protein; nucleotidyltransferase *length 1693 *molecular-weight 185191 *checksum 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1693;
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##residues 1-242 ##label RES
##cross-references EMBL:246862; NID:9599673; PID:9599674
                                                                                                                                                                                                                                                                                                       ##molecule_type genomic RNA
##residues 1-1693 ##label TAM
##cross-references GB:M73218; NID:g330023; PID:g330024
:NCE A48547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 1; L
Pred. No. 1.35e+00;
22; Mismatches 25
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Best Local Similarity 25.4%;
Matches 17; Conservative
29-May-1998
A40778; A48547
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                                                                                                                                                                                                                                                                                                                                              **residues
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Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.;
Daniel, R.A.; Dedani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Dedanizor, F.; Devine, K.M.; Duesterhoeft, A.;
Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabrer, C.; Ferrari, E.; Poulger, D.; Frizz, C.; Fujita,
M.; Fujita, Y.; Enma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Galightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Hags, K.; Haiech, J.; Harwood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.;
Kuita, M.; Levine, L.; Larindis, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Luber, J.; O'Reilly,
M.; Moestl, D.; Nakai, S.; Noback, M.; None, D.; O'Reilly,
M.; Moestl, D.; Portefelle, D.; Purnelle, B.; Rapoport, G.;
Rey, M.; Reynolds, S.; Rieger, M.; Rapoport, G.; Roch,
M.; Moestl, D.; Rayale, Y.; Sato, T.; Scanlon, E.;
Schwish, A.; Seror, S.J.; Satror, P.; Shin, B.S.; Solde,
B.; Sorckin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
Terpstra, P.; Tognoni, R.; Takagi, T.; Takahashi, H.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Winters, P.; Mapet, A.; Tamakohi, A.; Tanaka,
Fromplete, P.; Tognoni, A.; Tamakohi, A.; Tanaka,
K.; Yata, K.; Yoshikawa, H.; Pancher, E.; Wedler, H.; Wanmane,
K.; Yata, K.; Yoshikawa, H.; Tamahae, K.; Yata,
K.; Yata, K.; Yoshikawa, H.; Tamahae, K.; Yasunot,
K.; Yata, K.; Yoshikawa, H.; Yamamoto, H.; Yamanot, R.;
Koshikawa, H.; Danchin, A.;
Rocossion
Bacillus subtlis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-242 ##label KUN
##cross-references GB:299124; GB:AL009126; NID:92636442; PID:e1184632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as
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Apric. Blol. Chem. (1989) 53:2341-2346
Purification and some properties of two enzymes from a
beta_glucanase hyperproducing strain, Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tezuka, H.; Yuuki, T.; Yabuuchi, S.
Agric. Biol. Chem. (1989) 53:2335-2339
Construction of a beta-glucanase hyperproducing Bacillus
subtilis using the cloned beta-glucanase gene and a
multi-copy plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; nucleic acid sequence not shown;
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##residues 1-23,'S',25-82,'S',84-242 ##label TEZ
##cross-references DbBJ:D00518; NID:9216243; PID:9216
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##residues 1-2
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#journal
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catalyzes the hydrolysis of 1,4-beta-D-glucosidic bonds in
lichenin and other 1,3- and 1,4-beta-linked polysaccharides
*superfamily licheninase
extracellular protein; glycosidase: hydrolase; polysaccharide
degradation; pyroglutamic acid
                source was hyperproducing strain HL-25 with gene from strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                                                                                   #domain signal sequence *status predicted *label SIG\
*product licheninase *status predicted *label MAT\
*modified_site pyrrolidone carboxylic acid (Gln) (in
mature form) (partial) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore, J.T.; Fristrom, D.; Hammonds, A.S.; Fristrom, J.W.
Dev. Genet. (1990) 11:299-3309
Characterization of IMP-E3, a gene active during imaginal
disc morphogenesis in Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cfac protein precursor - Escherichia coli plasmid NTP113 #formal_name Escherichia coli 05-Jan-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A61046 *type complete ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster) *formal_name Drosophila melanogaster 31-Dec-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                       the amino ends of the mature forms of E-1 and E-2 are pyroglutamic acid and glutamine, respectively
                                                                                                                                                                                                                                                                                                                                                                                            #length 242 #molecular-weight 27268 #checksum 4439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 LALISPAYNKFDCGENRSVQIYGYGLYEVRM-KPAKNTGIVSSFFTYTGPTDGTP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ene FlyBase:ImpE3
##cross-references FlyBase:FBgn0001255
membrane protein
XY #length 331 #molecular-weight 36583 #checksum 8221
XY
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 85;
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##residues
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Best Local Similarity 25.5%;
Matches 14; Conservative
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$17404
$17400
Wu, D.; Gao, X.L.; Bai, Y.Y.; Aronson, A.I.
FEMS Microbiol. Lett. (1991) 81:31-36
Sequence of an operon containing a novel delta-endotoxin gene
from Bacillus thuringiensis.
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fimbrial operon of human enterotoxigenic Escherichia coli.
                                                                                                            ##cross.references GB:MS5661: NID:9145507; PID:9145510
##experimental_source enterotoxigenic strain, CFA/I-ST plasmid NTP113
##note
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parasporal crystal protein cryIIC - Bacillus thuringiensis
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Eur. J. Biochem. (1991) 197:337-343
Molecular cloning, expression and nucleotide sequence of wholecular cloning, a 14, edglucanese gene from Bacilius licheniformis. Predictive structural analyses of the
                                                                                                                                                                                                                                                                                                               Gaps
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licheninase (EC 3.2.1.73) - Bacillus licheniformis
endo-beta-1.3-1,4-D-glucanase; lichenase
#formal_name Bacillus licheniformis
21.Nov-1993 #sequence_revision 01-bec-1995 #text_change
S15388
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##Cross-references EMBL:X57279; NID:g39558; PID:g39559
CLASSIFICATION #superfamily licheninase
FEYWORDS glycosidase; hydrolase; polysaccharide degradation
SUWMARY #length 243 #molecular-weight 27435 #checksum 9335
                                                                                                                                                                                                                        plasmid
#length 869 #molecular-weight 97830 #checksum 9755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 LSLTSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPTDGTP 131
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                                                                                                                                                                                                                                                                         Score 85; DB 2; L
Pred. No. 1.85e+00;
14; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                              158 AFIQSQTINLSDSGKYKRLSISGNSALGITDTSY 191
                                                                                                                                                                                                                                                                                                                                                              Score 84;
                                                          ##status preliminary
##molecule_type DNA
##residues 1-869 ##label JOR
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##residue
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Best Local Similarity 27.8%;
Matches 15; Conservative
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#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, R.; Gas, S.; Barry III. C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Horrsby, T.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Horrsby, L.; Oliver, S.; Gsborne, J.; Quall, M.A.; Sagares, R.; Sulston, J.E.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

#file Deciphering the Diology of Mycobacterium tuberculosis from the complete genome sequence.
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*#cross-references GB:292669; GB:AL123456; NID:g3242271; PID:e304699;
                                                                                                                                                                                                                                                                                         501 FISEKYGNQGDSLRFELSNPTARYTLRGNGNSYNLYLRVSSIGSSTIRVTINGRVYTANV 560
                                                                                                                                                                                                                                                                                                                    #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
16-Dec-1998
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#checksum 9152
                                                                                                                                                          *checksum 8205
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#length 262 #molecular-weight 27280 #checksum 9
                                                                                                                                                                                                     Length 622;
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                                               ##residues 1-622 ##label WUD ##cross-references EMBL:X57252; NID:940283; PID:940286
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#superfamily enoyl-CoA hydratase homology
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hypothetical protein 1 - phage phi-C31
#formal_name phage phi-C31
                                                                                                                 plasmid
delta-endotoxin
#length 622 #molecular-weight 69729
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Pred. No. 2.52e+00;
26; Mismatches 26
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##molecule_type DNA
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Local Similarity 18.2%;
nes 12; Conservative
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DATE

OP-Sep-1995 #sequence_revision 20-Feb-1995 #text_change
ACCESSIONS
S18913
REFERENCE
#authors Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.F.
#submission submitted to the EMBL Data Library, November 1993
##scession s18913
##scession s18913
##molecule_type DNA
##residues
preliminary
##cross-references EMBL:X76288: NID:9432610; PID:9579071
##cross-references EMBL:X76288: NID:979071
##cross-references EMBL:X762888: NID:979071
##cross
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protein - protein database search, using Smith-Waterman algorithm
                                                                                                                         Wed Sep 1 16:15:23 1999; MasPar time 4.83 Seconds 544.173 Million cell updates/sec
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BACILLOLYSIN PRECURSOR
HYPOTHETICAL 76.2 KD P
BETA-GLUCANASE PRECURS
LATE EMBRYOGENESIS ABU
NABH-UBIQUINONE OXIDOR
HYPOTHETICAL 104.4 KD
NON-STRUCTURAL POLYPRO
NON-STRUCTURAL POLYPRO
BETA-GLUCANASE PRECURS
CFA/I FIMBRIAL SUBUNT
BETA-GLUCANASE PRECURS
HYPOTHETICAL 51.2 KD P
HYPOTHETICAL 51.4 KD P
TYROSINE-PROTEEN KIRAS
GTP CYCLOHYDROLASE II
                             Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL 19.0 KD P
NITROGEN REGULATION PR
RECEPTOR-TYPE ADENYLAT
NUCLEAR POLYADENYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENOLASE (EC 4.2.1.11)
TYROSINE-PROTEIN KINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL 7.3 KD PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mean 39.789; Variance 66.428; scale 0.599
                                                                                                                                                                                              >PCT-US99-13024-2
(1-93) from PCTUS9913024.pep (6 of 12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                               77977 seqs, 28268293 residues
                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Listing first 45 summaries
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NPRE_BACAM
VAIL_HISN
GUB_BACAM
GUB_BACAM
EMBB_PICGL
NGO3_PARDE
YM84_CAREL
YM84_CAREL
POLN_HEVPA
GUB_BACSU
CFAC_ECOLI
GUB_BACSU
YM60_YEAST
YXX 5_MYCTU
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Match Length DB
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Gap 11
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PUTATIVE FAMILY 31 GLU IMPORTIN BETA-3 SUBUNI VITELLOGENIN PRECURSOR GENOME POLYPROTEIN [CO STRUCTURAL PROTEIN VPB VITAMIN D-BINDING PROT VITAMIN D-BINDING PROT METHYLAALONYL-COA MUTA 70 KD CRYSTAL PROTEIN MADH-UBIQUINONE OXIDOR HYPOTHETICAL 108.4 KD STRUCTURAL PROTEIN VPB PUTATIVE PEPTIDASE IN MALIC ACID TRANSPORT P VITAMIN D-BINDING PROT 70 KD CRYSTAL PROTEIN NPB PUTATIVE PEPTIDASE IN MALIC ACID TRANSPORT P VITAMIN D-BINDING PROT 70 KD CRYSTAL PROTEIN M SSYS PROTEIN M SSYS PROTEIN ICO GENOME POLYPROTEIN [CO	ALIGNMENTS BPT4 STANDARD; PRT; 65 AA. BPT4 STANDARD; PRT; 65 AA. BB-1995 (REL. 31, CREATED) BB-1995 (REL. 31, LAST SEQUENCE UPDATE) BB-1995 (REL. 31, LAST SEQUENCE UPDATE) BB-1995 (REL. 31, LAST SEQUENCE UPDATE) CR 34.1. CR 24.1. CR 34.1. CR 24.1. CR 24.1. CR PHAGE T4. EES. DSDAWA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDA RES. SES. DSDAWA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDA RE.M.; THED (NOV-1994) TO THE SWISS-PROT DATA BANK. HEILCAL PROTEIN. HEILCAL PROTEIN. HEILCAL PROTEIN. 47.34; SCOICE 300; DB 1; Length 65; ALS 34. 7334 MW; C2D7CE2D CRC32; ALS 51. ALS 34. MISMATCHES STAGES AND S	AGPSYVKFQDNPVGSQT EE IRECTED RNA POLYM DNA STAGE; CALICI ATA T., ICHIKAWA IS E VITUS ISOLAT E AGENT OF ENTERI
YB79_YEAST IMB3_HUMAN YUI_ONCMY POLG_HCV1 VPB_VACCV VTDB_HUMAN WTAB_MUZB_MOUSE WTDB_HUMAN WUTA_RECAM WUTA_RECA	ALIGNMENTS PRT; 65 AA. ED) SEGUENCE UPDATE) ANNOTATION UPDATE IN GP34-GP35 INT RNA STAGE; TAILED SWISS-PROT DATA C2D7CE2D CRC32; SCOTE 300; DB 1 Pred. No. 1.60e- 3; Mismatches 3; Mismatches 1	SVRYKISIAGSCPLS; PRT; 1693 AA ED) SEGUTALICE UPDATE; ANNOTATION UPDATE; ANDARN; (HEV). AND VIRUSES, NO ., IIDA F., SHIK E Of the hepatit
6.6 6 954 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STANDARD; (REL. 31, CREATED); (REL. 31, LAST SEQ; (REL. 31, LAST ANN, 1. 1. 3. KD PROTEIN IN 1. 1. 3. KD PROTEIN IN 1. 3. KD PROTEIN IN 1. 3. KD PROTEIN IN NOV-1994) TO THE SW. C. (GES. 47.34, SC. 47.34; SC.	STANDARD; STANDARD; REL. 27, CREAT! REL. 37, LAST 4 REL. 37, LAST 4 REL. 37, LAST 5 REL. 37, LAST 5 REL. 37, LAST 6 REL. 37, LAST 6 REL. 37, LAST 6 REL. 37, LAST 6 ROSTRUS (STRAIN M) A POSITIVE-STRAIN M N.A. FOR STRAIN M N.A. FOR STRAIN M R.A. FOR STRAIN M FOR ST
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Matches
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERWOLYSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  572 FRISFVDGAVLEANGPERYNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTECLYTIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILPULA D.; Genes for alkaline protease and neutral protease from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                            .;
3
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                 Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 85006739.
VASANTHA N., THOMPSON L.D., RHODES C., BANNER C., NAGLE J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE; METALLOPROTEASE; ZINC; CALCIUM; ZYMOGEN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                             Score 100; DB 1; Length 169
Pred. No. 3.02e-03;
22; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BACILLOLYSIN PRECURSOR (EC 3.4.24.28) (NEUTRAL PROTEASE).
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                975 982 ATP (POTENTIAL).
1693 AA; 185215 MW; FFCB786D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 AA.
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PFAM: PF00099; zn-protease; 1. 
HSSP; P00800; 1TRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                             Match 15.8%;
Local Similarity 26.9%;
es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; K02497; G143249; -.
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                                                                                                                                                                                                                EMBL; D10330; G221705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 FAPGVSP 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDPSTGA 71
                                                                                                                                                                                                                                                            ATP-BINDING.
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NPRE_BACAM
P06832;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLLASMID SYM PNGR214A.
BACTERIA: PROTEGBACTERIA: ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97305956.
FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL
                                                    ZINC (CATALYTIC) (BY SIMILARITY)...
BY SIMILARITY...
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BC0147D4 CRC32;
                                                                                                                                                                                                                                                                    240 ISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes."; NATURE 387:394-401(1997).
                                                                                                                                                                                            Length 521;
                                                                                                                                                                                                          Pred. No. 5.71e-02;
19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 703;
            ACTIVATION PEPTIDE.
BACILLOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87; DB 1; L
Pred. No. 3.31e-01;
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A2BA53CE CRC32;
                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 76.2 KD PROTEIN 7411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMID; TRANSMEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                       703 AA
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                                                                                                                                                                                        Score 92;
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 PP 664 PP 76183 MW;
                                                                                                                                                      56840 MW;
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                                                                                                                                                                                      y Match
Local Similarity 27.8%;
hes 15; Conservative
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Best Local Similarity 26.000
18; Conservative
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2221
3521
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365
388
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228
364
365
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388
388
521 AA;
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                                                                                                                                                                                                                                                                                                       GENE 49:177-187(1986).
--:- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
--:- BETA-GLUCANSES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO
LICHENASE OF GERMINATING BARLEY.
--:- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                        BETA GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
BGLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PICEA GLAUCA (WHITE SPRUCE).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LALTSPSYNKFDCGENRSVQTYGYGLYEVRM-KPAKNTGIVSSFFTYTGPTEGTP 127
                                                                                                                                                                                                                                                   HOFEMEISTER J., KURTZ A., BORRISS R., KNOWLES J.;
"The beta-glucanase gene from Bacillus amyloliquefaciens shows extensive homology with that of Bacillus subtillis.";
GENE 49:177-187(1986).
                                                                                                                                       BACILLUS AMYLOLIQUEFACIENS.
BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86; DB 1; Length 239;
Pred. No. 4.66e-01;
20; Mismatches 18; Indels
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NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DONG J.Z., DUNSTAN D.I.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
-! SIMILARITY: BELONGS TO THE UPFOOL? FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14A3C78F CRC32;
                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8.
               239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29091; A29091.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PFAM: PF00722; 91ycosyl_hydro9; 1.
HSSP; P27051; 1GBG.
               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASE; GLYCOSIDASE; SIGNAL.
                                             08, CREATED)
08, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 25.5%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M15674; G143010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                          01-AUG-1988 (REL. 08,
01-JUN-1994 (REL. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 23
134 13
57 6
239 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                           01-AUG-1988 (REL.
                                                                                                                                                                                                                    STRAIN-BE 20/78;
MEDLINE; 87192007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMB8_PICGL
Q40863;
          GUB_BACAM
P07980;
                                                                                                                                                                       BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PICEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XU X., MATSUNO-YAGI A., YAGI T.;
"Structural features of the 66-KDa subunit of the energy-transducing MADB-ub/quinone oxidoreductase (NWH-1) of Paracoccus denitrificans."; ARCH. BIOCHEM. BIOPHYS. 296:40-48(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "DNA sequencing of the seven remaining structural genes of the gene cluster encoding the energy-transducing NADH-quinone oxidoreductase of Paracoccus denitrificans."

BIOCHEMISTRY 32:968-981(1993).

-!-CATALITIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

-!-COFACTOR: MAY BIND TWO 4FE-45 CLUSTER AND ONE 2FE-25 CLUSTER.

-!- SUBBUNIT: COMPOSED OF 14 DIFFERENT SUBBUNITS.

-!- SIMILARITY: BELONGS TO THE COMPLEX I 75 KD SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEOBACTERIA; ALPHA SUBDIVISION; RHODOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON-SULFUR (2FE-2S) (POTENTIAL). IRON-SULFUR (2FE-2S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 LGANILVRYLGEVAGNCPLSGAVSLCNPF-NLVIADEDFHKGLGFNNVYD 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.6%; Score 86; DB 1; Length 457; Best Local Similarity 34.0%; Pred. No. 4.66e-01; Matches 17; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3) (NADH DEHYDROGENASE 1, CHAIN 3) (NDH-1, CHAIN 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; $23948; $23948.

PROSITE; PS00641; COMPLEXI_75K_1; 1.

PROSITE; PS00643; COMPLEXI_75K_2; 1.

PROSITE; PS00643; COMPLEXI_75K_3; 1.

PFAM; PF00111; fer2; 1.

PFAM; PF00384; molybdopterin; 1.

OXIDOREDUCTASE; NAD; UBIQUINONE; IRON-SULFUR; 4FE-4S.
                                                                                                                                                                                                                                                                           EMBL; L47118; G1350545; -.
PROSITE; PS01133; UPF0017; 1.
SEQUENCE 457 AA; 51019 MW; AE7CB4CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 657-672 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M84572; G150601; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARACOCCUS DENITRIFICANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 13548;
MEDLINE; 92296779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93136200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARACOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO03_PARDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P29915;
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   888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOFER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER J., JIER M.
JOHASTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHASTON L., JONES M., KERSHAM J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTINORE B., O'CALLEAGAN M.,
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN R.,
WOHLDMAN R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WOHLDMAN P.,
                                                                                                                                                                                                                                     164 VRFTTEVAGITQMGQTGRG-EDSEITSYLNQTLESNMQGNIIDLCPVGALV-SKPYAFTA 221
                                                                                                                                                                                                                                                    11: :11 :: :1 : :11: :11: :24 VRYKISIAGSCPLYFRPOD-STGALVDSKSYAFST 82
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^{2}.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN. ZN_FING 43 83 C3HC4-TYPE.
                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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ن
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                                                                                                                            (POTENTIAL)
                                                                                                                                                                         Length 672;
                                                                                                                                                                                                        19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB 1; Length 932;
Pred. No. 4.66e-01;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III
IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (4FE-4S) (IRON-SULFUR (4FE-4S) (IRON-SULFUR (4FE-4S) (IRON-SULFUR (4FE-4S) (IRON-SULFUR (4FE-4S) (IRON-SULFUR (4FE-4S) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL):
SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER
                                                                                                                                                                         Score 86; DB 1; L. Pred. No. 4.66e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45C877B4 CRC32;
                                                                                                                                         40DB761A CRC32;
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                                                                                                                                                                                                                                                                                                                                   932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR: $28275; $28275.
WORMPEP; F54G8 4; CE05942.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
PFAM; PP00097; zf-C3HC4; 1.
HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             932 AA; 104438 MW;
                                                                                                                                           MW.
                                                                                                                                                                         13.6%;
larity 28.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-574 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.6%;
Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                         73028
                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.";
NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z19155; G6715; -.
 47
50
109
112
118
118
157
160
163
                                                                                                                                                                                                                                                                                                                                                                                                                                            CAENORHABDITIS ELEGANS
                                                                                                                                                                                       Local Similarity
                                                                                                                                         672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
MEDLINE; 94150718.
 47
50
109
1112
1118
1157
1160
207
                                                                                                                                                                                                                                                                                                       8
YMB4_CAEEL
Q03601:
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                                                                                                                                         SEQUENCE
                                                                                                                                                                          Query Match
 METAL
METAL
METAL
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M
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                                                                                                               01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE (RC 2.7.7.48); HELICASE).
HEPPATITIS E VIRUS (STRAIN BURMA) (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEPATITIS E VIRUS (STRAIN PAKISTAN) (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
CALICIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSAREV S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEGTERS L.J., MALIK I.A., IQBAL M., PURCELL R.H.; "Characterization of a prototype strain of hepatitis E virus.";
                                                                                                                                                                                                                                                                                                                                                              full length viral genome.";
vIROLOGY 185:120-131(1991).
-!- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
10-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.7.7.48); HELICASE!.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ë,
                                                                                                                                                                                                                                                                                                                                                  "Hepatitis E virus (HEV): molecular cloning and sequencing of
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILNE; 92024067.
MEDILMA.W., SMITH M.M., GUERRA M.E., HUANG C.-C., BRADLEY D.W.,
FRY K.E., REYES G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 1; Length 1693;
Pred. No. 4.66e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).

W; C560BE14 CRC32;
                                                                                                  PRT; 1693 AA.
282 TFTEGLEYLRNFQPDADELFNRK-LRFSAGDDAA 314
                               87
                 975 982 ATP
1693 AA; 185191 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M73218; G330024; -. PIR; A40778; MNWWHE.
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 92115700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAPGVSP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-BINDING.
                                                                               RESULT 9
ID POLN_HEVBU
AC P29324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLN_HEVPA
P33424;
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SEQUENCE
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셤
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PCT-US99-13024-2-06.rsp

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SEQUENCE OF
STRAIN-BR151
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P25733;
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95219081.
WOLF M., GECZI A., SIMON O., BORRISS R.;
WOLF M., GECZI A., SIMON O., BORRISS R.;
"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus
subtilis: characterization, mapping and construction of strains
deficient in lichenase, cellulase and xylanase.";
MICROBIOLOGY 141:281-290(1995).
                                                                                                                                                                                                                                                                   572 FRISEVDGAVLEINGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                   13-AUG-1987 (REL. 05, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 34, LAST ANNOTATION UPDATE)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
BGLS OR BGL OR LICS OR N159.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEZUMEN H., YUNKI T., YABBUCHI S.; "Construction of a beta-glucanase hyperproducing Bacillus subtilis using the cloned beta-glucanase gene and a multi-copy plasmid."; AGRIC. BIOL. CHEM. 53:2335-2339(1989).
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).
-!- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / BGSC1A1;
YOSHIDA K.-I., SANO H., SEKI S., ODA M., FUJIMURA M., FUJITA Y.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                            EMBL; M80581; G329998; -.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C120;
MEDLINE; 8427222.
MURPHY N., MCCONNELL D.J., CANTWELL B.A.;
"The DNA sequence of the gene and genetic control sites for the excreted B. subtilis enzyme beta-glucanase.";
NUCLEIC ACIDS RES. 12:5355-5367(1984).
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BACILLUS.
                                                                                                                                                                                                                     Score 86; DB 1; Length 1693; Pred. No. 4.66e-01;
                                                                                                                                                                                                                                             22; Mismatches 25; Indels
                                                                                                                                                                                  NP_BIND 975 982 ATP (POTENTIAL).
SEQUENCE 1693 AA; 185149 MW; FBCA2483 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                           242 AA.
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                                                                                                                                                                                                                    13.6%;
Local Similarity 25.4%;
hes 17; Conservative
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65 FDPSTGA 71
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P04957;
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Purification and some properties of two enzymes from a beta-glucanase hyperproducing strain. Bacillus subtilis HL-25.";
AGRIC. BIOL. CHEM. 53:234-2346(1989).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES IN BETA-D-GLUCANSES COWTAINING 1,3- AND 1,4-BONDS.
-!- BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-!- THE SEQUENCE OF STRAIN 168 IS SHOWN.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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                                                                                                                                      "Licr, a Bacillus subtilis transcriptional antiterminator protein the BglG family.";
J. BACTERIOL. 178:1971-1979(1996).
                                                    MEDLINE; 96178961.
SCHNETZ K., STUELKE J., GERTZ S., KRUGER S., KRIEG M., HECKER M.,
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01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
CFA/I FIMBRIAL SUBUNIT C PRECURSOR (COLONISATION FACTOR ANTIGEN I
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
A -> S (IN STRAIN HL-25).
A -> S (IN STRAIN HL-25).
P -> L (IN STRAIN STRAIN HL-25).
W; 3B62B79A CRC32;
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PFAM; PF00722; glycosyl_hydro9; 1.
HSSP; P27051; 1GBG.
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EMBL; D00518; D1000859; -.
EMBL; D3026; D1012364; -.
EMBL; Z46862; G599674; -.
EMBL; Z28340; G580948; -.
EMBL; Z29124; E1184632; -.
PIR; A22914; LXBS.
PIR; A070110; J00110
SUBTILIST; BG10476; BGLS.
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ilarity 25.5%;
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SEQUENCE OF 29-63.
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                                                                                                        The nucleotide sequence of the first two genes of the CFA/I fimbrial pperon of human enterotoxigenic Escherichia coll."; 41CROB. PATHOG. 6:297-309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEOURNCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDOMATION UPDATE)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                 MEDLINE; 92329981.
JORDI B.J.A.M., WILLSHAW G.A., VAN DER ZEIJST B.A.M., GAASTRA W.;
"The complete nucleotide sequence of region 1 of the CFA/I fimbrial
operon of human enterotoxigenic Escherichia coli.";
DNA SEQ. 2:257-263(1992).
PLASMID NTP513.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                     -i - FUNCTION: MAY SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIOBERAS J., PEREZ-PONS J.A., QUEROL E.;
"Molecular cloning, expression and nucleotide sequence of the endo-beral,3-1,4-D-glucanase gene from Bacillus licheniformis. Predictive structural analyses of the encoded polypeptide.";
EUR. J. BIOCHEM. 197:337-343(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS LICHENIFORMIS.
BACTERIA; FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 85; DB 1; Length 869; 32.4%; Pred. No. 6.55e-01;
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CFA/I FIMBRIAL SUBUNIT C.: 7AF76347 CRC32;
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                                                  SEQUENCE FROM N.A.
STRAIN-ENTEROTOXIGENIC;
MEDLINE; 89330163.
HAMERS A.M., PEL H.J., WILLSHAW G.A., KUSTERS J.G.,
VAN DER ZEIJST B.A.M., GAASTRA W.;
                                                                                                                                                                                                                                                                                                                                                EMBL; M55661; G145510; -.
ANTIGEN; SIGNAL; FIMBRIA; OUTER MEMBRANE; PLASMID.
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PLANAS A., JUNCOSA M., LLOBERAS J., QUEROL E.;
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P27051;
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HAHN M., PONS J., PLANAS A., QUEROL E., HEINEMANN U.;
"Crystal structure of Bacilius licheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase at 1.8-h resolution.";
FEBS LETT 374:221-224(1995)
-1- CATLVITC ACTIVITY: HYDROLYSIO FI 1,4-BETA-D-GLYCOSIDIC LINKAGES
-1- CATLVITC ACTIVITY: HYDROLYSIO FI 1,4-BETA-D-GLYCOSIDIC LINKAGES
-1- BETA-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
-1- BETA-GLUCANSES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO
LICHENASE OF GERMINATING BARLEY.
-1- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
*Essential catalytic role of Glu134 in endo-beta-1,3-1,4-D-glucan 4-glucanohydrolase from B. licheniformis as determined by site-directed
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                                                                                                                                                                                      [4]
MUTAGENESIS.
MUTAGENESIS.
MUTAGENESIS.
JUNCOSA M., PONS J., DOT T., QUEROL E., PLANAS A.:
JUNCOSA M., PONS J., DOT T., QUEROL E., PLANAS A.:
"Identification of active site carboxylic residues in Bi
licheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase licheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase licheniformis mutanenesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       >N: NO CHANGE I
3469842C CRC32;
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PIR; S15388; S15388.
PDB; 1GBG; 07-DEC-95.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PFAM; PF00722; G1ycosyl_hydro9; 1.
27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
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BETA-GLUCANASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOL. CHEM. 269:14530-14535(1994).
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010830;
01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27435 MW;
                                                                                                                                    'EBS LETT. 308:141-145(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%;
|larity 27.8%;
| Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                STRAIN-H37RV;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                              BACTERIÀ; FIRMICUTES; ACTINOBACTERIÀ; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 1; Length 449;
Pred. No. 1.79e+00;
18; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83; DB 1; Length 611;
Pred. No. 1.28e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                    EMBL; 274024; E249958; -.
EMBL; 274024; E248895; -.
HYPOTHETICAL PROTEIN; HYDROLASE.
HYPOTHETICAL PROTEIN; HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51437 MW; FE884F32 CRC32;
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL 67, 2 KD PROTEIN CY274.45C.
MTCY274.45C OR MTCY338.01C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 VRFQHLPVPFELYSDGIDLPVFE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|| || ::| |: || || 4 VKFQDNPVGSQTFSAGLHLRVFD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 249809; G854462; -.
PROSITE; PSG1133; UPF0017; 1.
PFAM: PF00561; abhydrolase; 1.
MYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.1%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                 MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.9%;
Similarity 27.1%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
Matches 16; Conser
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                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YM60_YEAST
Q03649;
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Gaps

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Search completed: Wed Sep 1 16:15:36 1999 Job time: 13 secs.

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protein - protein database search, using Smith-Waterman algorithm

MasPar time 9.48 Seconds 535.295 Million cell updates/sec Wed Sep 1 16:15:54 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-93) from PCTUS9913024.pep (6 of 12) 634 1 MEKFWAEFGGGYVQTPFLSE..........DSKSYAFSTSNDITSAAFVS 93 Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 37.991; Variance 71.901; scale 0.528 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No.
1	101	15.9	1577	7	054178	GLUCOSYLTRANSFERASE	1.060-02
7	100	15.8	1693	14	081876	COMPLETE GENOME SEOUEN	1.50e-02
m	96	15.1	114	14	041088	A606L PROTEIN.	5.836-02
4	92	14.5	299	14	065574	HYPOTHETICAL 32.4 KD P	2.20e-01
S	92	14.5	300	14	065581		2.20e-01
Q	92	14.5	337	7	044647	NEUTRAL PROTEASE (FRAG	2.208-01
7	83	14.0	266	7	084354	HYPOTHETICAL 63.5 KD P	5.816-01
æ	83	14.0	921	Ŋ	P90770		5.81e-01
σ	88	13.9	180	10	049984	PUTATIVE ETHYLENE RECE	7 996-01
10	87	13.7	239	7	045691	ENDO-BETA-1,3-1,4-GLUC	1.100+00
1	86	13.6	521	7	044677	NEUTRAL PROTEASE.	1.51e+00
12	98	13.6	974	S	023510	F54G8.4 PROTEIN.	1.51e+00
13	86	13.6	1693	14	069410	METHYL TRANSFERASE.	1.51e+00
14	86	13.6	1693	14	089444	UNNAMED PROTEIN PRODUC	1.51e+00
15	98	13.6	1693	14	081344	HEPATAITIS E VIRUS COM	1.51e+00
16	98	13.6	1693	14	081862	ORF 1.	1.51e+00
17	85	13.4	229	10	P93830	EARLY AUXIN-INDUCED PR	2.06e+00
18	84	13.2	229	10	049162	IAA17/AXR3-1 PROTEIN.	2.81e+00
19	84	13.2	622	7	045743	CRYIIC DELTA-ENDOTOXIN	2.81e+00
20	84	13.2	3443	14	011979	POLYPROTEIN.	2.81e+00

3.82e+000 3.82e+000 5.19e+000 7.02e+000
HYPOTHETICAL 27.3 KD PORF 1. ETHYLENE RESPONSE SENS NONSTRUCTURAL POLYPROTHEM PUTATIVE COAT PROTHEM. PUTATIVE COAT PROTHEM. PUTATIVE COAT PROTHEM. PROTHEM. 41.7 KD PENOLASE (EC 4.2.1.11) ETHYLENE RESPONSE SENS INSECTICIDAL CRYSTAL PUTATIVE READTHROUGH POLYPROTEIN (FRAGMENT) POLYPROTEIN (FRAGMENT) POLYPROTEIN (FRAGMENT) VC27A7L.1 PROTEIN (FRAGMENT) VC27A7L.1 PROTEIN (FRAGMENT) VC27A7L.1 PROTEIN (FRAGMENT) DOLYPROTEIN (FRAGMENT) POLYPROTEIN (FRAGMENT) VC27A7L.1 PROTEIN (FRAGMENT) DOLYPROTEIN (FRAGMENT) DOLYPROTEIN (FRAGMENT) DOLYPROTEIN (FRAGMENT) DA461.24P. TIEB PROTEIN (FRAGMENT) PARCRYSTALLINE SURFAC PROTEIN KINASE HOMOLOG
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ALIGNMENTS

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STRAIN-CHALLIS;
STRAIN-CHALLIS;
SULAVIK M.C., TARDIF G., CLEWELL D.B.;
SULAVIK M.C., TARDIF G., CLEWELL D.B.;
Identification of a gene, rgg, which regulates expression of glucosyltransferase and influences the Spp phenotype of Streptococcus gordonii Challis.'
J. BACTERIOL. 174.3577-3586(1992).
EMBL; 012643; G1054877; --
EMBL; M89776; G153795; --
EMBL; PFOM; PFO0128; alpha-amylase; 1.
TRANSFERASE.
SEQUENCE 1577 AA; 177805 MW; 7D58FEC2 CRC32;
LT 1 PRELIMINARY; PRT: 1577 AA. 054178 054247; 1577 AA. 054178. 054247; 1577 AA. 01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) 01-NOV-1998 (TREMBLACTOREL) 01-NOV-1998 (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 96157084.
VICKERMAN M.M., SULAVIK M.C., CLEWELL D.B.;
wholecular analysis of Streptococcus gordonii glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phase variants.";
DEV. BIOL. STAND. 85:309-314(1995).
    RESULT
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STRAIN-JURA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                572 FRTSFVDGAVLEANGPERYNLSFDASQSTMAÅGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARAMECIUM BURSARIA CHLORELLA VIRUS 1 (PBCV-1).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PHYCODNAVIRIDAE; PHYCODNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 FSSMSSNISFRVRLTASCAI -- LNPSYGRGRKSRNNSLNFTMSLSLMVFVISIKPSMSIK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLETE GENOME GENOME.
HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
CALICIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LI Y., LU Z., SUN L., ROPP S., KUTISH G.F., ROCK D.L.,
VAN ETTEN J.L.;
"Analysis of 74 kb of DNA located at the right end of the 330-kb
chlorella virus PBCV-1 genome.";
VIROLOGY 233:360-377 (1997).
EMBL; U42580; G2447164; ...
                                                                                                                                                                                                                                                                                                                                                                                                              ë,
                                                                                                                                                                                                                                                                                                                                                               Score 100; DB 14; Length 1693;
Pred. No. 1.50e-02;
22; Mismatches 24; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches 25; Indels
                                                                                                                                                                                                                                                   UCHIDA T.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; D11093; D1002342; -.
SEOUENCE 1693 AA; 184840 MW; 8952DD38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        065574 PRELIMINARY; PRT; 299 AA. 065574; CIREMELREL. 01, CREATED) 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE) HYPOTHETICAL 32.4 KD PROTEIN.
                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 96; DB 14;
Pred. No. 5.83e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 AA; 13257 MW; 1B75BE43 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AA.
PRT; 1693 AA
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1D 041088;
AC 041088;
DT 01-JAN-1998 (TREMBLREL. 05, CR DT 01-JAN-1998 (TREMBLREL. 05, LA DT 01-NOV-1998 (TREMBLREL. 08, LA DE AGOGL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                               Ouery Match 15.8%;
Best Local Similarity 26.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 15.1%;
Local Similarity 27.4%;
les 17; Conservative
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PRELIMINARY;
                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=UIGH179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 98022962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632 FAPGVSP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 KY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 SY 78
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081876
081876;
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                                                                                                                       VLCEK C., BENES V., LU Z., KUTISH G.F., PACES V., ROCK D.,
LETCHWORTH G.J., SCHWYZER M.;
"Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus I genome which exhibits a colinear gene arrangement with
the UL21 to UL4 genes of herpes simplex virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SCHOENBORKEN;
MEDLINE; 9613523.
SCHMITT J., KEIL G.M.;
"Identification and characterization of the bovine herpesvirus 1 UL7
gene and gene product which are not essential for virus replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 300;
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                                                                                                                                                                                                                                                                                                                    SCHWYZER M., PACES V., LETCHWORTH G.J., MISRA V., BUHI
LOWERY D.E., SIMARD C., BELLO L.J., THIRY E., VLCEK C.
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHWIZER M.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z48053; G971327; -.
EMBL; AJ004801; E1187337; -.
HYPOTHETICAL.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BOVINE HERPESVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JB 14,
1.20e-01;
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.5%; Score 92; DB 14; Le
Best Local Similarity 47.2%; Pred. No. 2.20e-01;
Matches 17; Conservative 9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AA; 32450 MW; 86377347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 14;
Pred. No. 2.20e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 PRFVCEVREIPAGPPTFTSSSITHLRV-EPSTGALL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 PREVCEVREIPAGPPIFISSSITHLRV-EPSTGALL 80
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337
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044647 PRELIMINARY: PRT;
044647;
01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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J. VIROL. 70:1091-1099(1996).
EMBL; X91751; G1006630;
SEQUENCE 300 AA; 33450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,
08,
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Best Local Similarity 47.2%;
Matches 17; Conservative
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06581
06581
01582
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
                                                           SEQUENCE FROM N.A.
STRAIN-COOPER, AND JURA;
MEDLINE; 95313343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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C34B7.2 PROTEIN.
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ID Q45691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVIS R.W.;
Genome Sequence of an Obligate Intracellular Pathogen of Humans:
Chlamydia trachomatis.";
SCIENCE 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 ISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
NEUTRAL PROTASE (FRABENT).
BACILLUS AMYLOLIQUERACIENS.
BACILLUS AMYLOLIQUERACIENS.
BACIERIA; FIRMICUIES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; DB 2; Length 337;
Pred. No. 2.20e-01;
19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 2; Length 566;
Pred. No. 5.81e-01;
25; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AEO01308, G3328771; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 566 AA: 63508 MW; CIAIC491 CRC32;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
YOSHIMURA K., MIYAZAKI T., NAKAHAMA K., KIKUCHI M.;
TAKEDA KENKYUSHO HO 44:42-50(1985).
EMBL: M64815; G142890; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 63.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLAMYDIA TRACHOMATIS.
BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
                                                                                                                                                                                                                                                                                                                                                                    337 337
337 AA; 36910 MW; 5A9BC52B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.2%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03,
05,
09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 ATSQL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGAL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997
01-JAN-1998
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVIS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                          PROTEASE
                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 8
P90770
P90770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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DDT ACC
DDT
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                                                                                                                                                                                                                                                                                                     BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HILLIER L., JIER M., JOHNSTON L., JOHNSTON L., JOHNSTON L., LIGHTING J., LLOYD C., MCMORRAY A., MORTIMONE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER B., STADEN R., SULSTON J., THERRY-MIEG J., THOMAS K., VAUGHAN K., WALERSTON R., WALSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRASSICA OLERACEA (CAULIFLOWER).
EUKARYOTA; VIRIDIALANTE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; BRASSICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 ERWFVEIVHGYVRQEYIFLPIG-RISLTIIGRRSTKYAGTRFLKRGANPTGNVANYVETE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                         EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHĀRNG Y.Y., SUN C.W., YAN S.L., CHOU S.J., CHEN Y.R., YANG S.F.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U87239; G2738025; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                              BERKS M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89; DB 5: Length 921;
Pred. No. 5.81e-01;
23; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 IPHTCPLAKIGPPVGKFAPPEVVSVRVPL-LHLSNFQGSDWSDL-SGKGYAL
                                                                                                                                       HARRIS B.;
SUBMITIED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                 BAYNES C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 88; DB 10; Le
Pred. No. 7.99e-01;
10; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 283220; E1344511; -.
SEQUENCE 921 AA; 106698 MW; 21DE4C35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 180 180
SEQUENCE 180 AA; 19859 MW; D9B072C1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           049984 PRELIMINARY; PRT: 16
049984 01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUE)
01-JUN-1998 (TREMBLREL. 06, LAST SANNOF)
PUTATIVE ETHYLENE RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 94150718.
WILSON R., AINSCOUGH R., ANDERSON K.,
BONFIELD J., BORTON J., CONNELL M., CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 QI-VWDMASSGNVADGRESSF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | | :|:| : |:: :|
61 HLRVFD-PSTGALVDSKSYAF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.7%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 13.9%;
Best Local Similarity 36.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 368:32-38(1994).
CAENORHABDITIS ELEGANS.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                  46 ADGYSNGDMFNSTWRADNVSMTSSGEMRLALTSPSYNKFDCGENRSVQTYGYGLYEVRM- 104
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SHIMADA H., HONJO M., MITA I., NAKAYAMA A., AKAOKA A., MANABE K.,
FURUTANI Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 ISSESGKYVLRDLSKPTGTQNNTYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACILLUS AMYLOLIQUEFACIENS.
BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB 2; Length 521;
Pred. No. 1.51e+00;
18; Mismatches 19; Indels
                                                                                                                                                                                                                                Score 87; DB 2; Length 239;
Pred. No. 1.10e+00;
26; Mismatches 34; Indels
                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENDO-BETA-1,3-1,4-GLUCANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NEUTRAL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 AA; 56725 MW; 64AFFE5F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          521 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                  105 KPAKNTGIVSSFFTYTGPTEGTP 127
                                                                                                                                                                                                                                                                                                                                                 DPSTGALVDSKSYAFSTSNDTTS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M36723; G143353; -. PFAM; PF00099; zn-protease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ULT 12
Q23510
Q23510
01-NOV-1996 (TREMBLREL. 01, CF
01-NOV-1998 (TREMBLREL. 08, LA
01-AUG-1998 (TREMBLREL. 07, LA
F54G8 4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOTECHNOL. 2:75-85(1985).
                                                                                                                                                                                                                                Query Match 13.7%;
Best Local Similarity 22.9%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.6%;
Best Local Similarity 27.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAENORHABDITIS ELEGANS
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             LT 11
Q44677
Q44677;
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MEDITHE; 95176571.
WIN S., PURCELL R.H., EMERSON S.U.;
"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
VIRUS GENES 9:23-32(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
UNNAMED PROTEIN PRODUCT.
UNNAMED FROTEIN PRODUCT.
VINDARE FROTEIN PROSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                       Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                          Indels
SEQUENCE FROM N.A.
HAWKINS T., AINSCOUGH R.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SIMILARITY CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; 222177; E1351235; -
EMBL; Z19155; E1351235; JOINED.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HEV037;
DONATI M.C., FAGAN E.A., HARRISON T.J.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, X98292; E1175751; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
XIN S.R., PURCELL R.H., EMERSON S.U.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86; DB 14; Le
Pred. No. 1.51e+00;
22; Mismatches 25;
                                                                                                                                                                                                                                                               Score 86; DB 5; L/Pred. No. 1.51e+00; 9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1693 AA; 185190 MW; 287742F6 CRC32
                                                                                                                                                                                                                974 AA; 109137 MW; 4D7558C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                        282 TFTEGLEYLRNFQPDADELFNRK-LRFSAGDDAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      13.6%;
|| Ilarity 38.2%;
|| Conservative
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05,
07,
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01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 Q69410 PRELIMINARY;
Q69410, 01-NOV-1996 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYL TRANSFERASE.
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-HEBEI;
MEDLINE: 93348763.
BI S.L., PURDY MA., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
BI S.L., PURDY MA., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
The sequence of hepatitis E virus isolated directly from a single source during an outbreak in China.";
VIRUS RES. 28.233-247(1993).
SEDUENCE 1693 AA: 185271 MW; EF762F9E CRC32;
                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                  Score 86; DB 14; Length 1693;
Pred. No. 1.51e+00;
22; Mismatches 25; Indels
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EMBL; L25547; G1209366; -.
EMBL; L25595; G784878; -.
SEQUENCE 1693 AA; 185122 MW; 0E56663A CRC32;
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Best Local Similarity 25.4%;
Matches 17; Conservative
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65 FDPSTGA 71
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632 FAPGVSP 638

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Search completed: Wed Sep $\,$ 1 16:16:22 1999 Job time : 28 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 7.22 Seconds 294.721 Million cell updates/sec Wed Sep 1 16:19:58 1999; Tabular output not generated. Run on:

>PCT-US99-13024-2 (1-100) from PCTUS9913024.pep (7 of 12) 683 1 MEKFMAEFGGGYVQTPFLSE.....STSNDITSAAFVSFMNSLIN 100 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

170751 segs, 21266608 residues

Searched:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part28 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part34 35:part35 36:part36 37:part37 38:part38 39:part39 Database:

Mean 27.671; Variance 122.380; scale 0.226 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Malate permease.	000	23 W14558 19 P95000 35 W75773	438 23 W1455 242 19 P9500 623 35 W7577	13.0 438 23 W1455 12.7 242 19 P9500 12.7 623 35 W7577
	209 209 209 209 209 209 209		37 37 37 37 37	35 35 35 35 35 35

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Gaps

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Length 65;

Score 300; DB 19; Length 65 Pred. No. 1.46e-17; 3; Mismatches 7; Indels

Query Match 43.9%; Best Local Similarity 82.1%; Matches 46; Conservative

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26 99

1 mekfmaeiwtricpnailsesnsvrykisiagscplstagpsyvkfqdnpvgsqtf ||||||||: | mekrwaefcqcrvqTpFLSESNSVRXKISIAGSCPLSTAGPSYVKFQDNPVGSQTF

RESULT 2 ID W76368 standard; Protein; 1693 AA.

4.33e+01 4.33e+01 4.33e+01 4.33e+01 4.33e+01 5.11e+01 5.11e+01 7.11e+01	t can also open lso ading 4).
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44444444444444444444444444444444444444	ard; Protein; 65 (first entry) x gene product. 11 fibre protein cular sleve. e T4. U13023. US-322760. BERG E B. 42/22. S3. derlived from T4 e into nano-stru e into nano-stru for into
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Vectors for expression of polypeptide(s) in Bacillus - contg. promoter and regulatory regions which control expression and secretion of protease(s) in Bacillus.

Disclosure: p: English.
Claimed replicon comprises a promoter and regulatory regions, capable of expressing alkaline and neutral protease genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                             Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation
Claim 10; Page 17-24; 29pp; Japanese.

This sequence represents a Hepatitis E viral hollow particle protein. This sequence represents a Hepatitis E viral hollow particle protein. This polypeptides can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 frtsfvdgavleangperynlsfdasgstmaagpfsptyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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           03-DEC-1998 (first entry)
Hepatitis E virus hollow particle protein #1.
Hollow particle protein; virus; antibody; detection; immunoassay;
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Neutral protease encoded by npr gene.
Protease; expression systems; substilin; neutral protease; ds.
Bacillus amyloliquefaciens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.1%; Score 96; DB 35; Length 1693; Best Local Similarity 26.9%; Pred. No. 4.71e+00; Matches 18; Conservative 21; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 92; DB 1; Length 520; Pred. No. 9.41e+00;
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                                                                                                                                          R 28-FEB-1997; 062445.
1 (DENK-) DENKA SEIKEN KK.
(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
NPI: 98-535037/46.
N-PSDB; V61687.
                                                                                                                        /note= "Partial sequence"
                                                                                            Location/Qualifiers
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Nagarajan V, Rhodes CS, Banner CDB,
N-PSDB, N91114.
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P94617 standard; protein; 520 AA.
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/note="Mature"
27..520
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Best Local Similarity 27.8%;
Matches 15; Conservative
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29-MAR-1985; 717800.
29-MAR-1985; US-717800.
                                                                                                              ...1693
                                                                                                                                                                                                                                                                                                                                                                                                                             1693 AA;
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                                                                               Hepatitis virus.
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                                                                infection
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Malate permease; mael gene; malic acid; succinate; succinic acid;
malonate; malonic acid; wine; malolactic fermentation;
deacidification; yeast; Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Replicable plasmidic expression vector - for transformation of Bacillus to direct expression of poly:peptide
Disclosure; Fig 4: 37pp; English.
The inventors claim a vector comprising a replicable plasmid containing the promoter and regulatory region of a gene selected from apr[Bamp] and npr[Bamp], for transformation of Bacillus to direct expression of polypeptide.
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                          239 issesgkyvlrdlskptgtqiitydlqnreynlp-gtlvssttnqfttssqraa
                                                                                                                                                                                                   01-DEC-1991 (first entry)
Sequence of neutral protease encoded by the npr[BamP] gene.
Bacillus expression vector; secretion vector.
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Pred. No. 9.41e+00;
19; Mismatches 18; Indels
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/note- "potential protein kinase
phosphorylation site"
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/note- "potential protein kinase
phosphorylation site"
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/label- Transmembrane_domain
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/label= Transmembrane_domain
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/label= Transmembrane_domain
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08-JUN-1984; US-618902.

29-MAR-1985; US-717800.

(GENE-) GENEX CORP.

Nagarajan V. Banner CDB, Rhodes CS;

WPI: 85-057299/10.

N PSDB; NS-0672.
                                                                                                                                                                                                                                                                                                                                                                                   28..221
/label Pro sequence
                                                                                                                                                                                                                                                                        Bacillus amyloliquefaciens.
Key Location/Qualifiers
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W06355 standard; Protein; 438 AA.
W06355;
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P51009 standard; Protein; 521
P51009;
01-DEC-1991 (first entry)
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Local Similarity 27.8%;
les 15; Conservative
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06-JUL-1984;
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PCT-US99-13024-2-07.rag

domain domain

domain region domain domain domain domain region

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Recombinant plasmids for stable integration of heterologous genes
Integration by homologous recombination
For integration by homologous recombination
Claim 8: Fig 1A-B; 18pp; French.
Claim 9: Fig 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant plasmid used in beer prodn. - obtd. by integrating lichenase gene derived from Bacillus subtilis, into vector bisclosure; Fig 4: 7pp: Japanese.
The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 laltspsynkfdcgenrsvqtygyglyevrm-kpakntglvssfftytgptdgtp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beer production; fermentation; barley; beta-glucan; hydrolysis;
lichenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89; DB 23; Length 438;
Pred. No. 1.57e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87; DB 19; Length 242;
Pred. No. 2.21e+01;
19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 vgppafs-glal-i-niargam-gsrpyifvgansseylgfvstfm 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONS-) CONSEIL INTERPROFESSIONNEL VIN BORDEAUX (OENO-) INST OENOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P95000 standard; Protein; 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-1997 (first entry)
Bacillus subtilis lichenase.
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Best Local Similarity 27.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-1987; 224615.
08-SEP-1987; JP-224615.
08-SEP 1987; JP-224615.
08-SEM 1987 BREWERIES KK.
WPI: 89-119863/16.
N-PSDB; N95000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.0%;
Best Local Similarity 39.1%;
Matches 18; Conservative
                                                                                                                                    Lonvaud A;
                                                        21-AUG-1995; FR-009959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis Y-25
                             009959
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                                                                                                                                 Denayrolles M, Lo
WPI; 97-195424/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA
                                                                                                                                                                                     N-PSDB; T62919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The soluted nucleic acid encoding malate permease and related vectors resoluted nucleic acid encoding malate degradation during fermentation to eliminate excessive acidity in wine care ilminate excessive acidity in wine care ilminate excessive acidity in wine care at the state of the malate permease (W06355) of Schizosaccharomyces pombe is the product of the mael gene (T42611) isolated from an S. pombe cannot library. The enzyme is constitutively expressed. It provides a simple and relatively inexpensive means of removing candate, during or after alcoholic fermentation. Recombinant saccharomyces cerevisiae strains expressing the S. pombe malate permease are able to degrade malate, partic, that present in wine must, thereby removing excess acidity from the wine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe; mael; recombinant plasmid; yeast; Lactobacillus lactis; mleS; selectable marker; integrate; P450-14DM; C14 lanosterol dimethylase; degradation; malic acid; growth medium; deacidify; fruit; vegetable juice; Saccharomyces cerevisiae; alcoholic fermentation; wine-making.
Schizosaccharomyces pombe.
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Pred. No. 1.57e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                               /label- Glycosylation
/note- "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Glycosylation
/note- "potential N-glycosylation site"
                                                                                                                            /label- Glycosylation
/note- "potential N-glycosylation site"
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Osothsilp-de-Eknamakul C; Pretorius IS, Subden RE;
WPI; 97-012090/01.
.40..160
/label- Transmembrane_domain
                                             75..192
label- Transmembrane_domain
                                                                                                                                                                             05. 225
label- Transmembrane_domain
                                                                                                                                                                                                                                                                                                            label - Transmembrane_domain
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/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label - Transmembrane_domain
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                                                                                                                                                                                                                                                           /label = Leucine_zipper
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W14558;
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larity 39.1%;
Conservative
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                                                                                                                                                                                                                                   214..235
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es 18; Conserv
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Sequence 438
                                                                                                 modified_site
                                                                                                                                                                                                                                                                                                                                    modified_site
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Best Loca Matches

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Gaps

5

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Gaps

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New insecticidal Bacillus thuringiensis toxins - useful for controlling legidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Heliocverpa zea Claim 14; Pages 28-30; 50pp; English.
This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control legidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                Amino acid sequence of lepidoteran-active HD573 toxin.
HD573 toxin: PCR: primer: amplification; Bacillus thuringlensis; probe; lepidoptera: pest; pesticide: Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringiensis.
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This hybrid protein is encoded by the beta-glucanase-H1 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the amylolique-faciens beta-glucanase and the carboxyl-terminal half of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label-amino terminal of beta-amyloliquefaciens
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Hybrid (1,3-1,4)-pre-beta-glucanase.
Hybrid pre-beta-glucanas; beer; animal feed; poultry.
Bacillus amyloliquefaciens, Bacillus macerans.
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16-FEB-1990; DR0044.
16-FEB-1989; DD-325800.
04-AuG-1989; DK-003848.
(CARL-) CARLSBERG A/S.
(CARL-) AAAD WISSENSCHAFT DDR.
BOTILSS R, Hofemaister J, Thomsen KK, Olsen O, Vonwettstein D; WPI; 90-275129/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.7%; Score 87; DB 35; Length 623 larity 18.2%; Pred. No. 2.21e+01; Conservative 26; Mismatches 26; Indels
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                                                                                                                                                                                                                                                  Muller-Cohn J, Narva KE, Schnepf HE; WPI; 98-506734/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R06621 standard; protein; 239 AA.
r 8
W75773 standard; Protein; 623 AA.
                                                02-DEC-1998 (first entry)
                                                                                                                                                                             17-SEP-1998.
13-MAR-1998; U05081.
13-MAR-1997; US-040512.
(MYCO) MYCOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562 ntttnn 567
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Matches
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New hepatitis E virus DNA from Pakistani strain SAR-55 - used for,

e.g. developing products for diagnosis of, and vaccination against

PT New hepatitis E virus infection

Disclosure: Pages 11-15: 204pp; English.

Disclosure: Pages 11-15: 204pp; English.

CC This represents a hepatitis E virus (HEV) open reading frame (ORF)-1

CC This represents a DNA sequence designated SAR-55. SAR-55 also encodes

CC This recombinant expression vector containing the SAR-55 nucleic acid

CC An be used to produce the HEV proteins, especially ORF-2 protein. The

C recombinant HEV proteins can be used as diagnostic agents and as vaccines

Cf or use against HEV infection. The detection and diseases caused by

CC HEV can be used for the diagnosis of infection and diseases. Such methods are

CC HEV and for monitoring the progression of such disease. Such methods are

CC COURSE of treatment of HEV infection and disease in a mammal. The

CC COURSE of treatment of HEV infection on disease in a mammal. The

CC ALLEA COURSE OF THE OFFICE OFFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus (HEV) ORF-1 protein.
Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
passive immunisation; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
nd______ beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mir. of food prods., esp. beer and animal feed (eg for feeding poultry). See also Q05833.
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Pred. No. 2.62e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                        Score 86; DB 1; Length 239;
Pred. No. 2.62e+01;
                                                                                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SV, Purcell RH, Robinson RA, Tsarev SA;
WPI: 98-568733/48.
N-PSDB; V71604.
                                                                                                                                                                                                                                                                                                                                                                                                             20; Mismatches
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1662
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Misc_difference 1244
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ilarity 25.4%;
Conservative
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.5%;
Matches 14; Conservative
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11-APR-1997; US-8403
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les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 fapgvsp 638
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Matches
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632 fapgvsp 638
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17-JUN-1988;
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19-JUN-1989;
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                                                                                                                                                                                                                                                            Query Match
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Matches
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The sequences given in R51264-66 are encoded by the hepatitis E virus (HEV) strain SAR-55. The cDNA sequence contains three open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production the virus proteins - useful for diagnosis or vaccine production the virus proteins - useful for diagnosis or vaccine claim 22; columns 57-66; 47pp; English.

Wally 29 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORFI sequence from ED-NANB.
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Protein encoded by ORF1 of ET-NANB (HEV) Burma strain DNA sequence.
Enterically transmitted non A non B hepatitis virus; ET-NANB;
Hepatitis E virus; HEV; Burma HEV isolate; vaccine;
diagnostic_probe.
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HEV strain protein encoded by ORF-1.
Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; antibody; detection; diagnosis; primates; stool suspension.
Hepatitis E virus strain SAR-55.
W09406913-A.
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Pred. No. 2.62e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                   07-JUN 1995; 475807.
25-JUL-1994; US-279823.
17-JUN 1988; US-2208997.
11-APR-1989; US-367486.
13-OCT-1989; US-367486.
05-JUL-1990; US-565888.
07-JUN-1995; US-456988.
07-JUN-1995; US-456988.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 12
R51264 standard; Protein; 1693 AA.
.r 11
W80196 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                  A non B Hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
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N-PSDB; Q45197.
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N-PSDB; V66321.
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                                                                                                                                                                                                                                                                                                                   20-OCT-1998.
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frames (ORFs). These proteins can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. The Proteins SAR-S5 CDNA was isolated from primates innoculated with stool suspensions obtained from hepatitis E patients.
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                                                                                                                                                                                                                                                                                                                         572 frtsfydgayletngperhnlsfdasqstmaagpfsltyaasaaglevryvaagldhray 631
                                                                                                                                                                                                                                                                                                                                                             572 frtsfydgavletngperhnlsfdasqstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                            3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by ORF 1 of the Burmese isolate of ET-NANB.
Enterically transmitted nonA/nonB hepatitis virus; identification;
HEV; ET-NANB; detection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis E virus DNA - useful for e.g. virus detection and viral
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                                                                                                                                                                                                                       Length 1693;
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Pred. No. 2.62e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                    Score 86; DB 10; Length 169
Pred. No. 2.62e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENELABS TECHNOLOGIES INC.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Columns 55-64; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note "not specified"
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W71209 standard; Protein; 1693 AA.
                                                                                                                                                                                                                    th 12.6%;
Similarity 25.4%;
17; Conservative
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Local Similarity 25.4%;
les 17; Conservative
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13-OCT-1989; US-420921.
05-APR-1990; US-505888.
25-JUL-1994; US-279823.
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US-208997.
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                                                                                                                                                                                                                                          Best Local Similarity
Matches 17; Conser
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WPI; 98-446186/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc_difference 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein useful in diagnosis, prophylaxis and treatment of antigenic protein useful in diagnosis, prophylaxis and treatment of antigenic protein useful in diagnosis, prophylaxis and treatment of protein the interesting in the present sequence is the protein prod. of ORF-1 from the present sequence is the protein prod. of ORF-1 from the retrieves (E.G. Protein Protein Protein Protein prod. of ORF-1 from the contentically transmitted non-A. non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than the NORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors ppic9-1779, -1780 and -1781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD525 toxin.
HD525 toxin. PCR: primer; amplification; Bacillus thuringiensis; probe; lepidoptera: pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 frtsfvdgavletngperhnlsfdasqstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86; DB 19; Length 1693;
Pred. No. 2.62e+01;
22; Mismatches 25; Indels 3; Gaps
                                                                                                                                                                                                                                                                /note="10 bp nucleic acid sequence TGGTNTTYGA has to be inserted between nucleotides and 127394 before these amino acid residues can be decoded"
                                                                                                                                          enteric transmission;
                                                                                                         26-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 ORF-1.
Hepatitis E virus; HEV: SAR-55 strain; enteric transmissi structural region; antigen; detection; antibody; vaccine;
                                                                                                                                                                                                                /note= "corresponding codon CAG"
misc_difference 1455..1693
                                                                                                                                                                                                                                                                                                                                                              03-0CT-1995; U13102.
03-0CT-1994; US-316765.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
EMETSON SU, PUICELL RH, TSATEV SA;
                                                                                                                                                                                                      Location/Qualifiers
                                                                         R91813 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W75774 standard; Protein; 633 AA
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Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                     LEGALITIS E VITUS.
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13-MAR-1998; U05081.
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WPI; 96-209320/21.
N-PSDB; T27394.
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65 FDPSTGA 71
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MINION MYCOGEN CORP.

MILET-COAD J, Narva KE, Schnepf HE;
MILET-COAD J, Narva KE, Schnepf HE;
MILET-COAD J, Narva KE, Schnepf HE;
MILET 98-506734/43.

Nari 98-506734/43.

Nari 98-506734/43.

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Best Local Similarity 23.7%; Pred. No. 3.10e+01;
Matches 14; Conservative 20; Mismatches 23; Indels
13-MAR-1997; US-040512.
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PCT-US99-13024-2-07.rpr

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm wed Sep 1 16:19:22 1999; MasPar time 7.09 Seconds 565.292 Million cell updates/sec MPsrch_pp Run on:

>PCT-US99-13024-2 (1-100) from PCTUS9913024.pep (7 of 12) 683 1 MEKFWAEFGGGYVQTPFLSE.....STSNDTTSAAFVSFMNSLIN 100 Title: Description: Perfect Score: Sequence:

Tabular output not generated.

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 39.393; Variance 75.747; scale 0.520 Statistics:

SUMMARIES

COMMARIES	Query e Match Length DB ID Description Pred. No.	14.9	13.5 299 2 S61248 hypothetical protein 3	13.5 521 1 HYBSN bacillolysin (EC 3.4. 3	9 13.0 438 2 S51876 C4-dicarboxylate tran 8.	9 13.0 566 2 G71525 probable OMP [leader 8	7 12.7 727 2 S17854 NADH dehydrogenase (u 1.	7 12.7 727 2 A33552	6 12.6 239 2 A29091 licheninase (EC 3.2.1 2.	6 12.6 521 2 139956 neutral proteinase (E 2.	6 12.6 574 2 S28275 hypothetical protein 2	6 12.6 1693 1 MNWWHE genome polyprotein - 2	5 12.4 242 1 LXBS licheninase (EC 3.2.1 3	5 12.4 331 2 A61046 ecdysone-induced memb 3.	5 12.4 869 2 C56617 cfaC protein precurso 3.	4 12.3	4 12.3 622 2 S17402	171 2 JQ2303 AL5 protein - pepper	171 2 S31878 AL4 protein - pepper 5.	262 2 D70961 probable echAl prote1 5	281 2 S38913 hypothetical protein 5	469 2 A55484 p52(Shc) protein - mo 5.4	0 473 0 COS776 transforming protoin R	c ITATOTA MITHITOTHISTOTHISTOCKETH DIOCETH 2
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Grobler, J.; Bauer, F.; Subden, R.E.; van Vuuren, H.J.J. Yeast (1995) 11:1485-1491
The mael gene of Schizosaccharomyces pombe encodes a permease for malate and other C(4) dicarboxylic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references GB:AE001308; GB:AE001273; NID:93328766; PID:93328771
##experimental_source serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe
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Science (1998) 282:754-759
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humans: Chlamydia trachomatis.
#cross-references MUID:99000809
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                                                              ISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                      36 LSTAGPSYV-KFQDNPVGSQTFSAGLHLRVFDPSTGALVDSKSYAFSTSNDTTS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G71525 #type complete
probable OMP [leader (19) peptide] - Chlamydia
(serotype D, strain UN3/Cx)
#formal_name Chlamydia trachomatis
13.5ep-1998 #sequence_revision 13.5ep-1998 #tex
21-Nov-1998
                         Indels
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                                                                                                                                                                                  S61876 *type complete
C4-dicarboxylate transport protein mael - f
Schizosaccharomyces pombe
#formal_name Schizosaccharomyces pombe
20-Jul-1996 #sequence_revision 13-Mar-1997
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  Pred. No. 3.52e-01;
19; Mismatches 18;
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ilarity 26.2%;
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Best Local Similarity 39.1%;
Matches 18; Conservative
  Best Local Similarity 27.8%;
Matches 15; Conservative
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S61876
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Submitted to the EMBL Data Library, January 1995
Nucleotide sequency and a 30-bb region of the bovine herpesvirus I genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium; extracellular protein; hydrolase; metalloproteinase;
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Bacillolysin (EC 3.4.24.28) precursor - Bacillus
amyloliquefaciens
Bacillus metalloendopeptidase; microbial metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.; Filpula, D. J. Bacteriol. (1984) 159:811-819
Genes for alkaline protease, and neutral protease from Bacillus amyloliquefaciens contain a large open reading frame between the regions coding for signal sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG(
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#product bacillolysin #status predicted #label MAT(
#binding_site zinc (His, His, Glu) #status predicted/
#active_site Glu, His #status predicted
#active_site Glu, His #status predicted
#status predicted #status predicted
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#formal_name Bacillus amyloliquefaciens
30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
05-Sep-1997
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#checksum 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-299 ##label VLC ##residues 1-299 ##label VLC ##cross-references EMBL:Z48053; NIO:9971311; PID:9971327 CLASSIFICATION #superfamily varicella-zoster virus gene 53 ps sUMMARY #length 2999 #molecular-weight 32379 #checks
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##cross-references GB:K02497; NID:g143248; PID:g143249
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Mitochondrial NADH:ubiquinone reductase: complementary DNA sequence of the import precursor of the bovine 75-kDa
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predicted #label TNP\
#product NADH dehydrogenase (ubiquinone) 75K chain
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30.5ep-1993 #sequence_revision 30.5ep-1993 #text_change
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#map_position 2q33-2q34
CLASSIFICATION #superfamily NADH dehydrogenase (ubiquinone) chain 11
                                                                                                                                                                                                                                                           Chow, W.; Ragan, I.; Robinson, B.H.
Eur. J. Biochem. (1991) 201:547-550
Determination of the CDNA sequence for the human
mitochondrial 75-kDa Fe-S protein of NADH-coenzyme
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metalloprotein; mitochondrion; NAD; oxidoreductase
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Pred. No. 1.66e+00;
18; Mismatches 34; Indels
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Local Similarity 27.3%;
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#authors Hofemeister, J.; Kurtz, A.; Borriss, R.; Knowles, J.
#Journal Gene (1986) 49:177-187
#title The beta-glucanase gene from Bacillus amyloliquefaciens shows extensive homology with that of Bacillus subtilis.
#cross_references_MUID:87192007
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neutral proteinase (EC 3.4.24..) - Bacillus amyloliquefaciens
#formal_name Bacillus amyloliquefaciens
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
18-Mar-1997
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The nucleotide sequence and some properties of the neutral protease gene of Bacillus amyloliquefaciens.
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16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
20-Mar-1998
#superfamily NADH dehydrogenase (ubiquinone) chain 11
iron-sulfur protein; membrane-associated complex:
    metalloprotein; mitochondrion; NAD; oxidoreductase
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glycosidase; hydrolase; polysaccharide degradation
#length 239 *molecular-weight 26928 *checksum 1611
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##residues 1-239 ##label HOF
##cross-references GB:M15674; NID:g143009; PID:g143010
##experimental_source strain BE20/78
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Hepatitis E virus (HEV): strain variation in the nonstructural gene region encoding consensus motifs for an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNWWHE #type complete
genome polyprotein - hepatitis E virus (strain Burma)
RNA-directed RNA polymerase (EC 2.7.7.48)
#formal_name hepatitis E virus
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                           #formal caenorhabditis elegans
12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
09-Sep-1997
$28275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                 S28275 #type fragment
hypothetical protein F54G8.4 - Caenorhabditis elegans
                                                                                #superfamily thermolysin
hydrolase; metalloproteinase
#length 521 #molecular-weight 56725 #checksum 6816
                                                                                                                                                                                                                           240 ISSESGKYVLRDLSKPTGTQNNTYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14/3; 51/2; 98/3; 213/2; 266/3; 294/3; 336/2; 381/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sulston, J. submitted to the EMBL Data Library, December 1992
                                                                                                                                                       Score 86; DB 2; Length 521;
Pred. No. 2.24e+00;
18; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #accession A407/b
##molecule_type genomic RNA
##residues 1-1693 ##label TAM
##cross-references GB:M73218; NID:g330023; PID:g330024
##cross-references GB:M73218; NID:g330023; PID:g330024
##cross-references GB:M73218; NID:g330024
##cross-references GB:M73218; NID:g330024
##cross-references GB:M73218; NID:g330024
##molecule_type DNA
##residues 1-521 ##label RES
##cross-references GB:M36723; NID:g143352; PID:g143353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-574 ##label SUL
##cross-references EMBL:219155; NID:96712; PID:96715
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                                                                                                                                                       12.6%;
Local Similarity 27.8%;
nes 15; Conservative
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Best Local Similarity 38.2%;
Matches 13; Conservative
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A40778
                                                                                                                                                                                                                                                                                                                                                                      (fragment)
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                                                                 #start_codon
CLASSIFICATION
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August, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.; Bolonio, A.; Braun, M.; Brignell, S.C.; Bron. S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.; Choi, S.K.; Codahl, J.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fulta, M.; Fulita, Y.; Freman, S.; Galizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.; C.; Fulta, Y.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.; Kashara, Y.; Rlaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Levine, A.; Liu, H.; Masuda, S.; Lazarevit, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; M.; Moesti, D.; Mediue, C.; Medina, N.; Mollado, R.P.; Mizuno, W.; Moesti, D.; Nakara, A.; Oudega, B.; Park, S. H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Perescott, A.M.; Presecon, E.; Pulic, P.; Porwolik, S.; Perescott, Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
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Microbiology (1995) 141:281-290
Genese encoding xylan and beta-glucan hydrolysing enzymes in
Bacillus subtilis: characterization, mapping and
construction of strains deficient in lichenase, cellulase
RNA-dependent RNA polymerase and an ATP/GTP binding site.
**Cross-references MUID:92271462
***accession A48547
                                                                                   572 FRISFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LXBS #type complete
licheninase (EC 3.2.1.73) precursor - Bacillus subtilis
1,3-1,4-beta-D-glucan 4-gluconohydrolase; beta-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           licheninase E-1; licheninase E-2

#formal_name Bacillus subtilis

30-Jun-1988 #sequence_revision 13-Mar-1998 #text_change

24-Sep-1998

140370; B69594; A22914; A90026; A90027; JU0110
                                                                                                                                                                                                                                                                                                                                                                                          Length 1693;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 1; Length 1693
Pred. No. 2.24e+00;
22; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
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##residues 1-24
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Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schletch, S.; Schroeter, R.; Scoffone, F.; Scklguchl, J.; Sekwaska, A.; Schroeter, R.; Scoffone, F.; Schlguchl, J.; Sekwaska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Taracaji, T.; Takahashi, H.; Takemaru, R.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, M.; Tamakoshi, A.; Tanama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catalyzes the hydrolysis of 1,4-beta-D-glucosidic bonds in lichenin and other 1,3- and 1,4-beta-linked polysaccharides #superfamily licheninase extracellular protein; glycosidase; hydrolase; polysaccharide degradation; pyroglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source was hyperproducing strain HL-25 with gene from strain
                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:299124; GB:AL009126; NID:g2636442; PID:e1184632; ##experimental_source strain 168 NCE NOSE A93526 thors
                                                                                                                                                                                                                                                                                     The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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Apric. Biol. Chem. (1989) 53:2341-2346
Purification and some properties of two enzymes from a
beta-glucanase hyperproducing strain, Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain C120
##note the authors translated the codon CAA for residue 29
Lys and CCA for residue 82 as Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Murphy, N.; McConnell, D.J.; Cantwell, B.A.
#journal Nucleic Acids Res. (1984) 12:5355-5367
#title The DNA sequence of the gene and genetic control sites in the excreted B. subtilis enzyme beta-glucanase.
#cross-references MUD:84272222
#accession A22914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tezuka, H.; Yuuki, T.; Yabuuchi, S.
Agric. Biol. Chem. (1989) 53:2335-2339
Construction of a beta-glucanase hyperproducing
subtilis using the cloned beta-glucanase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:X00754; NID:g39818; PID:g685236
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A90026
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*accession B69594
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#authors
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Jordi, B.J.; Willshaw, G.A.; van der Zeijst, B.A.; Gaastra,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1:869 ##label JOR
##cross-references GB:M55661; NID:9145507; PID:9145510
##experimental_source enterotioxigenic strain, CFA/I-ST plasmid NTP113
##note sequence extracted from NCBI backbone (NCBIN:108960,
NCBIP:108971)
                                                                                                                                                                                                                                                                                                                                                 Moore, J.T.; Fristrom, D.; Hammonds, A.S.; Fristrom, J.W. Dev. Genet. (1990) 11:299-309
Characterization of IMP-E3, a gene active during imaginal disc morphogenesis in Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C56617 *type complete
cfac protein precursor - Escherichia coli plasmid NTPll3
*formal_name Escherichia coli
05-Jan-1996 *sequence_revision 05-Jan-1996 *text_change
20-Mar-1998
                                                                                                                                                                                   A61046 *type complete ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster) *fromal_name Drosophila melanogaster 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change 16-Peb-1997
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                                                                          77 LALISPAYNKFDCGENRSVQTYGYGLYEVRM-KPAKNTGIVSSFFTYTGPTDGTP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid
#length 869 #molecular-weight 97830 #checksum 9755
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                                                                                                    ##cross-references FlyBase:FBgn0001255
DS membrane protein
X #length 331 #molecular-weight 36583 #checksum
Length 242;
                                    20; Mismatches 18; Indels
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Pred. No. 3.03e+00;
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Pred. No. 3.03e+00;
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Pred. No. 3.03e+00;
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Matches 11; Conservative
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Best Local Similarity
Matches 14; Conserv
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158 AFIQSQTINLSDSGKYKRLSISGNSALGITDTSY 191

Search completed: Wed Sep 1 16:19:39 1999 Job time : 17 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:18:08 1999; MasPar time 4.90 Seconds 576.427 Million cell updates/sec Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

>PCT-US99-13024-2 (1-100) from PCTUS9913024.pep (7 of 12) 683 1 MEKFWAEFGGGYVQTPFLSE......STSNDTISAAFVSFMNSLIN 100

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot37 1:swissprot

Mean 40.448; Variance 69.297; scale 0.584 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Pred. No.	5.568-43	3.05e-03	6.34e-03	1.08e-01	3.01e-01	5.88e-01	5.88e-01	5.88e-01	8.18e-01	8.18e-01	8.18e-01	8.18e-01	8.18e-01	1.14e+00	1.14e+00	1.57e+00	2.17e+00	2.17e+00	2.17e+00	2.17e+00	2.17e+00	2.17e+00	2.99e+00
	Description	HYPOTHETICAL 7.3 KD PR	NADH-UBIOUINONE OXIDOR	NON-STRUCTURAL POLYPRO	BACILLOLYSIN PRECURSOR	MALIC ACID TRANSPORT P	HYPOTHETICAL 76.2 KD P	NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	BETA-GLUCANASE PRECURS	LATE EMBRYOGENESIS ABU	HYPOTHETICAL 104.4 KD	NON-STRUCTURAL POLYPRO	NON-STRUCTURAL POLYPRO	BETA-GLUCANASE PRECURS	CFA/I FIMBRIAL SUBUNIT	BETA-GLUCANASE PRECURS	HYPOTHETICAL AL4 PROTE	SHC TRANSFORMING PROTE	SHC TRANSFORMING PROTE	HYPOTHETICAL 67.2 KD P	MAST/STEM CELL GROWTH	HYPOTHETICAL 145.8 KD	HYPOTHETICAL PROTEIN H
SUMMARIES	ID	Y15A_BPT4	NQ03_PARDE	POLN_HEVMY	NPRE_BACAM	MAE1_SCHPO	Y4II_RHISN	NUAM_HUMAN	NUAM_BOVIN	GUB_BACAM	EMB8_PICGL	YMB4_CAEEL	POLN_HEVBU	POLN_HEVPA	GUB_BACSU	CFAC_ECOLI	GUB_BACLI	YAL4_PHUV	SHC_MOUSE	SHC_HUMAN	YX45_MYCTU	KKIT_CHICK	YAE6_SCHPO	Y391_HAEIN
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д₽	Query Match	43.9	14.9	14.6	13.5	13.0	12.7	12.7	12.7	12.6	12.6	12.6	12.6	12.6	12.4	12.4	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.0
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HYPOTHETICAL 51.4 KD P TYROSINE PROTEIN KINAS MADH-UBIQUINONE OXIDOR MADH-UBIQUINONE OXIDOR GTP CYCLOHYDROLASE I I ENOLASE (EC 4.2.1.11) TYROSINE PROTEIN KINAS HYPOTHETICAL PROTEIN M HYPOTHETICAL 19.0 KD P NITROGEN REGULATION PR NIFU PROTEIN. RECEPTOR TYPE ADENYLATED HYPOTHETICAL 93.2 KD T PUTATIVE FAMILY 31 GLU HYPOTHETICAL 93.2 KD T PUTATIVE POLYPROTEIN (CO DELTA (L-ALPHA-AMINOAD VITAMIN D-BINDING PROT METHYLMALONYL-COA MUTA 70 KD CRYSTAL PROTEIN		PRT; 65 AA. ED) SEQUENCE UPDATE) ANNOTATION UPDATE) IN GP34-GP35 INTERGENIC REGION. RNA STAGE; TAILED PHAGES; MYOVIRIDAE	r DATA BANK. CRC32;	DB 1; Length 65; 5.56e-43; tches 7; Indels 0;	MEKFWAEIWTRICPNAILSESNSVRYKISIAGSCPLSTAGPSYVKFODNPVGSOTF 	E UPDATE) ION UPDATE) IN 3 (EC 1.6.5.3) (NADH THAIN 3). PDIVISION; RHODOBACTER GROUP; 1-15. subunit of the energy-transducin of Paracoccus denitrificans.
TYK_HUMAN HUMA_NEUCR GCH_ZEAST ENO_BORBU Y176_METTH YCB_PSEDE Y176_METTH YCB_PSEDE Y176_METTH YCB_SCHPO YBT JEAST YDSB_SCHPO YDSB_YDSB_YDSB_YDSB_YDSB_YDSB_YDSB_YDSB_	ALIGNMENTS	PRT; SEQUENCE UP ANNOTATION IN GP34-GP	SWISS-PROJ	Score 300; DB 1 Pred. No. 5.56e- 3; Mismatches	ISVRYKISIAGS(SUI OI OI BRCI
4449 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ANDARD; 31, CREAT 31, LAST 31, LAST KD PROTEIN RUSES, NO	N.A. V-1994) TO THE PROTEIN. AA; 7334 MW;	43.9%; Similarity 82.1%; 46; Conservative	RICPNAILSESN :: GYVQTPFLSESN	ANDARD; 25, CRE2 31, LAST 32, LAST 32, LAST 32, LAST 32, LAST 31, LAST ANDREDIC CHAIN 3) IFICANS. ACTERIA; ., AND SE .; AND SE .; TROM SE .; AND S
666677777777999990000		T4 ST) 1995 (REL. 1995 (REL. 1995 (REL. TICAL 7.3 1 34.1. OPHAGE T4.	FROM N., M.; D (NOV-19 ICAL PROT	Similar 46; Co	FMAEIWT : FMAEFGQ	2 3-PARDE STAND) 915; 915; 915; 915; 916; 917; 918; 918; 918; 918; 918; 918; 918; 918
225 25 25 25 25 25 25 25 25 25 25 25 25		15A_BP 39509; 1-FEB- 1-FEB- 17A- 17A- 17A- 17A- 17A- 17A- 17A- 17A	L1) KUTTER E.M.; SUBMITTED (NOV-1994) HYPOTHETICAL PROTEIN SEQUENCE 65 AA; 7;	Ouery Match Best Local S Matches	1 MEK1 1 HEL	NOO3_PARDE ST P29915; 01-ARF-1993 (REL. 01-FEB-1995 (REL. 01-NOV-1995 (REL. NADH-UBIQUINONE O DEHYDROGENASE 1, NOO3. PARACOCCUS DENITR BACTERIA; PROTEOB PARACOCCUS I] SEQUENCE FROM N.A STRAIN-ATCC 13548 MEDILINE; 9229779 XU X., MATSUNO-YA "Structural featul "Structural featul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.77.48); HELICASE).
HEPATITIS E VIRUS (STRAIN MYANMAR) (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                            29; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILIDE, 93227573.
AYE T.T., UCHIDA T., MA M.Z., IIDA F., SHIKATA T., ICHIKAWA M.,
RIKIHISA T., WINN K.;
                                                                                                        KU X., MATSUNO-YAGI A., YAGI T.;
"DNA sequencing of the seven remaining structural genes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM: PF00111; fer2; 1.
PFAM: PF00184; molybdopterin; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; IRON-SULFUR; 4FE-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON-SULFUR (2FE-2S) (FIRON-SULFUR (4FE-4S) (4FE-4
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(4FE-4S)
(4FE-4S)
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PROSITE; PSO0641; COMPLEXI_75K_1; 1.
PROSITE; PSO0643; COMPLEXI_75K_2; 1.
PROSITE; PSO0643; COMPLEXI_75K_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73028 MW;
                                        657-672 FROM N.A.
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ilarity 26.0%;
Conservative
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672 AA;
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RRANKER RRANKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- COFACTOR: BINDS AND REQUIRES A ZINC ATOM, WHICH IS ESSENTIAL FOR PROTECLYIC ACTIVITY. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: SECRETED.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE THERMOLYSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                      572 FRISFVDGAVLEANGPERYNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                           IS GENES 7:95-109(1993).
HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genes for alkaline protease and neutral protease from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS AMYLOLIQUEFACIENS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                    Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ARCC 23844;
MEDLINE; 85006739.
WASANTHA N., THOMPSON L.D., RHODES C., BANNER C., NAGLE J.,
FILPULA D.;
                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BACILLOLYSIN PRECURSOR (EC 3.4.24.28) (NEUTRAL PROTEASE)
                                                                                                                                                                                                                                                                               975 982 ATP (POTENTIAL).
1693 AA; 185215 MW; FFCB786D CRC32;
                                                                                                                                                                                                                                                                                                                                  14.6%; Score 100; DB 1; I
larity 26.9%; Pred. No. 6.34e-03;
Conservative 22; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A25415; HYBSN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K02497; G143249; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                           EMBL; D10330; G221705;
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 FAPGVSP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 FDPSTGA 71
                                                                                                                                                                                                                                                                ATP-BINDING.
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NPRE_BACAM
P06832;
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SEQUENCE
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51 VGSQTFSAGLHLRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS-FM 95

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 SPFADIDSGISIAAISLFGAAGASIRPPEWLAFANAALASGAFPIGLSPRVIAIAISQYA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (EC 1.6.5.3)
(EC 1.6.99.3) (COMPLEX I-75KD) (CI-75KD).
                                                                                                                                                                                                                                                                                                          MEDLINE; 97305956.
FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.,
PERRET X.;
                                                                                                                                                                                                 RHIZOBIUM SP. (STRAIN NGR234).
PLASMID SYM PWORB234A.
BACTERIA: PROTEOBACTERIA: ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                               NATURE 387:394-401(1997).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1- SIMILARITY: NONE OBVIOUS.
                                                                                                                                                                                                                                                                                                                                                              "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 1; Length 703; Pred. No. 5.88e-01; 20; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A2BA53CE CRC32;
                                                                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 76.2 KD PROTEIN Y4II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMID; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 AA.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 92037608.
CHOW W., RAGAN I., ROBINSON B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%;
ilarity 26.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452
664
76183 M
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                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432
644
703 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 KAK-FPIS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 DSKSYAFS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                    LT 6
Y4II_RHISN
P55492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 7
NDAM_HUMAN
P28331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                     2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96353430.
GROBLER J., BAUER F., SUBDEN R.E., VAN VUUREN H.J.J.;
"The mael gene of Schizosaccharomyces pombe encodes a permease for malate and other C4 dicarboxyllc acids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
ACTIVATION PEPTIDE.
BACILLOLYSIN.
ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
PRO147D4 CRC32;
                                                                                                                                                                                                                                                                                                      240 ISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                                                                                                                                         'n
                               HYDROLASE, METALLOPROTEASE; ZINC; CALCIUM; ZYMOGEN; SIGNAL. 27 POTENTIAL. PROPER 28 21 ACTIVATION PEPTIDE. CHAIN 222 521 BACILLOLYSIN METAL 364 364 ZINC (CATALTIC) (BY SIMILARIT METAL 368 368 2INC (CATALTIC) (BY SIMILARIT METAL 368 368 368 ZINC (CATALTIC) (BY SIMILARIT METAL 368 368 2INC (CATALTIC)
                                                                                                                                                                                                                               Score 92; DB 1; Length 521;
Pred. No. 1.08e-01;
19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89; DB 1; Length 438;
Pred. No. 3.01e-01;
11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 VGPPAFS-GLAL-I-NIARGAM-GSRPYIFVGANSSEYLGFVSTFM 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; FUNGI; ASCONYCOTA; ARCHTASCONYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MALIC ACID TRANSPORT PROTEIN (MALATE PERMEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         011F7FB6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                  438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
PFAM; PF00099; zn-protease; 1.
HSSP; P00800; 1TRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (REL. 34, CREATED)
                                                                                                                                                                                              56840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49304 MW;
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llarity 39.1%;
Conservative
                                                                                                                                                                                                                               Match 13.5%;
Local Similarity 27.8%;
es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U21002; G1171119; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPORT; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                       27
221
364
365
388
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321
353
438 AA;
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                                                                                                                                                                                                521 AA;
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MAE1_SCHPO P50537;

RESULT

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BACILLUS AMYLOLIQUEFACIENS
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GUB_BACAM
P07980;
         SEQUENCE MEDLINE;
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            MITOCHONDRION (BY SIMILARITY).

NADH-UBIQUINONE REDUCTASE 75 KD SUBUNIT.
IRON-SULEUR (4FE-45) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 IRFASEIAGVDDLGTTGRGN-DMQVGTYIEKMFMSELSGNIIDICPVGALT-SKPYAFTA 240
      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE 75 ND SUBUNIT PRECURSOR (EC 1.6.99.3) (COMPLEX I-75KD) (CI-75KD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
                                                                                                                                                                                                                                                                                     PFAM; PF00111; fer2; 1.
PFAM; PF00384; molybdopterin; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION; TRANSIT PEPTIDE; IRON-SULEUR; 4FE-45.
'Determination of the cDNA sequence for the human mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .88e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B9F33158 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87;
                                                                                                                                                                                                                                              MIM: 157655; -
PROSTE; PS00641; COMPLEX1_75K_1: 1.
PROSITE: PS00643; COMPLEX1_75K_2: 1.
PROSITE: PS00643; COMPLEX1_75K_3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUAM_BOVIN STANDARD; F
P15690;
O1-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQU
01-OCT-1996 (REL. 34, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 RPWETRKTESIDVMDAV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 SN-DTTSAAFVSFMNSL 98
                                                                                                                                                                                                                 EMBL; X61100; G38079; -.
                                                                                                                                                                                                                         PIR; S16382; S16382.
PIR; S17854; S17854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727 AA;
                                                                                                                                                                                                                                                                                                                                        24
53
64
75
78
128
1131
176
176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                               FRANSIT
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METAL
METAL
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IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 IRFASEIAGVDDLGTTGRGN-DMQVGTYIEKMFMSELSGNIIDICPVGALT-SKPYAFTA 240
                                                                            01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                        PROSITE; PS00641; COMPLEX1_75K_1; 1.
PROSITE; PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_3; 1.
PFAM; PF00111; fer2; 1.
PFAM; PF00184; molybdopterin; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION; TRANSIT PEPTIDE; IRON-SULFUR; 4FE-45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches 34; Indels
                                                                                                                                                    of the import precursor of the bovine 75-kDa subunit."; BIOCHEMISTRY 28:9452-9459(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON-SULFUR (4FE-45) (IRON-SULFUR (4FE-45) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.88e-01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9CAF139C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION
FROM N.A., AND PARTIAL SEQUENCE. 90122814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON-SULFUR
IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79442 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 27.3%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J02877; G163414; -. PIR; A33552; A33552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 RPWETRKTESIDVMDAV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 SN-DITSAAFVSFMNSL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
53
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Best Local Similarity
Matches 21; Conser
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457 AA; 51019 MW; AE7CB4CD CRC32;
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nes 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                             11
CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLN_HEVBU P29324;
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SEQUENCE
  SEQUENCE
                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                 YMB4_
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
-:- BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-:- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 LALTSPSYNKFDCGENRSVQTYGYGLYEVRM-KPAKNTGIVSSFFTYTGPTEGTP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOFEMEISTER J., KURTZ A., BORRISS R., KNOWLES J.;
"The beta glucanase gene from Bacillus amyloliquefaciens shows
extensive homology with that of Bacillus subtilis.";
GENE 49:177-187(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
,
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DONG J.Z., DUNSTAN D.I.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE UPF0017 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8.18e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
14A3C78F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LATE EMBRYGGENESIS ABUNDANT PROTEIN EMBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA-GLUCANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A29091; A29091.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PFAM: PF00722; 91ycosyl_hydro9; 1.
HSSP; P27051; 1GBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOPHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROLASE; GLYCOSIDASE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 239 BI
134 134 NI
57 86 BI
239 AA; 26928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L47118; G1350545; -. PROSITE; PS01133; UPF0017; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PICEA GLAUCA (WHITE SPRUCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M15674; G143010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                        MEDLINE: 87192007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 10
EMB8_PICGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
DISULFID
                      BACILLUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT J., COPERT J., COLLSON A.,
CRATTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOOPD C., MORTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPPA A., SAUNDERS D., SHOWNKEN R.,
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WOHLDMAN P.;
2.2. M. of contiguous nucleotide sequence from chromosome III of C.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN
                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                         232 LGANILVRYLGEVAGNCPLSGAVSLCNPF-NLVIADEDFHKGLGFNNVYD 280
                                                                                                                                                             Score 86; DB 1; Length 457; Pred. No. 8.18e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 1; Length 932;
Pred. No. 8.18e-01;
9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTALION UPDATE)
HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE 368:32-38(1994).
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                              11; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 83 C3HC4-TYPE.
932 AA; 104438 MW; 45C877B4 CRC32;
                                                                                                                                                                                                                                                                                                                     932 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 TFTEGLEYLRNFQPDADELFNRK-LRFSAGDDAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S28275; S28275.
WORNPEP: F5468.4; CE05942.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
PFAM; PF00097; zf-C3HC4; 1.
HSSP; P29590; 1BOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||: || || ||:| : | : ||:|::
55 TFSAGLH-LRVFDPSTGALVDSKSYAFSTSNDTT
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%;
38.2%;
   12.6%;
                          Local Similarity 34.0%;
hes 17; Conservative
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STRAIN-BR151
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             SSSE 2 2 2 5 8 5 6 8
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01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNORATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.7.7.48): HELICASE)
HERPATITIS E VIRUS (STRAIN BURMA) (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (REL. 28, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
16-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
17-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
18-DETAILS POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48); HELICASE].
18-DETAILTIS E VIRUS (STRAIN PAKISTAN) (HEV).
19-DETAILTISES: SSRNA POSITIVE-STRAND VIRUSES; NO DNA STAGE; CALICIVIRIDAE; CALICIVIRIDAE;
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MALIK I.A., 10BAL M., PUNCELL R.H.;
Characterization of a prototype strain of hepatitis E virus.";
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).
-!- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE ACENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                            'Hepatitis E virus (HEV): molecular cloning and sequencing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A40778; MNWWHE.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
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Pred. No. 8.18e-01;
22; Mismatches 25; Indels
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185191 MW; C560BE14 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length viral genome.";
VIROLOGY 185:120-131(1991).
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Matches 17; Conservative
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1693 AA;
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"Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction of strains deficient in lichenase, cellulase and xylanase.";
MICROBIOLOGY 141:281-290(1995).
                                                                                                                                                                                                                                                                                                                                                            572 FRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (REL. 05, CREATED)
01-NOV-1995 (REL. 32, LAST SEOUENCE UPDATE)
15-UTL-1988 (REL. 36, LAST ANNOTATION UPDATE)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
BAGIS OR BEL OR LICS OR NISB.
BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAK B.;
"LicT, a Bacillus subtilis transcriptional antiterminator protein of the BglG family.";
"BACTERIOL. 178:1971-1979(1996).
                                                                                                                                                                                                                                                                                                             Gaps
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"Construction of a beta-glucanase hyperproducing Bacillus subtilis
using the cloned beta-glucanase gene and a multi-copy plasmid.";
AGRIC. BIOL. CHEM. 53:2335-2339(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96178961.
SCHNETZ K., STUELKE J., GERTZ S., KRUGER S., KRIEG M., HECKER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-168 / BGSC1A1;
YOSHIDA K.-I., SANO H., SEKI S., ODA M., FUJIMURA M., FUJITA Y.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                         RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURPHY N., MCCONNELL D.J., CANTWELL B.A.;
"The DNA sequence of the gene and genetic control sites for the excreted B. subtilis enzyme beta-glucanase.";
NUCLEIC ACIDS RES. 12:5355-5367(1984).
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                                                                                                                                                                                                                                             Length 1693;
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                                                                                                                                                                                                                                                Score 86; DB 1; Len
Pred. No. 8.18e-01;
22; Mismatches 25;
                                                                                                                                                              ATP (POTENTIAL).

W; FBCA2483 CRC32;
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                       or send an email to license@isb-sib.ch)
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                                                                                                                                                                 982 ATE
185149 MW;
                                                                                                                                                                                                                                                   Query Match 12.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                            EMBL; M80581; G329998; -. POLYPROTEIN; TRANSFERASE;
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                                                                                                                                   ATP-BINDING.
NP_BIND 975 90
SEQUENCE 1693 AA;
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WOLF M., GECZI A.,
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SEQUENCE FROM N.A.
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MEDLINE; 84272222.
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          YUNGITY, TEZUKA H., YABUNCHI S.;
YUNGITY, TEZUKA H., YABUNCHI S.;
"Purification and some properties of two enzymes from a beta-glucanase hyperproducing strain, Bacillus subtilis HL-25.";
AGRIC. BIOL. CHEM. 53.2341-3346(1989).
-! CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4 BETA-D-GLYCOSIDIC LINKAGES
-! BETA-D-GLUCANS CONTAINING 1,3 - AND 1,4 -BONDS.
-! BETA-GLUCANASES OF BACILUS HAVE A SUBSTRATE RANGE SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-! THE SEQUENCE OF STRAIN 168 1S SHOWN.
-! SUBCELLULAR LOCATION: SECREFEED.
-! SUBCELLULAR LOCATION: SECREFEED.
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P25733;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
CFA/I FIMBRIAL SUBUNIT C PRECURSOR (COLONISATION FACTOR ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID NTP513.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: ::|:| ||: : :||::|| :|: || 36 LSTAGPSYVKFQ-DNPVGSQTFSAGLH-LRVFDPSTGALVDSKSYAFSTSNDTTS 88
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NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
A -> S (IN STRAIN HL-25).
A -> S (IN STRAIN HL-25).
P -> L (IN STRAIN HL-25).
P -> L (IN STRAIN HL-25).
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HAMERS A.M., PEL H.J., WILLSHAW G.A., KUSTERS J.G.,
VAN DER ZEIJST B.A.M., GAASTRA W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 1; L. Pred. No. 1.14e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBTILIST; BG10476; BGLS.
PROSTIE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PFAM: PF00722; glycosyl_hydro9; 1.
HSSP: P27051; 1GBG.
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EMBL; D00518; D1000559; -.
EMBL; D83026; D1012364; -.
EMBL; Z46862; G599674; -.
EMBL; Z28340; G580948; -.
EMBL; Z99124; E1184632; -.
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12.4%;
Best Local Similarity 25.5%;
Matches 14; Conservative
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STRAIN-ENTEROTOXIGENIC;
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PIR; JU0110; JU0110.
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137
60
24
83
204
242 AA;
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ACT_SITE
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MOD_RES
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"The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli."; MICROB. PATHOG. 6:297-309(1989).
                                                                                                                                                                                                                                                                         JORDI B.J.A.W., WILLSHAW G.A., VAN DER ZEIJST B.A.W., GAASTRA W.;
"The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";
DNA SEO. 2:257-263(1992).
-1- FUNCTION: MAY SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.14e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M5561; G145510; -.
ANTIGEN; SIGNAL; FIMBRIA; OUTER MEMBRANE; PLASMID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AFIQSQTINLSDSGKYKRLSISGNSALGITDTSY 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.4%;
Best Local Similarity 32.4%;
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                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           MEDLINE; 92329981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:18:39 1999; MasPar time 9.82 Seconds 556.004 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-100) from PCTUS9913024.pep (7 of 12) 683 Description: Perfect Score:

1 MEKFWAEFGGGYVQTPFLSE.....STSNDTTSAAFVSFMNSLTN 100 Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

[1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 38.557; Variance 74.296; scale 0.519 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Š.	1.858-02	596-02	.70e-02	53e-01	536-01	536-01	530-01	856-01	65e-01	100-01	10e-01	24e+00	24e+00	69e+00	30e+00	30e+00	30e+00	30e+00	30e+00	2.30e+00
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	Description	GLUCOSYLTRANSFERASE	COMPLETE GENOME SECUEN	A606L PROTEIN.	EARLY AUXIN-INDUCED PR	HYPOTHETICAL 32.4 KD P		NEUTRAL PROTEASE (FRAG	IAA17/AXR3-1 PROTEIN.		HYPOTHETICAL 63.5 KD P	C34B7.2 PROTEIN.	PUTATIVE ETHYLENE RECE	SCAFFOLDING PROTEIN PR	ENDO-BETA-1, 3-1, 4-GLUC	NEUTRAL PROTEASE.	C35A5.2 PROTEIN.	F54G8.4 PROTEIN.	METHYL TRANSFERASE.	HEPATAITIS E VIRUS COM	UNNAMED PROTEIN PRODUC
SUMMARIES	9	054178	081876	041088	P93830	065574	065581	044647	049162	011979	084354	P90770	049984	045996	045691	044677	018470	Q23510	069410	081344	089444
	DB	7	14	14	10	14	14	7	10	14	~	ທ	10	7	7	N	S	'n	14	14	14
	Length DB	1577	1693	114	229	299	300	337	229	3443	266	921	180	1546	239	521	574	974	1693	1693	1693
	% Query Match	14.8	14.6	14.1	13.5	13.5	13.5	13.5	13.3	13.2	13.0	13.0	12.9	12.9	12.7	12.6	12.6	12.6	12.6	12.6	12.6
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RESULT

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ORF 1. CRYIIC DELTA-ENDOTOXIN	HYPOTHETICAL 27.3 KD PORF 1.	NOC1 PROTEIN.	PROBABLE CARBOXYLESTER	P66SHC.	ETHYLENE RESPONSE SENS	ZC376.3 PROTEIN.	NONSTRUCTURAL POLYPROT	METALLOPROTEASE TOXIN-	HOMOLOGUE OF HYPOTHETI	NADH DEHYDROGENASE SUB	CAPSID PROTEIN PRECURS	. PUTATIVE COAT PROTEIN.	FLAGELLAR L-RING PROTE	HYPOTHETICAL 41.7 KD P	PUTATIVE METALLOPROTEA	ENOLASE (EC 4.2.1.11)	ETHYLENE RESPONSE SENS	INSECTICIDAL CRYSTAL P	PUTATIVE READTHROUGH P	PROTEIN KINASE HOMOLOG	GENOME POLYPROTEIN.	POLYPROTEIN (FRAGMENT)
Q81862 Q45743	P96404 038022	P79065	023267	015290	038846	001303	039221	068892	P94412	001388	036185	065847	067609	083762	068424	031312	049231	052764	065848	023540	003463	068469
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22	53	25	56	27	78	58	30	31	32	33	34	32	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

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WEDLINE; 92276337.
SULAVIK M.C., TARDIF G., CLEWELL D.B.;
SULAVIK M.C., TARDIF G., CLEWELL D.B.;
Identification of a gene, rgg, which regulates expression of glucosyltransferase and influences the Spp phenotype of Streptococcus gordoni, Challis.";
J. BACTERIOL. 174:3577-3586(1992).
EMBL; M89776; G153795; -..
EMBL; M89776; G153795; -..
PPAM; PF00128; alpha-amylase; 1.
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                                                                                                                                                                                                                                                                                                STREPTOCOCCUS GORDONII.
BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CHALLIS.
WEDLINE: 96157084.
WICKERMAN M.M., SULAVIK M.C., CLEWELL D.B.;
"Molecular analysis of Streptococcus gordonii glucosyltransferase phase variants.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 QDDGTVKKNFAVELNGKILYFDAETGALVDSNEYQFQQGTSSLNNEF 285
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054178; 054247; 01. CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SHOUNCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL.
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SEQUENCE 1577 AA; 177805 MW; 7D58FEC2 CRC32;
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SEQUENCE OF 1-96 FROM N.A.
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RESULT
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VIRUSES; DSDNA VIRUSES, NO RNA STAGE: PHYCODNAVIRIDAE; PHYCODNAVIRUS.
                                                                                                                                                                                                                                                                                             HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
CALICIVIRUS.
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VAN ETTEN J.L.;
"Analysis of 74 kb of DNA located at the right end of the 330-kb
chlorella virus PBCV-1 genome.";
VIROLOGY 237:360 377 (1997).
EMBL: U42580: G2447164: -.
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                                                                                                                                                                                                                              Length 1693;
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                                                                                                                                                                                                                        Score 100; DB 14; Length 16
Pred. No. 2.59e-02;
22; Mismatches 24; Indels
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Pred. No. 9.70e-02;
18; Mismatches 25; Indels
                                                                                                                                                                     SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; D11093; D1002342; -.
SEQUENCE 1693 AA; 184840 MW; 8952DD38 CRC32;
                       01, CREATED)
01, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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P93830
P93830
P93830
01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATIC
EARLY AUXIN-INDUCED PROTEIN IAA17.
EARLY AUXIN-INDUCED PROTEIN IAA17.
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
1693
 PRT;
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08,
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Best Local Similarity 26.9%;
Matches 18; Conservative
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Local Similarity 27.4%;
nes 17; Conservative
                                                  01-JAN-1999 (TREMBLREL. 0'COMPLETE GENOME SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                            041088;
01-JAN-1998 (TREMBLREL. 0)
01-JAN-1998 (TREMBLREL. 0)
01-NOV-1998 (TREMBLREL. 0)
A606L PROTEIN.
PRELIMINARY;
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                          (TREMBLREL.
                                                                                                                               SEQUENCE FROM N.A.
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MEDLINE, 98022962
                                                                                                                                                                                                                                                                                                                                    632 FAPGVSP 638
                                                                                                                                              STRAIN-UIGH179;
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                         01-NOV-1996
01-NOV-1996
                                                                                                                                                            JCHIDA T.;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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"Nuclectide sequence analysis of a 30-kb region of the bovine herpesvitus I genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SVR-YKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDPSTGALVDS-KS-YA 79
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                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA;
VYSOTSKAIA V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., BUEHLER
COMMAY A.B., COMMAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI
SHINN P., SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A.,
THEOLOGIS A.;
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EMBL: 049073; G2618723; -.
EMBL: AC000104; G2341044; -.
EMBL: AFC40631; G291756; -.
MENDEL; 7119; ARAth;1524;6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MISSING (IN REF. 2).
197 P -> PFIVGYWIRALFLEI (IN REF. 2).
218 A -> GMYELL (IN REF. 2).
229 RAMEKCKSRA -> MHIFTLIKF (IN REF. 2529 RAMEKCKSRA -> MHIFTLIKF (IN REF. 25288 MW. 00A134E6 CRC32.
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                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 98004476.
MID J., HARTER K., THEOLOGIS A.;
"Protein-protein interactions among the Aux/IAA proteins.";
PROC. NATL. ACAD. SCI. U.S.A. 94:11786-11791(1997).
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23; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVINE HERPESVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 32.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 SFTMGKHGGEEGMIDFMN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 -FSTSNDTTSAAFVSFMN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.8%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-COOPER, AND JURA;
MEDLINE; 95313343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 98146427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-JURA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 5
Q65574
Q65574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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PCT-US99-13024-2-07.rspt

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ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACERE; RABBIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 VRSYRKNYMVSCQKSSGGPEAAFVKVSMDGAPYLRKIDLRMYK-SYDELSNALSNMFSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 VR-YKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDPSTGALVDS-KS-YA- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIZE CHLOROTIC DWARF WAIKAVIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; SEQUIVIRIDAE;
WAIKAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDDICK B.B., HABERA L.F., LAW M.D.;
"Nucleotide sequence and taxonomy of maize chlorotic dwarf virus within the family Sequiviridae.";
J. GEN. VIROL. 78:1165-1174(1997).
EMBL; U67839; G2160664; -.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
SECUENCE FROM N.A.
MEDLINE: 98146427.
ROUSE D., MACKAY P., STIRNBERG P., ESTELLE M., LEYSER O.;
"Changes in auxin response from mutations in an AUX/IAA gene.";
SCIENCE 279:13731-13731-1998).
EMBL; AF040632; G291758; --
SEQUENCE 229 AA; 25304 MW; 2D88B037 CRC32;
                                                  240 ISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                            ς.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 91; DB 10; Length 229;
Pred. No. 4.85e-01;
22; Mismatches 33; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1193 VDSQERRYGGYLRIWHDPNGSLDEGVEFAMSTNLEPPPGAFVKY 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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  18;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                                                                                                                                                                                                                       CREATED)
                                                                                                                                                                                                        PRT;
  19;
                                                                                                                                                                                                                                                       96,6
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31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
13.3%;
Best Local Similarity 22.1%;
Matches 17; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 FTMGKHGGEEGMIDFMN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 FSTSNDTTSAAFVSFMN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                  01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                            01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IAA17/AXR3-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-TENNESSEE (TN);
MEDLINE; 97296968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 14; Conserv
15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                             71 8
049162
049162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o11979;
011979;
     Matches
                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification and characterization of the bovine herpesvirus 1 UL7 gene and gene product which are not essential for virus replication
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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044647
044647
044647
044647
044647
04-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
NEUTRAL PROTESTE (FRAGMENT)
BACILLUS AMYLOLIOUPERCIENST
BACTERIA, FIRMICUTES, BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷
                                                                                                                                                                                                                                                                            Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.5%; Score 92; DB 14; Length 300; 47.2%; Pred. No. 3.53e-01;
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                                                                                                                                                                                                                                                                       Score 92; DB 14; Length 299
Pred. No. 3.53e-01;
9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                            SCHWYZER M.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 248053, 5971327; -.
EMBL, A004801; E1187337; -.
HYPOTHETICAL PROTEIN.
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVINE HERPESVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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YOSHIMURA K., MIYAZAKI T., NAKAHAMA K., KIKUCHI M.;
TAKEDA KENKYUSHO HO 44:42-50(1985).
                                                                                                                                                                                                                       299 AA; 32379 MW; A3897D4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AA; 32450 MW; 86377347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA; 36910 MW; 5A9BC52B CRC32;
                                                                                                                                                                                                                                                                                                                                                                           45 PRFVCEVREIPAGPPTFTSSSITHLRV-EPSTGALL 79
                                                                                                                                                                                                                                                                                                                                                                                                        46 PRFVCEVREIPAGPPTFTSSSITHLRV-EPSTGALL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :| :: | |: || |: || || SYV-KFQDNPVGSQTF-SAGL-HLRVFDPSTGALV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SCHOENBOEKEN;
MEDLINE; 9135223.
SCHMITT J., KEIL G.M.;
"Identification and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70:1091-1099(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
                                                                                                                                                                                                                                                                         Query Match 13.5%;
Best Local Similarity 47.2%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 47.2%;
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M64815; G142890; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G1006630;
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                                               SEQUENCE FROM N.A.
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EMBL; X91751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
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                                                                                                                                                                                                                          SEQUENCE
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Q65581
Q65581;
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Matches
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RESULT

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"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                      NATÜRE 368:32-38(1994).
EMBL; Z83220; E1344511; -.
SEQUENCE 921 AA; 106698 MW;
                                                                                                                                                                                                                                                                                                    271 QI-VWDMASSGNVADGRESSF 290
                                                                                                                                                                                                                                                                                                                             :: | | :|:| : |:: :|
61 HLRVFD-PSTGALVDSKSYAF 80
                                                                                                                              13.0%; 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLOSTRIDIUM CELLULOLYTICUM
                                                                                                                                                                        20; Conservative
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Best Local Similarity 3
                                                                                                                              Query Match
Best Local Similarity
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STRAIN-ATCC 35319;
MEDLINE; 96218696.
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NON_TER
SEQUENCE
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049984
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Q45996
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WILSON R., AINSCOUGH R., CONNELL M., COPSET T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAM P., HAMKINSTEN J., LAISTER M., JOHNSTON L.,
LIGHTWING J., LLOYD C., MCMORRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPPAR A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONHAMMER E., STADEN R., WALERSTON R.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 IAESYLQQSFLSEDTYIR-KSAIIGA-GLSGSSEA-LELLSEAIETQDLYEQL-L-ILNA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FGGGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                                                                    STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITIOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequence of an Obligate Intracellular Pathogen of Humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89; DB 2; Length 566;
Pred. No. 9.10e-01;
25; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. AEO01308; G332871; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 566 AA: 63508 MW: C1A1C491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HARRIS B.;
SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                   08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                               CHLAMYDIA TRACHOMATIS.
BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 AA.
                                                               566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
                                                               PRT;
                                                                                                                                                                    HYPOTHETICAL 63.5 KD PROTEIN. CT350.
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05,
09,
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Local Similarity 26.2%;
les 17; Conservative
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01-JAN-1998 (TREMBLREL. 0
01-JAN-1999 (TREMBLREL. 0
C34B7. 2 PROTEIN.
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              trachomatis.";
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                                                                              084354;
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomati
SCIENCE 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                    STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-D/UW-3/CX;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 STGAL 72
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084354
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P90770
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BRASSICA OLERACEA (CAULIFLOWER).
BUKARYOTS, VITOLILANTE, STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACERE; BRASSICA.
                                                                                                                                                                  212 ERWFVEIVHGYVRQEYIFLPIG-RISLIIIGRRSTKYAGIRFLKRGANPIGNVANYVETE 270
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHĀRNG Y.Y., SUN C.W., YAN S.L., CHOU S.J., CHEN Y.R., YANG S.F., SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U87239; G2738025; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE; CLOSTRIDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAGES S., BELAICH A., TARDIF C., REVERBEL-LEROY C., GAUDIN C., BELAICH J.P.,
Interaction between the endoglucanase Cela and the scaffolding protein Cipc of the Clostridium cellulolyticum cellulosome.";
J. BACTERIOL. 178:2279-2286(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 IPHTCPLAKIGPPVGKFAPPEVVSVRVPL-LHLSNFQGSDWSDL-SGKGYAL
                                                         Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 35319;
PAGES S., BELAICH A., FIEROBE H.P., TARDIF C., GAUDIN C.,
                                                                                                            34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 045996;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SCAFFOLDING PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.9%; Score 88; DB 10; 36.5%; Pred. No. 1.24e+00;
                                                                               Pred. No. 9.10e-01;
21DE4C35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 AA; 19859 MW; D9B072C1 CRC32;
                                                         Score 89; DB 5;
                                                                                                               23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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01-JUN-1998 (TREMBLREL. 06, LAST SEQU
01-JUN-1998 (TREMBLREL. 06, LAST ANNO
01-JUN-1998 (TREMBLREL. 06, LAST ANNO
DUTATIVE ETHYLENE RECEPTOR (FRAGMENT)
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                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 35319;
STRAIN-ATCC 35319;
STRAINEL-LEROY C., TARDIF C., BELAICH A., BERNADAC A., GAUDIN C.,
BELAICH J.;
"Molecular study and overexpression of the Clostridium cellulolyticum celCF cellulase gene in Escherichia coli.";
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U40345; G3386344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 ADGYSNGDMFNSTWRADNVSMTSSGEMRLALTSPSYNKFDCGENRSVQTYGYGLYEVRM- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
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AC Q44677
AC Q44677
AC Q44677
DT OL-NOV-1996 (TREMBLREL. 01, CREATED)
DT OL-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT OL-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE NEUTRAL PROTEASE.
S BACILLUS AMYLOLIQUEFACIENS.
C BACIELUS.
C BACILLUS.
N [1]
BELAICH J.P.; Sequence analysis of scaffolding protein CipC and ORFXp a new scapesin-containing protein from C.cellulolyticum : comparison of various cohesin domains and subcellular localization of ORFXp."; SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                          Score 88; DB 2; Length 1546;
Pred. No. 1.24e+00;
17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87; DB 2; Length 239;
Pred. No. 1.69e+00;
26; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                             1061 AYDASL-LDVVSHAAGPIVKNRAVNFSSSASNGSISFL-FLDNTITD 1105
                                                                                                                                                                                                                                                                                                                                                                                                  STRAID-NCIB B565;
VAN RENSBURG P. VAN ZYL W.H., PRETORIUS I.S.;
VAN RENSBURG P. VAN ZYL W.H., PRETORIUS I.S.;
VAN BENSBURG P. VAN ZYL W.H., PRETORIUS I.S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U60830; G1480672; -
PROSITE: PSG10134; G1XCGSYL_HYDROL_F16; 1.
SPG0/ENCE 239 AA; 26969 MM; 8BD1DE7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 PRELIMINARY; PRT; 239 AA.
045691 045691 01.00V-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENDO-BETA-1, 3-1, 4-GLUCANASE.
                                                                                                                                                                                                                                           1 27 POTENTIAL.
28 1546 SCAFFOLDING PROTEIN.
1546 AA; 158629 MW; 7BBIlADF CRC32;
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.7%;
Best Local Similarity 22.9%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                               SEQUENCE
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SEQUENCE FROM N.A.

SHIMDA H., HONJO M., MITA I., NAKAYAMA A., AKAOKA A., MANABE K.,

FURUTANI Y.;

J. BIOTECHNOL. 2:75-85(1985).
                                                                                                                                                                                      240 ISSESGKYVLRDLSKPTGTQNNTYDLQNREYNLP-GTLVSSTTNQFTTSSQRAA 292
                                                                                                                                                                                                       ;
                                                                                                                             Score 86; DB 2; Length 521;
Pred. No. 2.30e+00;
18; Mismatches 19; Indels
                                                                                                  521 AA; 56725 MW; 64AFFE5F CRC32;
                                                                                                                                                                                                                                                      completed: Wed Sep 1 16:19:05 1999
ne : 26 secs.
                                                      EMBL; M36723; G143353; -. PFAM; PF00099; zn-protease; 1.
                                                                                                                             Query Match 12.6%;
Best Local Similarity 27.8%;
Matches 15; Conservative
                                                                                   PROTEASE.
SEQUENCE
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Job time
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:23:00 1999; MasPar time 4.06 Seconds 52.355 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (8-17) from PCTUS9913024.pep (8 of 12) 82 Title: Description: Perfect Score:

1 FGQGYVQTPF 10 Sequence:

170751 segs, 21266608 residues PAM 150 Gap 11 Searched:

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part13 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part39 31:part31 32:part32 33:part33 33:part39 39:part39

Mean 17.449; Variance 54.450; scale 0.320 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score Ma	tch	Match Length DB	DB	QI	Description	Pred. No.
3 6	4.6	30	80	R40072	Hib OMP P2 peptide OM	7.026+01
3	4.6	43	œ	R40095	OMP P1-	7.02e+01
3	4.6	341	-	R07043	ene	7.02e+01
9	9.	341	г	R07042	P3 gene product of Ha	7.02e+01
3 64	9:	342	13	R66880	H. influenzae protein	7.02e+01
3 64	9	342	13	R66879	H. influenzae protein	7.02e+01
3 64	9.	361	13	R66877	H. influenzae P2 enco	7.02e+01
3 64	9	361		R05999	P2 gene product of Ha	7.02e+01
3 64	9.	362	٦	P90098	P2 antigen of Haemoph	7.02e+01
3 64	۰.	363	13	R66878	pNV-2 fusion construc	7.02e+01
3 64	9	390	23	W21678	Haemophilus influenza	7.02e+01
1 62	62:12	196	17	R97616	Cephalosporin amidohy	1.13e+02
1 62	62.2	5069	30	W52846	A. mediterranei rifam	1.13e+02
0	0.1	613	32	W55964	Serratia marcescens S	1:43e+02
0	0.1	613	7	R36774	Serratia esterase.	1.43e+02
6	8.	211	38	W85101	Thyroid hormone recep	1.81e+02

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Gaps

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Score 53; DB 8; Length 30; Pred. No. 7.02e+01; 4; Mismatches 1; Indels

Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative

6 yaqgyletrf 15 ::|||::| |

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Thyroid hormone recep 1.81e+02 H. Pylori ORF O6ep106 1.81e+02 Helicobacter pylori 7 1.81e+02 Helicobacter pylori 7 1.81e+02 B. subtilis ECB deacy 1.81e+02 DNA polymerase which 1.81e+02 DNA polymerase which 2.28e+02 CFTR LIOTYP. 2.88e+02 Aprotinin. 2.88e+02 Aprotinin. 3.88e+02 Aprotinin and and and and and and and and and an	ALIGNMENTS R40072 standard; peptide; 30 AA. R40072 standard; peptide; 30 AA. R40072 standard; peptide; 30 AA. R40072; standard; peptide; 30 AA. R40072; standard; peptide; 30 AA. R40072; standard; peptide oMP2-2 (53-81). Hammophilus influenzae; type b; Hib; outer membrane protein; P1; P2; P6; vaccine; antibody; detection; lipoglycopeptide conjugate; Synthetic. Location/Oualifiers M99315205-A. M9
WYSSS WYSSS WYSSSSS WYSSSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSSS WYSS	ALIGNMENTS R40072 standard; peptide; 30 AA. R40072; G4-FEB-1994 (first entry) H1b OMP P2 peptide OMP2-2 (53-81). Haemophius influenzae; type b; H1b; on p6; vaccine; antibody; detection; liponimmunogen. Synthetic. Key M59315205-A. G0-AGG-1993. O3-FEB-1993; CAO041. O3-FEB-1992; GB-002219. (CONN') CONNAGOHT LAB LTD. Chong P. Kandil A, Klein MH, Sia C; WPI; 93-25681/32. Synthetic Haemophilus influenzae conjury princetic oligo:saccharide(s) T-helper cell determinants and B-cell synthetic oligo:saccharide(s) T-helper cell determinants and b-cell synthetic oligo:saccharide(s) T-helper cell determinants and b-cell fastence of the Haemophilus influenzae type b (H1b) P2 and P6. These peptides may be used infection and antibodies against these kits to detect H. Influenzae in a sample comprise a immunogenic or immunostimuling comprise a immunogenic or immunostimuling sequence is represented as it is given sequence is represented as it is given
3 3 3 8 8 8 8 9 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	man mellints and man mellints and man mellints are mades are mare mare mare mare mare mare mare
0621 0621 0625 0625 0625 0626 0626 0626 0626 0626	first entry; (first entry; (first entry) peptide OMP2-2; influenzae; t; influenzae; t; influenzae; t; cantibody; dei Location/(ence 30
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44444444444444444444444444444444444444	R40072 standard R40072; (4-FEB-1994 (f H1b OMP P2 Pept Haemophilus inf FEB-1994 (f FEB-1994 (f FEB-1994 (f FEB-1993); (5-FEB-1993); (1-FEB-1993); (1-FEB
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Gaps

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Length 341;

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W09315205-A

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immunogen. Synthetic.

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Production of Haemophilus influenzae HibP2 protein - for the prevention of bacterial meningitis in animals Claim 15; Figure 7; 63pp; English.

To clone P2 into expression vector pET-11a (Novagen pET System Manual) a 1.kb fragment from full length P2 (in pNV-1) (see Q84354) was generated using PCR and oligos Q85350 and Q84353.
Oligo Q85350 anilowed the mature P2 protein to be cloned into the Nder site of pET 11a. Q84353 incorporated a BamHI site. The P2 fragment thus generated was digested with NdeI and BamHI, purified and ligated into pET11a previously cut with NdeI-BamHI. This resulted in mature P2 construct - pNV-6. The rest of the plasmid is Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R66880;
22-AUG-1995 (first entry)
H. influenzae protein P2 encoded by pNV-6.
Haemophilus influenzae type b; outer membrane protein; P2; pNV-6.
Haemophilus influenzae type b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene coding for protein P2 of Haemophilus influenzae type-B used for developing vaccines for protection against disease caused by the organism.

Claim 1: Page 8: 15pp: English.

Peptide may be used as a vaccine to the disease caused by H1 type b, as carrier for conjugation to oligosaccharide derived from Haemophilus. Protein may be used with other haptens as Sequence 341 AA;
                                                                                                                                                                                                                                                       04-DEC-1990 (first entry)
P3 gene product of Haemophilus strain Durot (OMP subtype 2L).
P3 gene; strain 1H; Influenza; vaccine; ds.
Haemophilus influenze.
                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1989; 313573.
22-DEC-1988; GB-030124.
01-FEB-1989; GB-002178.
(CONN-) CONNAUGHT LAB LTD.
WHISON RS, Tolan RW, Chong P, Fahim R, Mcverry P, Klein M; WPL; 90-0225607/30.
N-PSDB; Q06119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 1; Length 341; Pred. No. 7.02e+01; 4; Mismatches 1; Indels
      Score 53; DB 1; L
Pred. No. 7.02e+01;
                                                4; Mismatches
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23-JUL-1994; U08326.
23-JUL-1993; US-096181.
(NAVA-) NORTH AMERICAN VACCINE INC.
Lang S. PULLED JK, SOPER TS, Tai JY;
WPI; 95-075024/10.
N-PSDB; Q84357.
                                                                                                                                                                                          T 4
R07042 standard; protein; 341 AA.
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R66880 standard; Protein; 342 AA.
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Similarity 50.0%;
5; Conservative
    64.6%;
50.0%;
                                              Conservative
  Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic oligo:saccharide(s)
Table 11; Page 59; 99pp; English.
The sequences given in R40053-101 are peptide fragments derived from the sequences given in R40053-101 are peptide fragments derived from F2 and P6. These peptides may be used in a vaccine against Hib infection and antibodies against these peptides may be used in test kits to detect H. influencae in a sample. The vaccine may further comprise a immunosenic or inked to synthetic PRP as synthetic lipoglycopeptide conjugates to produce alternative vaccines.
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04-FEB-1994 (first entry)
Hib OMP PI-P2 hybrid peptide 1P13-2P2.
Haemophilus influenzae: type b; Hib; outer membrane protein; P1;
P6; vaccine; antibody; detection; lipoglycopeptide conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chong P. Kandil A, Klein MH, Sia C;
WPI: 93-258681/32.
Synthetic Haemophilus influenzae conjugate vaccine - comprising T-helper cell determinants and B-cell epitope(s) linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Claim 1; Page 8; 15pp; English.

Peptide may be used as a vaccine to the disease caused by H1 type b, as carrier for conjugation to oligosaccharide derived from Haemophilus. Protein may be used with other haptens as T-cell dependant antigen and carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R07043:
04-DEC-1990 (first entry)
P3 gene product of Haemophilus strain 8358 (OMP subtype 6U).
P3 gene; strain 1H; influenza; vaccine; ds.
Haemophilus influenzae.
EP-378929-0.
22-DEC-1990.
23-DEC-1989; 313573.
01-EE-1989; GB-002178.
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MINSON RS. Tolan RW, Chong P, Fahim R, McVerry P, Klein M; WPI: 90-225607/30.
N-PSDB: Q06120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 8; Length 43; Pred. No. 7.02e+01; 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kandil A, Klein MH, Sia C;
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                           .T 2
R40095 standard; peptide; 43 AA.
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/label- CHIBP2
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/label= C-P1
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Best Local Similarity 50.0%;
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03-FEB-1993; CA0041.
03-FEB-1992; GB-002219.
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8 FGQGYVQTPF 17
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WPI; 89-174562/24
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                                                                                                                                                                                                         22-Aug-1995 (first entry)
H. influenzae protein P2 encoded by pNV-3.
Haemophilus influenzae type b; outer membrane protein; P2; pNV-3.
Haemophilus influenzae type b.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 13; Length 342;
Pred. No. 7.02e+01;
4; Mismatches 1; Indels
   Length 342;
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Linfluenzee P2 encoded by pNV-1 cDNA.
Haemophilus influenzae type b; outer membrane protein; P2.
Haemophilus influenzae type b.
Score 53; DB 13; Length 342 Pred. No. 7.02e+01; ' 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                 (NAVA-) NORTH AMERICAN VACCINE INC.
Liang S, Pullen JK, Soper TS, Tai JY;
WPI; 95-075024/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tai JY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1994; U08326.
23-JUL-1993; US-096181.
(NAVA-) NORTH AMERICAN VACCINE INC.
Liang S, Pullen JK, Soper TS, Ta
WPI: 95-075024/10.
                                                                                                                                                          T
R66879 standard; Protein; 342 AA.
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64.6%;
larity 50.0%;
Conservative
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larity 50.0%;
Conservative
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22-JUL-1994; UO8326.
23-JUL-1993; US-096181.
 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                   59 yaqgyletrf 68
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Best Local :
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oligo (084348) was designed to be 40 bp 5' of the ATG start codon. The 3' oligo (08449) was designed to be 300 bp 3' of the stop codon. Both oligos contd. Sall restriction sites. The amplified DNA was used to transform E.coli and the resulting colonies isolated an analysed. Clones contg. a 1.4 kb fragment were chosen for DNA sequence analysis. One clone, designated pNv-1, was found to be identical to the published sequence for Hib strain Minn A (Munson, R. and Tolan, R.W. Infection & Immunity 57:88-94, Jan. 1989). The synthetic oligos used to sequence the DNA are indicated in the FT. The direction of sequencing was 5'-3'. The rest of pNv-1 is identical to pUCI8. The lac promotor is adjacent to the lower
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Claim 1, Page 8; 15pp; English.

Peptide may be used as a vaccine to the disease caused by H1 type b, as carrier for conjugation to oligosaccharide derived from Haemophilus. Protein may be used with other haptens as T-cell dependant antigen and carrier.
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Pred. No. 7.02e+01;
4; Mismatches 1; Indels
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N-PSDB; Q05372.
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Haemophilus influenzae P2 antigen; vaccines; pathogenic
type b strains.
Haemophilus influenzae type b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P2 gene product of Haemophilus strain 1H. P2 gene; strain 1H; influenza; vaccine; ds. Haemophilus influenzae. EP-378929-A. 25-JUL-1990. 22-DEC-1989; GB-030124. 01-FEB-1989; GB-030178. (CONN-) CONNAUGHT LAB LID.
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R05999 standard; protein; 361 AA.
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llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.6%;
Best Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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1-NOV-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 AA;
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Best Local Similarity
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vaccine; immunogen; respiratory disease.
Haemophilus influenzae strain 1479.
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15-NOV-1995; E04487.
17-NOV-1994; GB-023212.
(GLAX ) GLAXO GROUP LID.
                                                                                                                                                                                                                                                                                                                                                             US-740644.
US-006168.
                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996; U17698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 FGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                               WO9716207-A1.
                                                                                                                                                                                                                                                                                                                                                             31-OCT-1996;
02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                  09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
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Matches
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Wo9503069-A.

WO9503069-A.

O2-FEB-1993: US-095181.

PE 22-JUL-1994: UNRITH AMERICAN VACCINE INC.

Liang S. Pullen JK, Soper TS, Tai JY;

WPI: 95-075024/10.

N N-PSDB: O84355.

Production of Haemphilus influenzae HibP2 protein - for the prevention of bacterial meningitis in animals.

Production of Haemphilus influenzae HibP2 protein - for the prevention of bacterial meningitis in animals.

Production of Haemphilus influenzae HibP2 protein - for the prevention of bacterial meningitis in animals.

Production of Haemphilus influenzae type be (hib-P2) with 22 Aas of gene 10 of prevention of bacterial meningitis in animals.

Production of Haemphilus influenzae type be (hib-P2) with 22 Aas of gene 10 of phage T7 at the N-terminus that were derived from the pET-17b captesion vector (Novagen pET System Manual). To P2 into observed to print to phage T7 at the nature porint to be cloned into the BamHI site of peT-17b, thus yielding a fusion protein P2 to gene 10. The sequence of this oligo was Q84351. The extraneous 3' sequences were aliminated by introducing Ahol site about 10 protein to the Iranslation stop codon. This oligo (Q84352) contd. an Xhol site to allow it to be cloned into the Xhol site of pET-17b. PCR was used to generate a liminated by introducing Xhol site of peT-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminated by introducing Ahol site of per-17b. PCR was used to generate a liminate Animated Ahol site and the 3' ollgo contg. the BamHI site and the 3' ollgo contg. the Ahol site and the 3' ollgo contg. the Ahol site of per-17b. PCR was used to generate a limit to the BamHI site and will site and will site and will site and will site and wil
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                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1995 (first entry)
WYV-2 fusion construct of H. influenzae P2 with T7 gene 10 protein. Haemophilus influenzae type b; outer membrane protein; P2; pNV-2; fusion protein; fusion P-2; gene 10; major capsid protein; T7.
             used for producing immunogenic compsns. as vaccines and in diagnostic hybridisation assays.
Disclosure: fig 6: 20pp; English.
P2 antigen of Haemophilus influenzae (see corresp. N90033).
Isolated from type b strains, the P2 antigens are used as vaccines and to detect P2-specific RNA or DNA. Segments used as antigens and to detect p2-specific RNA or DNA. Segments used or antigens or their functional equivalents.
Sequence 362 AA;
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30-SEP-1997 (first entry)
Haemophilus influenzae outer membrane protein P2.
Fusion protein; protein dellvery; outer membrane protein P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 13; Length 363;
Pred. No. 7.02e+01;
4; Mismatches 1; Indels
                                                                                                                                                                              Length 362;
                                                                                                                                                                                                             1; Indels
                                                                                                                                                                             Score 53; DB 1; Le
Pred. No. 7.02e+01;
4; Mismatches 1;
DNA encoding Haemophilus influenzae P2 antigen
                                                                                                                                                                                                                                                                                                             LT 10
R66878 standard; Protein; 363 AA.
R66878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W21678 standard; Protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.6%;
similarity 50.0%;
5; Conservative
                                                                                                                                                                           64.6%;
Similarity 50.0%;
5; Conservative
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                            79 yaqgyletrf 88
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                                                                                                                                                                                                                                                                           8 FGGGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 AA;
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New recombinant DNA for producing fusion proteins - comprising microbial pathogen epitope inserted into Haemophilus influenzae P2 microbial pathogen epitope inserted into Haemophilus influenzae P2 protein loop 5, used in vaccine memorane in Page 40-43; 54pp. English.

Example 1: Page 40-43; 54pp. English.

The loop 5 portion of Haemophilus influenzae strain 1479 outer common protein P2 (W131678) provides a structure suitable for fusion with, and display of, one or more heterologous or homologous peptide sequences. A method is provided for producing a fusion protein comprising a P2 protein in which loop 5, or a portion of it, displays a heterologous or homologous peptide sequence which antigenically minics an epitope from a microbial pathogen. The cantigenically minics an epitope from a microbial pathogen. The exposed sequence) and used as an immunoapen against disease caused by H. Influenzae and/or the microbial pathogen. It is esp. used to treat infection by respiratory pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One-step conversion of cephalosporin C into 7-amino:cephalosporanic acid - allows environmentally friendly production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Slade A, Spence D W;
WPI; 96-268610/27.
N-PSDB; T29215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 23; Length 390;
Pred. No. 7.02e+01;
4; Mismatches 1; Indels
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Cephalosporin amidohydrolase.
Cephalosporin amidohydrolase; cephalosporin C; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-aminocephalosporanic acid; gac gene.
Pseudomonas vesicularis strain B965.
W09616174-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY ) UNIV NEW YORK STATE RES FOUND.
KYUNGYENOL Y, TIMOTHY FM;
WPI: 97-271883/24.
N-PSDB: T72476.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R97616 standard; Protein; 796 AA. R97616;
                                                                                                                                                    115..133
/label- Loop-3
155..175
/label- Loop-4
                                                                                     69..85
/label- Loop-2
                                                                                                                                                                                                                                                                              203..248
/label- Loop-5
                                                                                                                                                                                                                                                                                                                                                                                                           303..315
/label- Loop-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331..364
/label= Loop-8
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                                                           /label- Loop-1
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Similarity 50.0%;
5; Conservative
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21-AUG-1998 (first entry)
Serratia marcescens SR41 esterase sequence.
Serratia marcescens mutant M-1; FERM BP-4068; esterase;
S marcescens Sr41; FERM BP-467; higher productivity.
                                                                                                                                                           Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R36774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Warcolatopsis mediterranei rifamycin synthesis gene cluster - used
to produce rifamycin and rifamycin analogues
claim 6: Page 126-15: 205pp; English
claim 7: Page 126-15: 205pp; Page 126-15: 205pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. mediterranel rifamycin synthesis gene cluster fragment protein B. Amycolatopsis mediterranel: rifamycin; synthesis; gene cluster; polyketide synthase; actinomycete; ansamycin. Amycolatopsis mediterranel. WQ9807868-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             A cephalosporin anidohydrolase (R97616) was identified as the product of the gac gene (T29215) of Pseudomonas vesicularis strain B965. The enzyme is capable of converting cephalosporin C and its derivatives to 7-aminocephalosporanic acid and its derivatives, building blocks of semisynthetic cephalosporin antibiotics. The method is cheap, involves simple technology and is environmentally safe. The enzyme is obtd. by incorporation of the gac gene into a vector and expression in e.g. Escherichia coli. Sequence 796 AA;
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0
7-amino:cephalosporanic acid for prod. of cephalosporin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 17; Length 796; Pred. No. 1.13e+02;
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                                                          Disclosure; Page 32-36; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W52846 standard; Protein; 5069 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVS ) NOVARTIS AG.
Engel N, Schupp T, Toupet C;
WPI; 98-169172/15.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.2%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 100.0%;
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20-AUG-1996; EP-810551.
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OT ALSO

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LT 14 W55964 standard; Protein; 613 AA.

RESULT Ω

3455 fgggyv 3460

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FGQGYV 13

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                                                                                                                                                                                                              Serratia marcescens mutant M-1 - with high esterase productivity Example 3; Pages 10-13; 15pp; English.

The present sequence represents an esterase of Serratia marcescens. A S.marcescens mutant was produced and designated M-1 (FERM BP-4068). The M-1 mutant is obtained by treating S. marcescens Sr41 (FERM BP-467) with N-methyl-N'-nitro-N-nitrosoguandine. The M-1 mutant has a two fold higher productivity of esterase than the wild type organism. The mutant is used for producing M-1 esterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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N-FSEBS 17,0437, 042858.

New genes encoding esterase from Serratia - are contained in recombinant vectors and transformed cells with high esterase productivity, useful as hydrolytic reagent

Disclosure; Page 11-13; 16pp; English.

N-Methyl-N'-nitro-Noultrosoguandine and mutants selected on tributyrin medium, the mutant MI was identified. MI contains an allelic variant of C -> T at position 9. MI has 2.5 times greater esterase prod. than Sr41. The esterase is useful for carrying out hydrolytic reactions.

Sequence 613 AA;
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Pred. No. 1.43e+02;
1; Mismatches 3; Indels
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Pred. No. 1.43e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komatsubara S, Omori K, Shibatani T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sr41; M1; mutation; allele; variation; hydrolysis.
Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Wed Sep 1 16:23:25 1999 Job time: 25 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 15
R36774 standard; Protein; 613 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.0%;
60.0%;
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60.0%;
                                             25-NOV-1992; 120078.
13-APR-1992; JP-137502.
25-NOV-1991; JP-355440.
(TANA ) TANABE SEIYAKU CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANA ) TANABE SELYAKU CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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25-NOV-1991; JP-355440.
13-APR-1992; JP-137502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 fdegyhqtgf 45
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Best Local Similarity
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8 FGQGYVOTPF 17
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                                                                                                                                                                      WPI; 98-219117/20
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EP-837135-A2.
                           22-APR-1998.
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                                                                                                                                                  Shibatani
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:22:24 1999; MasPar time 5.25 Seconds 76.309 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (8-17) from PCTUS9913024.pep (8 of 12) 82 1 FGGGYVQTPF 10 Title: Description: Perfect Score: Sequence:

122810 seqs, 40068593 residues Searched:

PAM 150 Gap 11

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 24.385; Variance 32,736; scale 0.745 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES			
Result	9	Query	4	2	ţ		•	
. o	score	Match	Match Length	a :	di 	Description	Pred. No.	
~	57	69.5	262	~	S64050	hypothetical protein	1.13e+00	
7	55	67.1	509	~	C69491	probable acidCoA 11	2.77e+00	
m	55	67.1	1036	_	A34755	nitrogen regulatory p	2.77e+00	
4	54	65.9	547	7	A43832	heme-binding protein	4 300+00	
Ŋ	54	62.9	549	7	D64098	heme-binding protein	4.30e+00	
9	53	64.6	359	7	D64050	major outer membrane	6.66e+00	
7	53	64.6	361	7	A30542	major outer membrane	6.66e+00	
œ		64.6	371	~	S68072	or	6.66e+00	
6		٠	371	~	868069	major outer membrane	6.66e+00	
10	53		392	~	C69672	probable aspartate tr	6.66e+00	
11		64.6	936	~	B64567	cytochrome c blogenes	6.66e+00	
12		9.49	936	~	H71862	probable cytochrome C	6.66e+00	
13	52	63.4	9	~	JN0741	hypothetical 6.6K pro	1.02e+01	
14	52	63.4		Н	A24994	cellulose 1,4-beta-ce	1.02e+01	
15		63.4		7	A44766	defective chorion-1 f	1.02e+01	
16	51	62.2	340	7	G70432	conserved hypothetica	1.57e+01	
17	51	62.2	743	~	S19437	hypothetical protein	1.57e+01	
18	51	62.2	822	7	S26872		ä	
19	51	62.2	830	-	RNEGB2	RNA	H	
20	51	62.2	2301	7	T02323	hypothetical protein	1.57e+01	
21	20	61.0	234	7	F64595	membrane fusion prote	2.38e+01	
22	20	61.0	234	7	G71918	probable efflux trans	2.38e+01	
23	20	61.0	489	7	C64984	lysine-specific perme	2.38e+01	

	reversed polarity pro 2.38e+01 triacy1glycerol lipas 2.38e+01 hypothetical protein 3.60e+01 hypothetical protein 3.60e+01 hypothetical protein 3.60e+01	3.60e+ 3.60e+ 3.60e+	3.60e+	3.60e+ 3.60e+	1.60e+	.41e+	41e+	.41e+	41e+	.41e+	.41e+	YTS	ete GLO46w - yeast (Saccharomyces	335 ses cerevisiae svision 17-May-1996 #text_c		S.; Souciet, J.L. in Sequence Database, May 1996	ID:91322534; PID:e243943; PID:91322535	U	r-weight 29440 #checksum 290	57; DB 2; Length 262; No. 1.13e+00; ismatches 2; Indels 0; Gaps 0;			te ise (EC 6.2.1) fadD8 - Archaeoglobus	obus fulgidus evision 05-Dec-1997 #text_change		0 - 14	C.I.; McNeil, L.K.; Badger, J.H.;
	A54282 JS0763 T00728 PC1139	E71039 864610 E64610	871904 E71904	A43734 A57177	JC1298	577548	F64389	A26483	570844	104910	446112	ALIGNMENT	ap)	6 6 9		er, ote	Sel FEU	288	molecular	Score 5 Pred. N 2; Mi			comple comple	thaeoglo		Ayton, F K.A.; Richa, N.C.; N.C.; tton, G.	Reich,
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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, Sjournal Nature (1997) 390:364-370

*title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.
                                                                                                                                                                                                                                    ##molecule_type DNA
##residues 1-509 ##label KLE
##cross-references GB:AE000970; GB:AE000782; NID:g2689293; PID:g2648612;
FFICATION #superfamily acetate--COA ligase homology
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heme-binding protein A precursor - Haemophilus influenzae
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Mol. Cell. Biol. (1990) 10:1056-1065
nit-2, the major nitrogen regulatory gene of Neurospora
crassa, encodes a protein with a putative zinc finger
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#region zinc finger GATA motif
#length 1036 #molecular-weight 109295 #checksum 235
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##residues 1-1036 ##label FUY
##cross-references GB:M33956
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#cross-references MUID:90158568
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Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
KIrkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:465-512
Whole-genome random sequencing and assembly of Haemophilus
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#product heme-binding protein A #status predicted #label
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                                                                                                                                           #authors Hanson, M.S.; Slaughter, C.; Hansen, E.J.
#journal Infect. Immun. (1992) 60:2257-2266
#title The hbpA gene of Haemophilus influenzae type b encodes a
heme-binding lipoprotein conserved among heme-dependent
Haemophilus species.
#cross-references MUID:92267636
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##cross-references GB:M88134
##note extracted
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Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Budgherty, B.A.; Merrick, J.W.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hebblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
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#journal Infect. Immun. (1989) 57:88-94
#title Molecular cloning, expression, and primary sequence of outer membrane protein P2 of Haemophilus influenzae type b.
#cross-references MuID:89079316
#accession A30542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-359 ##label TIGR
##ross-references GB:U32699; GB:L42023; NID:g1573084; PID:g1573092;
TIGR:HI0139
                                                                                                                                                                                                                                    D64050 #type complete
major outer membrane protein P2 - Haemophilus influenzae
(strain Rd KW20)
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major outer membrane protein P2 precursor - Haemophilus
influenzae (type b)
#formal_name Haemophilus influenzae
07-Sep-1990 *sequence_revision 07-Sep-1990 *text_change
                                                                                           Gaps
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18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
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#length 549 #molecular-weight 60904 #checksum 3028
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#length 359 #molecular-weight 39375 #checksum 1781
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                                           Score 54; DB 2; Leury-Pred. No. 4.30e+00; Pred. No. 4.30e+00; Indels
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                                                   65.9%;
Similarity 85.7%;
6; Conservative
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Best Local Similarity 50.0%;
Matches 5; Conservative
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##residues 1-3
                                                     Query Match
Best Local Similarity
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#authors Hansen, E.J.; Pelzel, S.E.; Orth, K.; Moomaw, C.R.; Radolf,
J.D.; Slaughter, C.A.
#journal Infect. Immun. (1989) 57:3270-3275
#title Structural and antigenic conservation of the P2 porin protein
among strains of Haemophilus influenzae type b.
#cross-references MUID:90035390
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Mol. Microbiol. (1989) 3:1797-1803
Diversity of the outer membrane protein P2 gene from major clones of Haemophilus influenzae type b.
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#product major outer membrane protein P2 #status
experimental #label MAT
#length 361 #molecular-weight 39701 #checksum 4550
mature protein, was confirmed by protein sequencing
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Cossion A60116

**Cession A60116

**Monlecule_type protein

**Eresidues 21-42 **label HA2

**Eresidues 21-42 **label HA2

**Experimental_source type b, strains DL42, CH100, DL26, DV102, H234,

**Madigan, OA104, and SL103

***Norgard,
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M.V.; Miller, E.E.; Cope, L.D.; Pelzel, S.E.; Gaddy, B.;
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major outer membrane protein P2, antigenic variant tl -
Haemophilus influenzae
fformal_name Haemophilus influenzae
19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change
                                                                                                                   Infect. Immun. (1989) 57:1100-1107
Primary structure of the porin protein of Haemophilus
Influenzae type b determined by nucleotide sequence
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Pred. No. 6.66e+00;
4; Mismatches 1; Indels
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##residues 21-40 ##label HA3
##experimental_source type b, strain DL42
ENCE S09622
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Best Local Similarity 50.0%;
Matches 5; Conservative
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##cross-references EMBL:X73386; NID:g510590; PID:g510591
##cross-references EMBL:X73386; NID:g510590; PID:g510591
##cross-references EMBL:X73386; NID:g510590; PID:g510591
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#title Antigenic drift of non-encapsulated Haemophilus influenzae major outer membrane protein P2 in patients with chronic bronchiis is caused by point mutations.
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##experimental_source isolate t2
RDS membrane protein
XY #length 371 #molecular-weight 40945 #checksum 5124
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                                                                                        Duim, B. submitted to the EMBL Data Library, June 1993 S68072
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Pred. No. 6.66e+00;
...matches 1; Indels
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Dulm, B.
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##molecule_type DNA
##residues 174-188;215-234;257-283 ##label DUW
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August, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotlin, A.; Brochert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Borouillet, S.;
Bruschl, C.V.; Caldwell, B.; Capuano, V.; Carter N.W.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fuljta,
M.; Fuljta, Y.; Fume, S.; Galizzi, A.; Galderon, N.; Ghis,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Klaerr-Banchard, M.; Knoph, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medique, C.; Medina, N.; Mellado, R.B.; Mizuno,
M.; Neynolds, S.; Rieger, M.; Nivolla, C.; Rochay, E.;
Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Vasarotti, A.; Vasumoto,
Winters, P.; Winter, A.; Vasarotti, A.; Takaa, K.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.;
Winterbol, M.; Vashikawa, H.F.; Zumstein, E.;
Winterbold, M.; Va
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The complete genome sequence of the Gram-positive bacterium
Bacillus subtilis.
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#journal J. Bacteriol. (1989) 171:6187-6196
#title Characterization of the gene for a protein kinase which phosphorylates the sporulation-regulatory proteins spoolA #cross-references MUD:90036708
#accession C33496
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##molecule_type DNA
##residues 1-392 ##label KUN
##cross-references GB:299111; GB:AL009126; NID:92633699; PID:e1184990;
##cross-references PID:92633771
                                                                                                                                                                                                                                                                                       #formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                     probable aspartate transaminase (EC 2.6.1..) - Bacillus
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C69672; C33496
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S FGOGYVOTPF 17
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cytochrome c blogenesis protein - Helicobacter pylori (strain
26695)
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TIGR:HP0378
:Y #length 936 #molecular-weight 106359 #checksum 8931
                                                                                                                                                                                                                                                                                                                                                                                                                           Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
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probable cytochrome C-type biogenesis protein - Helicobacter
pylori (strain J99)
#formal_name Helicobacter pylori
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                                                                                                                                             Gaps
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09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
10-Oct-1997
B64567
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12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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#title The complete genome sequence of the gastric pathogen #accession B64567
                                                                   #length 392 #molecular-weight 43448 #checksum 5874
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Pred. No. 6.66e+00;
3; Mismatches 2; Indels
                                                                                                    Score 53; DB 2; Length 392;
Pred. No. 6.66e+00;
4; Mismatches 1; Indels
                                 *superfamily aspartate transaminase aminotransferase
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Similarity 50.0%;
5; Conservative
                                                                                                      64.6%;
Similarity 50.0%;
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Best Local Similarity
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O'Neill, G.; Goh, S.H.; Warren, R.A.J.; Kilburn, D.G.; Miller
Jr., R.C.
Gene (1986) 44:325-330
                                                                                                                                        ##residues 1-336 ##label ARN ##cross references GB:AE001528; GB:AE001439; NID:g4155575; PID:g4155589 ##experimental_source strain J99
#journal Nature (1999) 397:176-180
#title Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
#cross-references MUID:99120557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title Sequence analysis of the left end of the Bacillus subtilis
bacteriophage SPP1 genome.
#cross-references MUID:93328123
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JN0729
Graf, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso,
J.C.
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hypothetical 6.6K protein · phage SPP1
hypothetical protein 50
#formal_name phage SPP1
03-Feb-1994 *sequence_revision 03-Feb-1994 *text_change
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#length 936 #molecular-weight 106452 #checksum 7770
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Pred. No. 6.66e+00;
3; Mismatches 2; Indels
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Pred. No. 1.02e+01;
2; Mismatches 3; Indels
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X #length 60 #molecular-weight 6692 #checksun
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##residues 1-60 ##label CHA
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50.0%;
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50.0%;
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                                                                                                                                 ##molecule_type DNA
##residues 1-9
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                     222 FGSAYIELPF 231
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8 FGQGYVQTPF 17
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*superfamily Cellulomonas cellulose 1,4-beta-cellobiosidase A: bacterial cellulose-binding domain homology; Streptomyces endo-1,4-beta-xylanase A homology extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide degradation; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
the amino-terminal sequence of the mature protein (residues 42-71) has been determined (M.L. Langsford, unpublished data)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waring, G.L.; Hawley, R.J.; Schoenfeld, T.
Dev. Biol. (1990) 142:1-12
Multiple proteins are produced from the dec-1 eggshell gene
in Drosophila by alternative RNA splicing and proteolytic
cleavage events.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain Streptomyces endo-1,4-beta-xylanase A homology #1abel SXY, #1abel SXY # region 7-residue repeats (P-T-P-T-[S/T])\ #domain bacterial cellulose-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrolyses 1,4-beta-D-glucosidic linkages in cellulose and releasing cellobiose from the non-reducing ends of the
                                                                                                                        annotation: X-ray crystallography, 1.8 angstroms, residues 42-173,'G',175,'RR'178-353
                                                                                                                                                                                                                       White, A.; Withers, S.G.; Gilkes, N.R.; Rose, D.R. Biochemistry (1994) 33:12546-12552 Crystal structure of the catalytic domain of the beta-1, 4-glycanase Cex from Cellulomonas fimi. annotation; X-ray crystallography, 1.8 angstroms, residues 42-173, 'G', 175, 'RR'178-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#product cellulose 1,4-beta-cellobiosidase #status
experimental #label MAT\
                                                               #authors White, A.; Withers, S.G.; Gilkes, N.R.; Rose, D.R. #submission submitted to the Brookhaven Protein Data Bank, July 1994 #cross-references PDB:2EXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *binding_site carbohydrate (Asn) (covalent) #status
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#formal_name Drosophila melanogaster
#formal_name Drosophila melanogaster
03-mar-1993 #sequence_revision 03-mar-1993 #text_change
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#active_site Glu *status experimental\
#disulfide_bonds *status experimental\
#disulfide_bonds *status predicted
#length 484  #molecular-weight 51291  #checksum 9660
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##molecule_type mRNA
1-1123 ##label WAR
##cross-references GB:M35887; NID:q157181; PID:q157182
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Pred. No. 1.02e+01;
4; Mismatches 1,
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Best Local Similarity 50.0%;
Matches 5; Conservative
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#title
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                          ##cross-references FlyBase:FBgn0000427
# #length 1123 #molecular-weight 127959 #checksum
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                                                                      Length 1123;
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                                                                      Score 52; DB 2; Len
Pred. No. 1.02e+01;
3; Mismatches 2;
                                                                      Query Match 63.4%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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8 FGQGYVQTPF 17
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 3.79 Seconds 74.682 Million cell updates/sec Wed Sep 1 16:20:53 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (8-17) from PCTUS9913024.pep (8 of 12) 82 1 FGGGVQTPF 10 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 24.996; Variance 29.785; scale 0.839

Statistics:

	Pred No.		3.49e-01	9.37e-01	1.52e+00	2.46e+00	2.46e+00	2.46e+00	2.46e+00	3.94e+00	3.94e+00	6.29e+00	6.29e+00	6.29e+00	9.95e+00	1.56e+01	2.44e+01	2.44e+01							
	Description		HYPOTHETICAL 29.4 KD P	NITROGEN CATABOLIC ENZ	HEME-BINDING PROTEIN A	OUTER MEMBRANE PROTEIN		OUTER MEMBRANE PROTEIN	PUTATIVE AMINOTRANSFER	EXOGLUCANASE PRECURSOR	DEFECTIVE CHORION-1 FC	60S RIBOSOMAL PROTEIN	HYPOTHETICAL 84.9 KD P	DNA-DIRECTED RNA POLYM	LYSINE-SPECIFIC PERMEA	THYROID RECEPTOR INTER	ESTRADIOL 17 BETA-DEHY	G2-SPECIFIC PROTEIN KI	ENDOGLUCANASE F PRECUR	G2-SPECIFIC PROTEIN KI	ACULEACIN A ACYLASE PR	DNA POLYMERASE I (EC 2	DNA POLYMERASE I (EC 2	ESTRADIOL 17 BETA-DEHY	HYPOTHETICAL PROTEIN M
SUMMARIES	ID		YGE6_YEAST	NIT2_NEUCR	HBPA_HAEIN	OM21_HAEIN	OM22_HAEIN	OM25_HAEIN	PATA_BACSU	GUX_CELFI	DC11_DROME	RL3_DROME	YCR6_YEAST	RPOD_EUGGR	LYSP_ECOLI	TR10_HUMAN	DHB2_MOUSE	NIMA_EMENI	GUNF_CLOCE	NIM1_NEUCR	AAC_ACTUT	DPO1_HAEIN	DPO1_CHLAU	DHB2_RAT	Y718_METJA
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of	Query Match		69.5	67.1	62.9	64.6	64.6	64.6	64.6	63.4	63.4	62.2	62.2	62.2	61.0	59.8	59.8	59.8	59.8	59.8	59.8	59.8	59.8	58.5	58.5
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                     FU Y - H., MARZLUF G.A.;
FU Y - H., MARZLUF G.A.;
FU Y - H., MARZLUF G.A.;
FI Y - H., MARZLUF G.A.;
Site-directed mutagenesis of the 'zinc finger' DNA-binding domain of the nitrogen-regulatory protein NIT2 of Neurospora.";
MOL. MICROBIOL. 4:1847-1852(1990).
- I- FUNCTION: MAJOR NITROGEN REGULATORY PROTEIN. DURING CONDITIONS OF NITROGEN LIMITATION IT TUNNS ON THE EXPRESSION OF GENES FOR ENZYMES WHICH ARE REQUIRED FOR THE USE OF A VARIETY OF SECONDARY NITROGEN SOURCES, INCLUDING NITRATES, PURINES, AMINO ACIDS, AND
                                                                                                         FU Y.-H., MARZLUF G.A.;
"nit.2, the major nitrogen regulatory gene of Neurospora crassa,
encodes a protein with a putative zinc finger DNA-binding domain.";
MOL. CELL. BIOL. 10:1055-1065(1990).
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                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR.
INDUCTION: BY LACK OF A PRIMARY NITROGEN SOURCE.
SIMILARITY: HIGH TO OTHER FUNGAL NITROGEN REGULATORY PROTEINS.
SIMILARITY: TO GATA TRANSCRIPTION FACTORS IN THE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; ZINC-FINGER; NUCLEAR PROTEIN; NITRATE ASSIMILATION; REPEAT.

3 X APPROXIMATE REPEATS.
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RR->GG: ABOLISH DNA-BINDING.
                                         EUKARYOTA; FUNCI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES; SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1036;
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GL->DV: ABOLISH DNA-BINDING.
KR->NS: ABOLISH DNA-BINDING.
W: CCDE5BEB CRC32;
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) NITROGEN CATABOLIC ENZYME REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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PROSYTE; PSO0344; GATA_ZN_FINGER; 1.
PFAM; PF00320; GATA; 1.
HSSP; P17429; SGAT.
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P33950;
01-FEB-1994 (REL. 28, CREATED)
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66.7%;
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                                NEUROSPORA CRASSA.
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FGQGYVQTP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T00627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743
755
765
768
789
                                                                                                                                                              MUTAGENESIS
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ZN_FING
MUTAGEN
MUTAGEN
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MUTAGEN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HANSON M.S., HANSEN E.J.;
"Molecular cloning, partial purification, and characterization of a haemin-binding lipoprotein from Haemophilus influenzae type b.";
MOL. MICROBIOL. 5:267-278(1991).
-I- FUNCTION: IMPORTANT ROLE IN HEME ACQUISITION OR METABOLISM.
-I- SUBCELLULAR LOCATION: ATTACHED TO THE INNER MEMBRANE BY A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELIGEMENT R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERIGCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LUI L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                              HANSON M.S., SLAUGHTER C., HANSEN E.J.;
"The hbpA gene of Haemophilus influenzae type b encodes a
heme-binding lipoprotein conserved among heme-dependent Haemophilus
                                                                                                                                                 BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HEME-BINDING PROTEIN A PRECURSOR (HEMIN-BINDING LIPOPROTEIN).
HBPA OR DPPA OR H10853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEME-BINDING PROTEIN A.
N-ACYL DIGLYCERIDE (PROBABLE).
KA -> NS (IN STRAIN DL42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> N (IN STRAIN DL42)
-> N (IN STRAIN DL42)
-> I (IN STRAIN DL42).
-> V (IN STRAIN DL42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSSIBLE FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-DL42 / SEROTYPE B;
MEDLINE; 92267636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5220E11D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INNER MEMBRANE; SIGNAL; LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01040; SBP_BACTERIAL_5;
PFAM; PF00496; SBP_bac_5; 1.
HSSP; P23847; 1DPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFECT. IMMUN. 60:2257-2266(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M88134; G148941; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DL42 / SEROTYPE B; MEDLINE; 91251755.
                                                                                                           HAEMOPHILUS INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN FAMILY 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VENTER J.C.;
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PCT-US99-13024-2-08.rsp

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SACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
FAEMOPHILUS.
                                   SEQUENCE FROM N.A.
STRAIN-SEROTYPE B;
MEDLINE; 89079316.
                                                                                                                                            SEQUENCE FROM N.A. STRAIN-SEROTYPE B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 FGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 YAQGYLETRF 87
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P46027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCIENCE 269:496-512(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIMILARITY: TO PHOTOBACTERIUM STRAIN SS9 OMPH.
                                                                                                                                                                                                                                                                                                  STRAIN-RD / KW20;
MEDLINE; 95350630
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FREISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M.,
MCKENNEY R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.E., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                      Gaps
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                                                                                                                                                                                                                                 HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
          Score 54; DB 1; Length 547;
Pred. No. 1.52e+00;
1; Mismatches 0; Indels
                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53; DB 1; Length 359;
Pred. No. 2.46e+00;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
OUTER MEMBRANE PROTEIN P2.
40615FB6 CRC32;
                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
0UTER MEMBRANE PROTEIN P2 PRECURSOR (OMP P2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; H10139; -.
OUTER MEMBRANE; TRANSMEMBRANE; PORIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM22_HAEIN STANDARD; PRT; 361 AA. P20149; 01-FEB-1991 (REL. 17, CREATED) (REL. 17, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) OUTER MEMBRANE PROTEIN P2 PRECURSOR (OMP P2).
                                                                                                                                          359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39375 MW;
         65.9%;
llarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.6%;
Similarity 50.0%;
5; Conservative
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                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                       Local Similarity
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 FGGGYVQTPF 17
                                                             528 GYVQSPF 534
                                                                                                                                                                                                                     OMPP2 OR HI0139.
                                                                                      11 GYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                    VENTER J.C.;
                                                                                                                                                                                                                                                             HAEMOPHILUS
                                                                                                                                        OM21_HAEIN
P43839;
            Query Match
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                                    Matches
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                                                                                                                                                                                    MEDLINE; 90158127.

MUNSON R.S. JR., BAILEY C., GRASS S.;

MUNSON R.S. JR., BAILEY C., GRASS S.;

Diversity of the outer membrane protein P2 gene from major clones of Haemophilus influenzae type b.";

MOL. MICROBIOL. 3:1797-1803(1989).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-SEROTYPE B;
MEDLINE; 89173105.

MODIAN C., CLAUSELL A., CAPRA J.D., ORTH K.,
MOOMAN C.R., SLAGGHTER C.A., LATIMER J.L., MILLER E.E.;

Primary structure of the porin protein of Haemophilus influenzae
type b determined by nucleotide sequence analysis.";

INFECT. IMMUN. 57:1100-1107(1989).

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.

-1- SIMILARITY: TO PHOTOBACTERIUM STRAIN SS9 OMPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN-T1, AND T2;
MEDLINE; 94293786.
DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;
"Antigenic drift of non-encapsulated Haemophilus influenzae major
MONSON R.S. JR., TOLAN R.W. JR.;
"Modecular cloning, expression, and primary sequence of outer
membrane protein P2 of Haemophilus influenzae type b.";
INFECT. IMMON. 57:88-94(1989).
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HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 21 361 OUTER MEMBRANE PROTEIN P2. SEQUENCE 361 AA; 39701 MW; 291391ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 1; Le
Pred. No. 2.46e+00;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03359; G148959; -.
EMBL; A09003; G412251; -.
PIR; A30542; A30542.
PIR; S09622; S09622.
OUTER MEMBRANE; TRANSMEMBRANE; PORIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
OUTER MEMBRANE PROTEIN P2 PRECURSOR (OMP P2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA.
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50.0%;
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Best Local Similarity
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DISULFIDE BONDS
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                                                                                                                                                                                                                                                                               LT 8
GUX_CELFI
P07986;
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                 DUIM B., DANKERT J., JANSEN H.M., VAN ALPHEN L.;
"Genetic analysis of the diversity in outer membrane protein P2 of
"Genetic analysis of the diversity in outer membrane protein P2 of
non-encapsulated Haemophilus influenzae.";
MICROB. PATHOG. 14:451-462(1993).
-!- SUBCELLULUAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- THE SEQUENCE OF STRAIN TI IS SHOWN HERE.
-!- SIMILARITY: TO PHOTOBACTERIUM STRAIN SS9 OMPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTONIEWSKI C., SAVELLI B., STRACIER P.,
"The spoild gene, which regulates early developmental steps in
Bacillus subtilis, belongs to a class of environmentally responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
outer membrane protein P2 in patients with chronic bronchitis is
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 1; Length 371; Pred. No. 2.46e+00; 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                               P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCANLAN E., DEVINE K.M.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                               OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                          K -> Q (IN T2).
A -> T (IN T2).
S -> T (IN T2).
; 982A22A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATA_BACSU STANDARD: PRT; 392 AA. P16524: 01-AUG-1990 (REL. 15, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PUTATIVE AMINOTRANSFERASE A (EC 2.6.1.-).
                                                                                                                                                                                                                                                                                          EMBL: X73383; E1192128; -.
OUTER MEMBRANE; TRANSMEMBRANE; PORIN; SIGNAL.
           caused by point mutations.";
MOL. MICROBIOL. 11:1181-1189(1994).
                                                                                                                                                                                                                                                                                                                                                                             40901 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIOL. 172:86-93(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 361-392 FROM N.A. MEDLINE; 90094275.
                                                                                                                                                                                                                                                                                                                                                                                                    64.6%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                             EMBL; X73386; G510591; -.
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                                                                                                                                                                                                                                                                                                                            21 3
184 1
224 2
273 2
371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B FGOGYVQTPF 17
                                                          STRAIN-T1, AND T2;
MEDLINE; 94018553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 YAQGYLETRF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATA OR UAT.
BACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                          VARIANT
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (REL. 08, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-AUG-1988 (REL. 37, LAST SEQUENCE UPDATE)
EXOGLUCANASE PRECURSOR (EC 3.2.1.91) (EXOCELLOBIOHYDROLASE) (1,4-BETA-CELLOBIOHYDROLASE) (BETA-1,4-GLYCANASE CEX) / ENDO-1,4-BETA-XYLANASE B (EC 3.2.1.8) (XYLANASE B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITRE; 92104156.
GILKES N.R., CLAEYSSENS M., AEBERSOLD R., HENRISSAT B., MEINKE A., MORRISON H.D., KILBURN D.G., WARREN R.A.J., MILLER R.C. JR.; "Structural and functional relationships in two families of beta-1,4-glycanases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHITE A., WITHERS S.G., GILKES N.R., ROSE D.R.;
"Crystal structure of the catalytic domain of the beta-1,4-glycanase cex from Cellulomonas fimi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           JR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELLULOMONAS FIMI.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; MICROCOCCINEAE; CELLULOMONADACEAE; CELLULOMONAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'NEILL G., GOH S.H., WARREN R.A.J., KILBURN D.G., MILLER R.C. JI
"Structure of the gene encoding the exoglucanase of Cellulomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVE SITE GLU-274.
MEDLINE; 91340691.
TULL D., WITHERS S.G., GILKES N.R., KILBURN D.G., WARREN R.A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "colutamic acid 274 is the nucleophile in the active site of a retaining' exoglucanase from Cellulomonas fimi."; J. BIOL. CHEM. 266:15621-15625(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 42-353.
MONEM V., BIRSAN C., WARREN R.A.J., WITHERS S.G., ISUBMITTED (NOV-1997) TO THE PDB DATA BANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 42-353.
STRAIN-ATCC 484;
                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 1; Le
Pred. No. 2.46e+00;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOCHEMISTRY 33:12546-12552(1994).
                                                                                                                                                                                                                                                                                                                                                                                 uuery Match
Best Local Similarity 50.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 YGEGYVRLSF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 87055250.
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MEDLINE; 94250631.

AM REDLINE; 94250631.

AM CLEDD A.M., LINDHORST T., WITHERS S.G., WARREN R.A.J.;

MICLEDD A.M., LINDHORST T., WITHERS S.G., WARREN R.A.J.;

"The acid/base catalyst in the exoglucanase/xylanase from
"The acid/base catalyst in the exoglucanase/xylanase from
"The acid/base catalyst in the exoglucanase/xylanase from
"The acid/base catalyst in the exoglucanase from detailed

"The acid/base catalyst in the exoglucanase from detailed

"The acid/base catalyst in the exoglucanase from detailed

"The acid/base acid/base acid/base and xylan. Has also weak

"The acid/base acid/base and the acid/base polymer catalyst in the proposition of the cellulose polymer catalyst in the acid/base and cellulose and cellulos
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                                                                                                              "Insights into transition state stabilization of the beta-1,4-glycosidase Cex by covalent intermediate accumulation in active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR PROTEOLYSIS.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL-HYDROLASES)
-!- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95284032.
XU G.-Y., ONG E., GILKES N.R., KILBURN D.G., MUHANDIRAM D.R.,
HARRIS-BRANDICS M., CARVER J.P., KAY L.E., HARVEY T.S.;
"Solution structure of a cellulose-binding domain from Cellulomonas
fimi by nuclear magnetic resonance spectroscopy.";
BIOCHEMISTRY 34:6993-7009(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.
-!- THE LINKER REGION (ALSO TERMED "HINGE") MAY BE A POTENTIAL SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER ("HINGE") (PRO-THR BOX).
CECLULOSE-BINDING (BY SIMILARITY).
PROTON DONOR.
NUCLEOPHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00331; 91ycosyl_hydro3; 1.
PFAM; PF00553; CBD_1; 1.
CELLULOSE DEGRADATION; HYDROLASE; GLYCOSIDASE; REPEAT; SIGNAL;
MEDLINE; 98400502.
NOTENBOOM V., BIRSAN C., NITZ M., ROSE D.R., WARREN R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOGLUCANASE. CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB: 2HIS; 14-OCT-98.
PROSITE; PS00561; CBD_BACTERIAL; 1.
PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
                                                                                                                                                                                                                             NAT. STRUCT. BIOL. 5:812-818(1998).
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                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 377-484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1EXG; 03-JUN-95.
PDB; 1EXH; 03-JUN-95.
PDB; 1EXP; 27-JAN-97.
PDB; 2XYL; 18-MAR-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356
376
484
168
274
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                                                                             WITHERS S.G.:
                                                                                                                                                                                                mutants."
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ACT_SITE
ACT_SITE
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    REAL PROPERTY PRESENTATION OF THE PROPERTY PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEC-1 GENE BY ALTERNATIVE RNA SPLICING AND PROTECLYTIC CLEAVES DEC-1-FUNCTION: THE DEC-1 FEMALE-STERILE LOCUS PROTEIN IS REQUIRED FOR PROPER ASSEMBLY OF THE DROSOPHILA EGGSHELL.

-!-ALTERNATIVE PRODUCTS: MULTIPLE PROTEINS ARE PRODUCED FROM THE DEC-1 GENE BY ALTERNATIVE RNA SPLICING AND PROTEOLYTIC CLEAVAGE EVENTS.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 91032553.
WARING G.L., HAWLEY R.J., SCHOENFELD T.;
"Multiple proteins are produced from the dec-1 eggshell gene in Drosophila by alternative RNA splicing and proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 1123 DEFECTIVE CHORION-1 FC125 PROTEIN. 493 788 12 X 26 AA TANDEM REPEATS. 1123 AA; 127959 MW; 99218239 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
EURARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 1; Length 1123;
Pred. No. 3.94e+00;
3; Mismatches 2; Indels
                                                                                               Length 484;
                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A44766; A44766.
FLYBASE; FBGN0000427; dec-1.
CHORION; EGGSHELL; REPEAT; ALTERNATIVE SPLICING; SIGNAL.
                                                   E->A, D, G: REDUCED ACTIVITY
                                                                                               Score 52; DB 1; L
Pred. No. 3.94e+00;
                                                                 2624B193 CRC32;
                                                                                                                                                                                                                                                                                       01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
101-EBB-1913 (REL. 17, LAST ANNOTATION UPDATE)
DEFECTIVE CHORION-1 FC125 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL3_DROME STANDARD; PRT; 415 AA. 016797; 15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                               4; Mismatches
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208 240
302 308
382 481
168 168
484 AA; 51291 MW;
                                                                                               63.4%;
50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                Local Similarity
                                                                                                                                                             186 LGNGYIETAF 195
                                                                                                                                                                               : | | | | :: |: |
8 FGQGYVQTPF 17
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DC11_DROME
P18169;
 DISULFID
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                                                MUTAGEN
SEQUENCE
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SEQUENCE
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EMBL; X59720; E264490; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                           SEQUENCE FROM N.A. CHANG Y., HOHELSEL J.D., O'KANE C.J.; CHAN H.Y.E., ZHANG Y., HOHELSEL J.D., O'KANE C.J.; SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-:- FUNCTION: THE L3 PROTEIN IS A COMPONENT OF THE LARGE SUBUNIT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOLLE P. A., GILLIQUET V., BERBEN G., DUMONT J., HILGER F.; The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chromosome III, reveals the presence of seven open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                   CYTOPLASMIC RIBOSOMES.
--- SUBCELLULAR LOCATION: CYTOPLASMIC.
--- SIMILARITY: BELONGS TO THE L3P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                 DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA: DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
14-POTHETICAL 84-9 KD PROTEIN IN PMPI-FENZ INTERGENIC REGION.
17-ROTOLOG OR YCR26C OR YCR246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 1; Length 415;
Pred. No. 6.29e+00;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-244 FROM N.A.
POHL F., RICHTERICH P., WURST H.;
SUBMITTED (MAR-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEAST 8:205-213(1992).
-!- SIMILARITY: TO YEAST YEL016C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 0 BY SIMILARITY.
415 AA; 46784 MW; FAD30713 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FLYBASE; FBGN0020910; RpL3.
PROSITE; PS00414, RIBOSOMAL_L3; 1.
PFAN: PF00297; L3; 1.
RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 244-743 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 62.2%;
Local Similarity 71.4%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF016835; G2384754;
60S RIBOSOMAL PROTEIN L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92245758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 GYVOTPF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCR6_YEAST
P25353;
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SEQUENCE
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    BIOL. CHEM. 257:3265-3275(1982).
    FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INFO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEPIZ-PLASCENCIA G.M., RADEBAUGH C.A., HALLICK R.B.;
"The Euglene gracilis chloroplast rpob gene. Novel gene organization
and transcription of the RNA polymerase subunit operon.";
NUCLEIC ACIDS RES. 18:1869-1878(1990).
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OROZCO E.M., HALLICK R.B.;
"Euglena gracilis chloroplast transfer RNA transcription units. II.
Worleotide sequence analysis of a tRNAVal-tRNAAsn-tRNAArg-tRNALeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
                                                                                                                                      ä
                                                                                                 Score 51; DB 1; Length 743; Pred. No. 6.29e+00; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00623; RNA_pol_A; 1.
MENDEL; 5016; EUGGT; RROC2;1.
TRANSCRIPTION; DNA_DIRECTED RNA POLYMERASE; CHLOROPLAST.
CONFLICT 593 593 I -> II (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; EUGLENOZOA; EUGLENIDA; EUGLENALES; EUGLENA.
                                                                                                                                                                                                                                                                                                     01-NOV-1991 (REL. 20, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DNA-DIRECTED RNA POLYMERASE BETA" CHAIN (EC 2.7.7.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> II (IN REF. 2).
L -> R (IN REF. 2).
003F633F CRC32;
                                                 114 135 POTENTIAL.
743 AA; 84915 MW; 957CE7AF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51;
PIR; $19437; $19437.

PIR; $27380; $27380.

HYPOTHETICAL PROTEIN; TRANSMEMBRANE.

TRANSMEM 114 135 POTENTI

SEQUENCE 743 Aa; 84915 MW; 957CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 586-830 FROM N.A.
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                                                                                                   62.2%;
ilarity 60.0%;
Conservative
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EMBL, M22010, G336887; -...
EMBL, X70810, G415792; -...
PIR, S19259; RNEGB2.
PIR, S34554; S34554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.28;
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                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                      563 FPQGYIE-PF 571
                                                                                                                                                                                                      8 FGGGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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688
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MEDLINE; 90245579.
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MEDLINE; 82142472
                                                                                                                                                                                                                                                                                                                                                                                          EUGLENA GRACILIS.
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J. BIOL. CHEM
                                                                                                                                                                                                                                                       LT 12
RPOD_EUGGR
P23581;
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                                                                                                                                      Matches
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-!- FUNCTION: PERMEASE THAT IS INVOLVED IN THE TRANSPORT ACROSS THE CYTOPLASMIC MEMBRANE OF LYSINE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-!- INDUCTION: HIGH, IN ANAEROBIC MEDIA OF LOW PH, CONTAINING LYSINE.
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELLIS J., CARLIN A., STEFFES C., WU J., LIU J., ROSEN B.P.; "Topological analysis of the lysine-specific permease of Escherichia
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-KIZ. / MG1655;
MEDLINE: 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / BHB2600;
RICHTERICH P., LAKEY N., GRYAN G., JAEHN L., MINTZ L., ROBISON K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coll K-12."; SCIENCE 277:1453-1474(1997).
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEFFES C., ELLIS J., WU J., ROSEN B.P.; "The lysP gene encodes the lysine-specific permease."; J. BACTERIOL. 174:3242-3249(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN B.P.;
SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (OCT-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
Pred. No. 6.29e+00;
                                                                                                                                                                                                                                                                                                                                                                  01-WAY-1992 (REL. 22, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                           488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000305; G1788480; -.
PIR; S24560; S24560.
ECOGENE: EG1137; LVSP.
PROSITE; PS00218; AMINO_ACID_PERMEASE; 1.
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY, AND SEQUENCE OF 1-6. MEDLINE; 96032017.
                      Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M89774; G466778; -.
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYSINE-SPECIFIC PERMEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G40590
                                                                                                                        280 FPEVYIRTPF 289
                                                                                                                                                               | : |::|||
8 FGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BPR2;
MEDLINE; 92250419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYSP OR CADR.
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                                                                                                                                                                                                                                                                       LY 13
LYSP_ECOLI
P25737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. BACTERIO [2] REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.";
MOL. ENDOCRINOL. 9:243-254(1995).
-- FUNCTION: THYROLD RECEPTOR INTERACTING PROTEINS (TRIPS)
-- FOURTION: THYROLD RECEPTOR MITH THE LIGAND BINDING DOMAIN OF THE THYROLD RECEPTOR (TR). TRIP10 REQUIRES THE PRESENCE OF THYROLD HORMONE FOR ITS INTERACTION.
-- IISSUE SPECIFICITY: EXPRESSED MOST ABUNDANTLY IN SKELETAL MUSCLE, HEART AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A.
MEDLINE, 95295737.
LEE J.W., CHOI H.-S., GYURIS J., BRENT R., MOORE D.D.;
TWO classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
 neases; 1.
TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          015642;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOYATION UPDATE)
THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 1; Length 488;
Pred. No. 9.95e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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B0E7230B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA
                                                                                                                                                                                                                                                                                                                          PERIPLASMIC.
                                                                                                                                                                   PERIPLASMIC.
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                                                                                                                                                                                                                                              CYTOPLASMIC.
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FFAM; PF00324; aa_permeases;
TRANSPORT; AMINO-ACID TRANSPO
                                                                                                                                                                                                                                                                                                                                                                                                    61.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                 470
121
488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 YGQNYVEEGF 93
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TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of mouse 17beta-hydroxysteroid dehydrogenase type 2, and analysing expression of the mRNAs for types 1, 2, 3, 4 and 5 in mouse embryos and adult tissues.";
BIOCHEM. J. 325:199-205(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STOFFEL W., WEISS B.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: CAPABLE OF CATALYZING THE INVERCONVERSION OF
TESTOSTERONE AND ANDROSTENEDIONE, AS WELL AS ESTRADIOL AND
ESTRONE. ALSO HAS 20-ALPHA + HSD ACTIVITY. USES NADH WHILE EDH17B3
USES NADPH (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NAD(+) - ESTRONE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL). SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                          JT 15
DHB2_MOUSE STANDARD; PRT; 381 AA.
P51558, 008898;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ESTRADIOL 17 BETA-DEHYDROGENASE 2 (EC 1.1.1.62) (17-BETA-HSD 2)
HSD1782 OR EDH1782.
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X95517; E289833; --
EMBL; X95685; E223346; --
MGD; MGI:1096386; HSD17B2.
PROSITE; PS00061; adh_SHORT; 1.
HSSP; P14061; 1FDV.
STERNID BIOSYNTHESIS; OXIDOREDUCTASE; NAD; MULTIGENE FAMILY;
TRANSMEMBRANE; SIGNAL-ANCHOR.
SIGNAL-ANCHOR.
SIGNAL-ANCHOR.
                                                                                                                                                                    Score 49; DB 1; Length 115;
Pred. No. 1.56+01;
3; Mismatches 1; Indels
                                                                                                     NON_TER 1 1
DOMAIN 60 115 SH3.
SEQUENCE 115 AA; 12848 MW; E678DBE7 CRC32;
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALB/C, TISSUE-LIVER;
MEDLINE; 97344259.
                                                                                                                                                                      Ouery Match 59.8%;
Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 1-358 FROM N.A.
                              EMBL; L40379; G695376; -. PROSITE; PS50002; SH3; 1. PFAM; PF00018; SH3; 1. SH3 DOMAIN.
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                            101 GEGYVPTSY 109
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Gaps
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                                                 Score 49; DB 1; Length 381;
Pred. No. 1.56e+01;
2; Mismatches 1; Indels
                                                  Length 381;
BY SIMILARITY.
QA -> RP (IN REF. 2).
6A3B8BC8 CRC32;
                                                                                                                                                              Search completed: Wed Sep 1 16:21:06 1999 Job time: 13 secs.
                         381 AA; 41835 MW;
                                                 59.8%;
Similarity 62.5%;
5; Conservative
                                                           Local Similarity
                                                                                                  296 YGQDYVHT 303
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8 FGOGYVOT 15
ACT_SITE
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:21:25 1999; MasPar time 5.97 Seconds 91.381 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (8-17) from PCTUS9913024.pep (8 of 12) 82 1 FGGGYVQTPF 10 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 23.872; Variance 31.947; scale 0.747 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Pred. No.	001007 6	4.38e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	6.83e+00	1.06e+01	1.06e+01	1.63e+01	1.63e+01
	Description	TONG-ATTACHMENT AND TO THE PROPERTY.	PUTATIVE G2-SPECIFIC P		OUTER MEMBRANE PROTEIN	MAJOR OUTER MEMBRANE P	OUTER MEMBRANE PROTEIN	MAJOR OUTER MEMBRANE P	OUTER MEMBRANE PROTEIN	F21C3.4 PROTEIN.	KIAA0547 PROTEIN.	CYTOCHROME C BIOGENESI	ORF50.	BETA-1,4-XYLANASE PREC	LEPIDODACIYLUS MOESTUS	HYPOTHETICAL 37.1 KD P					
SUMMARIES	8	028347	013839	062260	048025	048225	001452	068632	068634	068635	068631	068633	068630	001450	019672	060294	025141	038080	059277	P87432	067489
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	% Query Match	67.1	62.9	64.6	64.6	9.49	9.49	9.49	9.49	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	63.4	63.4	62.2	62.2
	Score	55	54	23	23	53	53	53	53	53	23	53	23	53	53	53	23	52	52	51	51
	Result No.		7	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20

1.63e+01	1.63e+01	1.63e+01	1.63e+01	2.51e+01					2.51e+01				2.51e+01	3.82e+01	3.82e+01	3.82e+01		3.82e+01	3.82e+01	3.82e+01	3.82e+01	3.82e+01	3.82e+01	3.82e+01				
TGF PROTEIN.	F13P17.19 PROTEIN.	POLYKETIDE SYNTHASE.	RIFAMYCIN POLYKETIDE S	MEMBRANE FUSION PROTEI	PUTATIVE MEMBRANE FUSI	NEOPULLULANASE.	RK2=GLIAL-SPECIFIC HOM	REVERSED POLARITY.	LIPASE (EC 3.1.1.3).		SIMILAR TO MAIZE TRANS	T01B7.6 PROTEIN.	TRP-LIKE PROTEIN.	HYPOTHETICAL 12.0 KD P	REP PROTEIN.	U0002M.	OMP1 PROTEIN (FRAGMENT	OMP1 (FRAGMENT).	MAJOR OUTER MEMBRANE P	HYPOTHETICAL 45.1 KD P	425AA LONG HYPOTHETICA	ACETYL COA: BENZYLALCO	CDC42-INTERACTING PROT	SALT-TOLERANT PROTEIN.			509 AA.	
092734	080784	052545	052789	025327	068961	P71093	026441	024477	059932	059933	048572	022047	046129	P94122	P75004	050462	080020	069304	068623	P95139	059244	064988	18	P97531	ALIGNMENTS		PRT;	, CREATED)
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ATE) T SEQUENCE UPDP T ANNOTATION UP SE (FADD-8). GLOBALES; ARCHA 49558; JF., WHITE C N M., HICKEY E. CRAHAM D.E., CRENEY K., AD MAN J.F. AD MAN J.F. AD MAN J.F. MCDOR MAN J.F. MCDO	55; DB 1; No. 2.79e+ Mismatches	
5 S S S S S S S S S S S S S S S S S S S	55; No. ; 1sma1	
T 1 12.31 13.347 14.363.47 15.347 16.243.47 16.243.47 16.248.47 16.248.47 16.248.47 16.248.47 17.348.41 18.348.47 18.348.37 18.34	Score 55; Pred. No. 1; Misma	
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NARY RELL RELL RELL ROTA, NOTA, NOTA	67.1%; 60.0%; vative	
T 1 O13347 O23347 O1-JAN-1998 (TREMBLREL. 05, O1-JAN-1998 (TREMBLREL. 05, O1-JAN-1998 (TREMBLREL. 06, O1-JAN-19932. ARCHAEOGLOBUS (TUGIDUS. ARCHAEOGLOBUS. OLGAN A304 / ARCHAEOGLOBUS. OLGAN A304 / ARCHAEOGLOBUS. OLGAN A304 / ARCHAEOR N-1, KERLAN N-1, ONGEN N-1, KERLAN N-1, ONGEN N-1, MASON N-1, SPRIGGS T., ARCHAEOR N-1, ONGEN N-1, ON	Query Match 67.1% Best Local Similarity 60.0% Matches 6; Conservative	334
PRI B (TI B B (TI B B C TI B C T	nilar CC	/GVPE
COUNT IN TO TROP THE SECONDARD	ch 1 Sim 6;	325 FTEGYVGVPF : 8 FGGGYVQTPF
1 028347 028347 01-34N-19 01-10N-19 01-10N-19 10NG-CHA-19 10NG-CHA-19 10NG-CHA-19 10NG-CHA-19 10 10NG-CHA-19 10 10NG-CHA-19 10 10NG-CHA-19 ARCHAREOGO EXTRAIN-V MEDILINE; KICKHAREOGO KICKHAREOGO KICKHAREOGO FILESCHAREOGO KIRKNESS PETERSON T. N. SADOW P. W. SADOW P. P. SA	Mat Loca les	25 F – F
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EMBL; Z81547; E1347158; -.
PROSITE; PSO0518; ZINC_FINGER_C3HC4; 1.
ZINC-FINGER.
                                                                                                                                                                                                                   OUTER MEMBRANE PROTEIN P2 (FRAGMENT).
                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                                                                                                                                PRT;
                                                     64.6%;
||arity 66.7%;
|Conservative
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50.08;
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Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                      Query Match
Best Local Similarity
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Matches 5; Conserv
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                                                                                               177 GQGYIKCPF 185
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                                                                                                                    9 GQGYVQTPF 17
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                                 SEQUENCE
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Q48025
Q48025;
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MEDLINE: 94150718.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSON J., PERCY C., RIFKEN L., ROOPEA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WATERSTON J.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITIONDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                   ö
                                01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PUTATIVE G2-SPECIFIC PROTEIN KINASE C19E9.02 (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                              DB 3; Length 722;
                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATTHEWS L.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07, CREATED)
07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATÜRE 368:32-38(1994).
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                 SCHIZOSACCHAROMYCES POWBE (FISSION YEAST),
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                              Score 54; DB 3; L
Pred. No. 4.38e+00;
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286A8C12 CRC32;
                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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            722 AA
            PRT;
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722 AA; 82689 MW;
                               (TREMBLREL. 06, C
(TREMBLREL. 06, I
(TREMBLREL. 08, I
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60.0%;
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nes 6; Conservative
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062260 062260,
01-4UG-1998 (TREMBLREL. 0'
01-AUG-1998 (TREMBLREL. 0'
01-AUG-1998 (TREMBLREL. 0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
            PRELIMINARY;
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CAENORHABDITIS ELEGANS
                                                                                                                   SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                       182 FTQSYVGTPY 191
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8 FGQGYVQTPF 17
                                                                                                                                         SEQUENCE FROM N.A.
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                                                                        SPAC19E9.02
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SEQUENCE
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013839;
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STRAIN=12;
MEDLINE; 94245383.
BELL J., GRASS S., JEANTEUR D., MUNSON R.S.;
"Diversity of the P2 protein among nontypeable Haemophilus influenzae isolates.";
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE; 94018553.
DUIM B., DANKERT J., JANSEN H., VAN ALPHEN L.;
DUIM B., DANKERT J., JANSEN H., VAN ALPHEN L.;
Wenetic analysis of the diversity in outer membrane protein P2 of non-encapsulated Haemophilus influenzae.";
MICROB. PATHG. 14:451.462(1993).
EMBL; X73392; G860954; -.
SEQUENCE 357 As, 39093 MW; 95AD9567 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 2; Length 344; Pred. No. 6.83e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB 2; Length 357; Pred. No. 6.83e+00; 4; Mismatches 1; Indels
                                                Length 209;
                                                                                              2; Indels
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LAST ANNOTATION UPDATE)
                                                Score 53; DB 5; Le
Pred. No. 6.83e+00;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFECT. IMMUN. 62:2639-2643(1994).
EMBL: U08206; 6559998; -.
1 1 1 SEQUENCE 344 AA; 37781 MW; 257B8DC5 CRC32;
209 AA; 24425 MW; D1978DC1 CRC32;
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64.6%;
50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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B FGGGTVQTPF 17
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-32-82E;
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SEQUENCE
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MEDLINE: 94293786.
DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;
Antigenic drift of non-encapsulated Haemophilus influenzae major outer membrane protein P2 in patients With chronic bronchitis is caused by point mutations:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-30-77C;
STRAIN-30-77C;
REGELINK A G. DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK P.,
VAN ULSEN P., DANKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF052556; G2981123;
NON_TER
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068632
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068632
068632;
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
HARMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                          BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                           MEDLINE; 93084371.

SIKKEMA D.J., MURPHY T.F.;

SIKKEMA D.J., MURPHY T.F.;

"Molecular analysis of the P2 porin protein of nontypeable Haemophilus influenzae.";

INFECT. IMMUN. 60:5204-5211(1992).

EMBL; M93270; G148967;

OUTER MEMBRANE; PORIN; SIGNAL.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 2; Length 357; Pred. No. 6.83e+00;
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Pred. No. 6.83e+00;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
OUTER MEMBRANE PROTEIN P2.
C5E6B40D CRC32;
                                                                O01452 PRELIMINARY; PRT; 357 AA.
001422.
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
001-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caused by point mutations.";
MOL. MICROBIOL. 11:1181-1189(1994).
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357 AA; 39215 MW;
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50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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SEQUENCE FROM N.A.
78 YAQGYLETRF 87
                        8 FGQGYVQTPF 17
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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BUINE, 94293786.

DUIM B., VAN ALPHEN L., ELJK P., JANSEN H.M., DANKERT J.;

"Antigenic drift of non-encapsulated Haemophilus influenzae major outer membrane protein P2 in patients with chronic bronchitis is caused by point mutations ";

MOL. MICROBIOL. 11:1181-1189(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94293786.

DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;

Mattgenic drift of non-encapsulated Haemophilus influenzae major outer membrane protein P2 in patients with chronic bronchitis is caused by point mutations.";

MOL. MICROBIOL. 11:1181-1189(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGELINK A.G., DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK P., VAN ULESN P., DARKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF052552; G2981127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGELINK A.G., DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK P., VAN ULER P., DANKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1999) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF052553; G2981129; ...
NON_TER 365
SEQUENCE 365 AA; 39953 MW; 3567EC05 CRC32;
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                                                  01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
HARAMOPHIUS INFUNENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O68635 PRELIMINARY; PRT; 365 AA.
068635, 068635, 01-806-1998 (TREMBLREL. 07, CREATED)
01-A0G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
HAEMOPHILUS INFLUENZAE.
HAEMOPHILUS.
HAEMOPHILUS.
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364 AA; 39839 MW; 147EB78E CRC32;
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364 AA.
PRT;
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"Antigenic drift of non-encapsulated Haemophilus influenzae major
outer membrane protein P2 in patients with chronic bronchitis is
caused by point mutations.";
MOL. MICROBIOL. 11:1181-1189(1994).
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DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;

DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;

"Antigenic drift of non-encapsulated Heemophilus influenzae major outer membrane protein P2 in patients with chronic bronchitis is caused by point mutathons.";

MOL. MICROBIOL. 11:1181-1189(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=30-77B;
STRAIN=30-77B;
REGELINK A.G., DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK P.,
VAN ULSEN P., DANKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF052549; G2981121; -.
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REGELINK A.G., DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK P., VAN ULSEN P., DANKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
HAEMOPHILUS INFUUENZAE.
HAEMOPHILUS INFUUENZAE.
HARMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
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Pred. No. 6.83e+00;
 Length 365;
                              1; Indels
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01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
Score 53; DB 2; L
Pred. No. 6.83e+00;
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                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                           365 AA.
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                                                                                                                                           PRT;
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64.6%;
50.0%;
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Local Similarity 50.0%;
                            5; Conservative
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 Query Match
Best Local Similarity
                                                                        8 FGOGYVOTPF 17
                                                       71 YAQGYLETRF 80
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SEQUENCE
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DUIM B., VAN ALPHEN L., EIJK P., JANSEN H.M., DANKERT J.;

*Antigenic drift of non-encapsulated Haemophilus influenzae major outer membrane protein P2 in patients with chronic bronchitis is caused by point mutations.;

MOL. MICROBIOL. 11:1181-1189(1994).
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01-AUG-1998 (TREMBLEEL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST SEQUENCE UPDATE)
MAJOR OUTER MEMBRANE PORIN P2 VARIANT (FRAGMENT).
HARMOPHILUS INFUUENAAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HARMOPHILUS.
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-30-77A;
RECELINK A.G., DAHAN D., MOLLER L.V.M., COULTON J.W., EIJK
RYAN ULSEN P., DANKERT J., VAN ALPHEN L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AFOS2548; G2981119; -.
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MEDLINE; 93084371.
SIKKEMA D.J., MURPHY T.F.;
"Molecular analysis of the P2 porin protein of nontypeable Haemophilus influenzae.";
INFECT. IMMUN. 60:5204-5211(1992).
EMBL; M93268; G148965;
PFAM; PF00267; Gram-ve_porins; 1.
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Pred. No. 6.83e+00;
4; Mismatches 1; Indels
                                                                                                                                              Length 368;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                           Score 53; DB 2; Le
Pred. No. 6.83e+00;
4; Mismatches 1;
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EMBL; AF052551; G2981125; -.
NON_TER 1 1
NON_TER 368 368
SEQUENCE 368 AA; 40510 MW;
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Similarity 50.0%;
5; Conservative
                                                                                                                                           Query Match 64.6%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                    71 YAQGYLETRF 80
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SEQUENCE
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068630;
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001450;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., MILSON BONEIELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COLLSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LICHTNING J., LLOYD C., MORNERARA, A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SKITH A., SONNHAAMER E., STABÈN R., SULTON J., HOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
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MEDLINE; 98290545.
NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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                                                                                                                                          Score 53; DB 2; Length 390;
Pred. No. 6.83e+00;
4; Mismatches 1; Indels
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OUTER MEMBRANE; PORIN; SIGNAL.
SIGNAL
1 20 POTENTIAL.
CHAIN 21 390 OUTER MEMBRANE PROTEIN P2.
SEQUENCE 390 AA; 42941 MW; 0E424362 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
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EMBL: 271261; E1345956; -.
SEQUENCE 584 AA; 66338 MW; 10A646D4 CRC32;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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GOGYVOTP 16
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RA OHARA O;

RT *Prediction of the coding sequences of unidentified human genes. IX.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro.*;

RD DNA RES. 5: 313-39(1998)

SQ SEQUENCE 686 AA; 75583 MW; B5C954CA CRC32;

QUETY MATCh

Best Local Similarity 66.7%; Pred. No. 6.83e+00;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 ARGYVQDPF 37

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QY 9 GGGYVQTPF 17

Search completed; Wed Sep 1 16:22:04 1999
Job time : 39 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:25:40 1999; MasPar time 4.56 Seconds 172.419 Million cell updates/sec Run on:

Tabular output not generated

>PCT-US99-13024-2 (57-93) from PCTUS9913024.pep (9 of 12) 232 1 SAGLHLRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS 37 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

| jpart| 2. part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part11 12:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 34:part34 35:part30 31:part36 37:part37 38:part38 39:part39

Mean 22.786; Variance 86.998; scale 0.262 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					
∷ So. ∷ :	Score	Match	Match Length DB	8 :	DI CI	Description	Pred. No.
-	73	31.5	. 272	7	R07522	Alpha-Trichosanthin e	2.30e+01
~	73	31.5	272	'n	R25577	Ribosome inactivating	2.300+01
m	73	31.5	345	10	R52824	GTP-cyclohydrolase II	2.300+01
4	70	30.2	820	13	R71802	N-acetylheparosan fra	4 140+01
2	99	29.3	119	34	W77551	Nickel-binding peripl	6 110+01
9	99	29.3		37	W72935	Mycobacterium tubercu	6.119+01
7	9	29.3		14	R80530	B. sphaericus SLP.	6.11e+01
80	29	28.9			W41513	N. meningitidis alpha	7.42e+01
6	99	28.4		23	W21704	Luffin-A.	8 996+01
0	99	28.4	248	7	R37294	Plant type I RIP Luff	8.99e+01
_	99	28.4		14	R74180	Type I ribosome-inact	8.99e+01
~	99	28.4		٣	R12468	Luffa cylindrica bios	8 996+01
m	99	28.4			R63906	Type I ribosome-inact	8 99-401
4	99	28.4			W25141	Luffin-A (a ribosome	8 996+01
15	99	28.4		10	R53731	Luffin (ribosome inac	8.99e+01
و	99	28.4			R29909	Drod of the lifeton	101000

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od. of tase ccr-	H. Pylori cytopiasmic Myxoma virus MA56 gen	Sequence encoded by R	cile to	C. difficile toxin A	Antigenic surface pro	ncephal1	Recombinant vaccinia	Sequence containing J	SFV4 non-structural p	Clostridium difficile	C. difficile toxin A.	Trichosanthin-like pr	nthes kiril	Maleate isomerase.	Maleate isomerase.	E. coli ADSS protein.	Amino acid sequence o	Soybean heat shock pr		E2 protein of Canine	H. pylori cytoplasmic	Flavivirus v3 antiqen	Sequence of neutral p	wine retr	CCVInsavc spike prote
O 10 1	W20634 W15104	R05109	R95014	R95017	P93305	R85479	R10424	R05597	R25138	W68387	R95016	R07519	R25574	R98392	R98391	W40594	W46470	P50063	W59912	R31038	W20641	P71739	P51009	W32096	R27819
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99	9 20	5 5	65	65	65	65	65	65	65	65	65	9	64	64	64	9	63	63	63				62		
118	507	21	23	24	25	56	27	58	53	30	31	32	33	34	32	36	37	38	33	40	41	42	43		45

ALIGNMENTS

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18-001-1990; U01816.
104-ARR-1990; U01816.
104-ARR-1990; U01816.
11 Platek M, Chow T, Fry K;
12 Platek M, Chow T, Fry K;
13 Platek M, Chow T, Fry K;
14 Platek M, Chow T, Fry K;
15 Platek M, Chow T, Fry K;
16 Platek M, Chow T, Fry K;
17 Recombinant trichosanthin protein - with selective inhibitory effect
18 PR-PSDB; Q06350.
19 Platek MP-PSDB; English.
19 Platek M-PSDB; English.
19 Platek M-PSDB; English.
25 Example: Figl 19; 1020p; English.
26 Coding for TCS in a T.kirilowii genomic library. Five clones were contently isolated and sequenced, including clone 3.
27 Phey were found to have homology to the alpha-TCS coding sequence.
27 See also Q06343-9 and Q06351.
                              R07522;
06-FEB-1991 (first entry)
Alpha-Trichosanthin encoded by insert sequence from clone 3.
trichosanthin (TCS); Human Immunodeficiency Virus; inhibition Trichosanthes Kirilowii.
                                                                                                                                                                  1..23
/label-signal peptide
                                                                                                                 Location/Qualifiers
 T
R07522 standard; protein; 272 AA.
                                                                                                                                   24..272
/label-alpha-TCS
                                                                                                                                                                                               WO9012097-A
                                                                                                                                protein
                                                                                                                                                                  region
RESULT
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Gaps ; 0 Query Match 31.5%; Score 73; DB 2; Length 272; Best Local Similarity 39.1%; Pred. No. 2.30e+01; Matches 9; Conservative 8; Mismatches 6; Indels

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97 gylvnttsyffnepdaataskfv 119

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RESULT

Length 345;

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amino-2,4-(1H,3H)-pyrimidindion);
- rib-4 gene: 6,7-dimethyl-8-ribityllumazine (DMRL)-synthase;
- rib-5 gene: riboflavin-synthase;
- rib-3 gene: L-3,4-dihydroxy-2-butanone-4-phosphate (DBP)-synthase.
                                                                           Score 73; DB 10; Length 345
Pred. No. 2.30e+01;
4; Mismatches 9; Indels
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R71802 standard; Protein; 820
                                                                           Query Match
Best Local Similarity 50.0%;
Matches 14; Conservative
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17-AUG-1993; FR-010050.
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19-0CT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequences and expression vectors encoding riboflavin genes - are useful for the prodn. of riboflavin in eukaryotes claim 1, Page 4-6; Edpp; German.

The riboflavin genes isolated from S. cerevisiae allow the prodn. of riboflavin in eukaryotes. The gene products are: rib-1 gene: quanosine triphosphate (GTP)-cyclohydrolase II (transforming GTP to 2,5-diamino-4-7. pyrimidine-5-phosphate);

- rib-7 gene: #TP-reductase (transforming 2,5-diamino-6-ribosylamino-4-7. phosphate into 2,5-diamino-ribitylamino-3,4-(14,3H)-pyrimidine-5-phosphate (DRAP));

- rib-2 gene: (DRAP)-deaminase (formation of 5-amino-6-ribityl
                                                                                                                                                                                                                                                   Nucleic acid encoding trichosanthin protein - which can be used inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV expression

Example 7: Fig 19: 53pp; English.

The clone pQ30E, containing a 0.6kb insert, which was isolated from a T.kirilowin library (see Q26501), was used as a probe to isolate additional sequences homologous to alpha-TCS, i.e. other members of the RIP multi-gene family. Four unique cloned inserts were identified and designated pQ2, pQ3, pQ12 and pQ24. Each insert see Q26499-Q26508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riboflavin; expression; rib-1; guanosine triphosphate;
GTP-cyclohydrolase II; rib-7; HTP-reductase; rib-2; DRAP-deaminase;
rib-4; DMRL-synthase; rib-5; riboflavin-synthase; rib-3;
                                  Ribosome inactivating protein deduced from p03.
TCS: alpha-trichosanthin; Radix trichosanthin; abortifacient; RIP; multi-gene family; Maxim; HIV-infected human T cells; human immunodeficiency virus; probe.
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Pred. No. 2.30e+01;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buitrago Sema MJ, Garcia Ramirez JJ,
Revuelta Doval JL, Sanios Garcia MA;
WPI; 94-177113/22.
                                                                                   Trichosanthes kirilowii.
Key Location/Qualifiers
standard; Protein; 272 AA.
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/label= signal
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39.1%;
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GTP-cyclohydrolase II.
                        13-JAN-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae
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04-APR-1989; US-333184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1992; 238904.
19-NOV-1992; DE-238904.
(BADI ) BASF AG.
                                                                                                                                                                                                       (GENE-) GENELABS INC..
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Legoux R, Lelong P, Salome MLV;

WPI: 95-100554/14.

N-PSDB: 066268.

New DNA encoding enzyme for fragmenting N-acetyl:heparosan -
related protein, vector, transformed cells, etc.

Claim 2; Page 38-40; 54pp; French.

An enzyme which degrades high mol.wt. N-acetylheparosan into
fragments of lower mol.wt. (More suitable for use as pharmaceutical
staring materials) can be obtained from E.coli (K5) SEBR 3282. The
DNA sequence (086268) coding for the enzyme was isolated in a
CC plasmid (p838.7) which has been deposited in E.coli RRI strain as
CNCM I-1352. The deduced amino acid sequence (R71802) has homology
Sequence 820 AA;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                           N-acetylheparosan fragmentation enzyme.
N-acetylheparosan; polysaccharide K5; fragmentation; degradation; pharmaceutical starting material.
Escherichia coli (K5) ESERR 3282 (CNCM I-1013).
Key
binding_site 384.387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leu or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461..464
/label- potential_lipoprotein_attachment_site
/note= "Asn-X1-X2-Ser motif (X1-11e, Leu or Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411..414
/note=."Asn-X1-X2-Ser motif (X1=1le, Leu or and X2-Val, lle or Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "strongly charged C-terminal region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.2%; Score 70; DB 13; Length 820; Best Local Similarity 34.3%; Pred. No. 4.14e+01; Matches 12; Conservative 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "Asn-X1-X2-Ser motif (X1-11e, Leu and X2-Val, 11e or Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.14e+01;
9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Asn-X1-X2-Ser motif (X1-11e, and X2-Val, 11e or Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motif (X1=11e,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 gvsikdfgaqngilndnkd-aftkslhsfssvfvp 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and X2=Val, Ile or Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and X2-Val, Ile or Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Asn-X1-X2-Ser
                                                114 glale-fddstgellaskattwdahndt 140
                                                                              Ä.
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for

1;

Gaps

Length 129;

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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M. tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Host cell expressing surface layer protein fusion protein - used for host presentation of antigens and vaccine prodn.

Disclosure: Fig. 6: 95pp; English.

A probe based on the N-terminal sequence of B. sphaericus P-1 (LMG P-13655) surface layer protein was used to screen an HindIII-generated library to isolate the slp gene. Promoter regions of the gene are used in genetic constructs providing surface expression of heterologous proteins in P-1 hosts.
                                                             New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis Claim 1: Page 223; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surface layer protein; SLP; fusion protein; vaccine; antigen; surface expression; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W41513 standard; Protein; 371 AA.
W41513;
W7-1998 (first entry)
W meningitidis alpha-2,3-sialyltransferase protein.
Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid; biologically active oligosaccharide; sialyl-modified protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 1252; 6.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 37; I
6.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ltlrllaasagilsaa-afaapaqanpvddafia 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|: :: |:| ||| |::::| |:| :
62 LRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..30
/label- Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desomer J, Dhaese P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R80530 standard; Protein; 1252 AA. R80530;
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Local Similarity 31.3%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.3%;
Best Local Similarity 26.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1994; GB-000650.
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WO9747749-Al.
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10-JUN-1997; CA0390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sphaericus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-1995; E00147
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WPI; 95-263827/34.
N-PSDB; 099430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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   WPI; 98-
N-PSDB;
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      셤
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This sequence represents a Staphylococcus aureus protein, that based on homology with an Escherichia coll protein, is a nickel-binding periplasmic protein precursor, and is encoded by a DNA sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides.

Conditions which may be treated include bacterial infections, especially respiratory, cardiac, gastrointestinal, central nervous, eye, kidney, crimary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. Pylori infection.
                                                      30-0CT-1998 (first entry)
Nickel-binding periplasmic protein precursor.
Stabhylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "residues designated X are unspecified, and represented as Xaa in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in vaccines and for treatment of bacterial infections of respiratory tract and central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences from Staphylococcus aureus WCHU29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM FUC.
Black MT, Burnham MKR, Hodgson JF, Knowles DJC,
Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1999 (first entry)
Mycobacterium tuberculosis antigen CFPBA.
Mycobacterium tuberculosis; antigen; vaccine; immunological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STAT-) STATENS SERUM INST.
Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB,
Rosenkrands I, Weldingh K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.11e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 tvelnlkeayqpalaelamprpyvfvspkd 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGLHLR-VFDPSTGALVDSKSYAFSTSND 85
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 6
W72935 standard; Protein; 129 AA.
      Z
W77551 standard; Protein; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.3%;
Best Local Similarity 23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1998; DK0132.
05-JAN-1998; US-070488.
02-APR-1997; DK-000376.
18-APR-1997; US-044624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1996; US-027032.
                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference 1..119
                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1997; 307485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98-252940/23.
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Gaps

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8; Indels

57

Matches

g ò Pred. No.

PCT-US99-13024-2-09.rag

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Best Local Similarity 39.1%;
Matches 9: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimeric ribosome-inactivating protein - also chimeric ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing chimeric ribosome-inactivating protein precursors containing chimeric ribosome-inactivating protein Ribosome Inactivating Claim 2: Column 117-118: 121pp; English.

The sequences given in W21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins (RIP's), which may be used in the construction of the internal peptide linker. The proRIP has a selectively removable internal peptide linker. The proRIP has a selectively removal of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPS are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 268 RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein possible make the previous provide protein prossible make the machime provide protein prossible make the machime provide protein prossible make the provide protein prossible make the machime make the provide protein prossible make the provide protein processible make the processible to provide protein processible make the processible make the
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                                                                                                                                                                                                               claim 31; Page 38; 50pp; English.
This sequence represents an alpha-2,3-sialyltransferase which has been isolated from Neisseria meningitidis. The protein can be used as a reagent for adding a sialic acid residue to an acceptor having a terminal galactose residue, e.g. in synthesis of biologically active oligosaccharides or sialyl "modified proteins or lipids. The nucleic acid sequence can be used for the recombinant production of
                                                                                                       N-PSDB; V04125.
Nucleic acid sequence encoding Neisseria
alpha-2,3-sialy1:transferase - useful to add sialic acid to acceptor
with terminal galactose residue for synthesis of biologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N 91ycosidase; glycosidic bond; liver; rat; ribosomal 288 RNA; cellular proliferation; HIV-infected T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138..148
/note= "Position of possible insertion of internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 29; Length 371;
Pred. No. 7.42e+01;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                possible. The RIP can be used to make cytotoxic conjugates
Sequence 248 AA:
                                                               Gilbert M, Jennings MP, Wakarchuk WW, Young WPI; 98-052313/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W21704 standard; Protein; 248 AA.
                        10-JUN-1996; US-019520.
(CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morgan AER, Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                   alpha-2,3-sialyltransferase.
Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%;
Local Similarity 47.1%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 iktfddgtgnligsssy 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1997.
11-JUN-1990; 535636.
11-JUN-1990; US-535636.
09-DEC-1992; US-987927.
26-JAN-1995; US-378761.
(DOWC.) DOWELANCO.
  06-JUN-1997; US-872485
10-JUN-1996; US-019520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hey TD, Molywar, 97-309831/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luffa cylindrica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5635384-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W21704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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Length 248;

DB 23;

28.4%; Score 66;

Query Match

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13-MAY-1992; U09487.

14-NOV-1992; U09487.

15-MAY-1992; U5-901707.

16-NOV-1992; U5-901707.

17-MAY-1992; U5-901707.

18-CAMA ) XOMA CORP.

18 Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

19 MPI; 93-16761720.

10 MPI; 93-16761720.

11 MPI; 93-16761720.

12 Cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo bisclosure; Page 95-96; 163pp; English.

17 Cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo bisclosure; Page 95-96; 163pp; English.

17 The Invention covers analogues of the invention have a cysteine and the analogues of the invention have a cystein carresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of cricin A chain. The analogues are pref. Joined via a distubhide cell, e.g. inkage to a molecule which specifically binds to a target cell, e.g.
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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01-JAN-1996 (first entry)
Type I ribosome-inactivating protein luffin.
Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-1993 (first entry)
Buth type I RIP Luffin.
Type I ribosome-inactivating protein; ricin; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; loofah.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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/note- "in ricin A-chain and the Type I RIPS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                              Indels
8.99e+01;
8;
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Pred. No. 8.99e+01;
6; Mismatches 8
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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label see above
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                                                                                                                                                    73 gylvnstsyffnesdaklasgyv 95
                                                                                                                                                                                             73 gylvnstsyffnesdaklasgyv 95
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                                                                                                                                                                                                                                                                                                                                                 T 10
R37294 standard; protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 11
R74180 standard; protein; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.4%;
larity 39.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an antibody fragment.
Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_difference
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standard; Protein; 248 AA.

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Polynucleotide(s) encoding gelonin analogues - having a cystein residue for intermolecular bonding for the prodn. of immuno-toxins(s) by Sciosure; Figure 4; 66pp; English.

Pacciosure; Figure 4; 66pp; English.

Analogues of Type I RIP are defined as non-naturally occurring polypeptides that share the ribosome-inactivating activity of the natural protein but differ in AA sequence. Preferred analogues have a cys available for disulfide bonding located at a posn. it its AA sequence from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy terminus of the analogue. (R74176 is the sequence of ricin A-chain RTA, which is a Type I RIPP). The primary AA to the carboxy terminus of the analogue. (R74176 is the sequence of ricin A-chain RTA, which is a Type I RIPP). The primary AA sequence of the Type I RIPS gelonio, BRIP, mormordin II, luffin (see Islam et al. Agricultural Biological Chem., 54(5) 1343-45 1991], alphatrichosanthin (see Ho et al., 31. 1810. Chem., 54(5) 1343-45 1991], alphatrichosanthin (see Ho et al., BAL). Chem., 265, 8670-74 (1990), momordin I (see Ho et al., BAL). Chem., 264(12) 6629-37 1989), poskewed antiviral protein isolated from 2 seeds (see Kung et al., Agric. 3. Biochem., 183, 465-70 (1989) are individually aligned with the primary sequence of the ricin A-chain (see Halling et al., Nucleic Acids Res., 13, 6 and caporin (see Halling et al., Nucleic Acids Res., 13, 6 and caporin et al., Achain and the Type I RIPS are indicated in FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWI: 91-184-584-53.
Wew protein of Luffa cylindrica, extracted form seeds - is used for inhibiting protein synthesis in viral proliferation.
Claim 1, Ffg 1, 6pp; Japanese.
The protein is prepd. by extraction from seeds of L. cylindrica.
It has protein synthesis inhibiting activity and is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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3.99e+01;
~~hes 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 3; Length 248;
Pred. No. 8.99e+01;
6; Mismatches 8; Indels
                                                                                                                  Better MD, Carroll SF, Lane JA, Lei SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.4%; Score 66; DB 14
Best Local Similarity 39.1%; Pred. No. 8.99e+
Matches 9; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1991 (first entry)
Luffa cylindrica bioactive protein.
Protein synthesis inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 gylvnstsyffnesdaklasgyv 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GALVDSKSYAFSTSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GALVDSKSYAFSTSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 12
R12468 standard; Protein; 248
R12468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAY-1991.
22-SEP-1989; 247410.
22-SEP-1989; JP-247410.
(SUMO.) SUMITOMO CHEM IND KK.
WPI; 91-181458/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 gylvnstsyffnesdaklasgyv
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Similarity 39.18;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting viral growth. See also J0112999.
                                                      US-787567.
US-988430.
                16-MAY-1995.
09-DEC-1992; 988430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                  Bernhard SL, Bette:
WPI; 95-193480/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 AA;
                                                                                             (XOMA ) XOMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luffa cylindrica.
                                                   04-NOV-1991;
09-DEC-1992;
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셤
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RESULT

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DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in evaryotic cells without causing cell death claim 4: Column 117-120; 186pp; English. W25141 shows a Luffin-A (ribosome inhibitory protein, RIP) protein which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different RIPs may be produced with an internal linker including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W25141;
U2-DEC-1997 (first entry)
U2-DEC-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynuclectide(s) encoding type I ribosome-inactivating proteins
T therapeutic agents.
T therapeutic agents.
T therapeutic agents.
Signature of the first state of the first state of the first state of the nine RIPs described in R63903-R63911.
C RIPs are key components of cytocoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 28.4%; Score 66; DB 26; Length 248; Local Similarity 39.1%; Pred. No. 8.99e+01; les. 9; Conservative 6; Mismatches 8; Indels
                                                                                   Type I ribosome inactivating protein luffin.
Type I ribosome inactivating proteins; luffin; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                             Better MD, Carroll SS, Studnicka GM, Carroll SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W25141 standard; Protein; 248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 gylvnstsyffnesdaklasgyv 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y TD, Morgan AER, Walsh TA;
I; 97-362934/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GALVDSKSYAFSTSNDTTSAAFV 92
                                                         (first entry)
                                                                                                                                                                                   graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5646026-A.

08-JUL-1997.

11-JUN-1990. 535636.

09-DEC-1992. US-987927.

11-JUN-1990. US-355636.

26-JUN-1995. US-37561.
                                                                                                                                                                                                                                                                                24-NOV-1994.
112-MAY-1994; U05348.
112-MAY-1993; US-064691.
(XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-006804/01.
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maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs can be used in the construction of therapeutic coxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing viewer, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to then converted to active RIP proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Luffin: ribosome inactivating protein; RIP; loofah; inhibition;
protein translation; protein synthesis; viral proliferation.
Luffa cylindrica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 24; Length 248;
Pred. No. 8.99e+01;
6; Mismatches 8; Indels
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R53731 standard; Protein; 276 AA.
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(TORA.) TORAY IND INC.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:25:00 1999; MasPar time 4.63 Seconds 320.071 Million cell updates/sec Run on:

Tabular output not generated.

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PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

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Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 32.689; Variance 57.122; scale 0.572

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##ncalccule_type DNA ##residues 1-345 ##label GOF ##cross-references EMBL:23794; NID:9536040; PID:9536041; MIPS:YBL033c ##experimental_source strain S288C

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senerics #introns	41/2;	83/1;	16	2/1; 186/1;	; 604/1; 613/3; 653,	3/2; 1082/3	2/3;
SUMMARY	1169/3; #length 1	9/3; 1 th 122	207	/1 #molecular	-weight 136273 #c	checksum	2236
Query Match Best Local Simi. Matches 9;	illarity Conser	31. y 37. ervati	7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Score 7 Pred. N 7; Mi	DB 2; Length 1 1.96e+00; atches 8; Inde	222; 1s 0;	Gaps 0
Db 788 LHLRTF	LHLRTFSVKINKFVSSNAYPI	FVSSNA	YPI	SSG 811			
QY 60 LHLRVF	LHLRVFDPSTGALVDSKSYAF	TVDSKS	YAF	STS 83			
RESULT 2 ENTRY TITLE	S45767 probable		#ty	<pre>#type complete GTP cvclohvdrolase</pre>	TI (BC 3 5 4 2	ָר מפסט מפסט	ŧ
	(Sa	ccharo	myc	es cerevis			,
ALIERNAIE_NAMES ORGANISM DATE	#form 26-Au	ın YBL al_nam g-1994	6 33 8 8 8	<pre>protein YBL033c; protein YBL0417 #formal_name Saccharomyces cerev 26-Aug-1994 #sequence revision 0</pre>	YBLO417 es cerevisiae vision 09-Sep-1994	# Fx + C	Change
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	\$45767; \$4656 \$45745	7; S46 5	565	; \$50971	;		
#authors	Gotte	au, A. offoss	ە ب	Onniaux, J.L P · van Dock	.L.; Purnelle, B.;	Skala,	J.; de
#submission	submi	tted t	0 (Prote	្ត	August	1994
#accession ##molecule		7 DNA					

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##residues 1-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *superfamily yeast cyclohydrolase II; cyclohydrolase homology GTP; hydrolase; riboflavin biosynthesis
                Skala, J.; van Dyck, L.; Purnelle, B.; Goffeau, A. Yeast (1994) 10[Suppl.A]:S13-S24

The sequence of an 8.8 kb segment on the left arm of chromosome Saccharomyces cerevisiae reveals four new open reading frames including homologs of animal DNA polymerase alpha-primases and bacterial GTP cyclohydrolase
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##molecule_Lype DNA
##csidues
1345 ##label SKA
##cross-references EMBL:X74738; NID:9511140; PID:9511141
##experimental_source strain $288C;
BNCE
Short Short Saiz, J.; Santos, M.A.; Plaza, M.A.; Revuelta, J.L.
uthors Saiz, J.; Santos, M.A.; Plaza, M.A.; Revuelta, J.L.
uthors committed to the EMBL Data Library, February 1993
escription Cloning and sequencing of the RIB1 gene from Saccharomyces
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hypothetical protein April 333 - Archaeoglobus fulgidus
#formal_name Archaeoglobus fulgidus
05-Dec-1997 *sequence_revision 05-Dec-1997 *text_change
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#cross-references MUID:98049343
#accession H69418
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Pred. No. 2.75e+00;
4; Mismatches 9; Indels
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##cross-references SGD:S0000129; MIPS:YBL033c
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larity 50.0%; Pred. No. 2
Conservative 4; Mismat
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##molecule_type DNA
##stabel KLE
##cross-references GB:AE001010; GB:AE000782; NID:g2689333; PID:g2649225;
##cross-references GB:AE01010; GB:AE000782; NID:g2689333; PID:g2649225;
##CR:AF1353
##molecular-weight 39283 #checksum 2579
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Characterization of the aac(6')-Ik gene of Acinetobacter sp.
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#formal_name Prevotella ruminicola
22-Nov-1993 #sequence_revision 26-May-1995 #text_change
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gene aac(6')-Ik protein - Acinetobacter sp.
#formal_name Acinetobacter sp.
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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#superfamily 6'-N-acetyltransferase
#length 145 #molecular-weight 16638 #checksum 8491
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##cross-references GB:L29510; NID:g847646; PID:g847647
##experimental_source Acinetobacter sp. 6
                                                                                                                                                                        2.75e+00;
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Larity 28.1%; Pred. No. 2.75e+00;
Conservative 12; Mismatches 11
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3.86e+00;
                                                                                                                                                  DB 2;
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12; Misma
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Pred. No.
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#accession 140238
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57.1%;
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30.6%;
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#product oncofetal trophoblast glycoprotein 514 #status
predicted #label MAT
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                                                                                                                                                                                                                          *authors Machado, H.B.; Yates, M.G.; Funayama, S.; Rigo, L.U.; Steffens, M.B.; Souza, E.M.; Pedrosa, F.O. afournal can. J. Microbiol. (1995) 41:674-684 title The ntrBC genes of Azospirillum brasilense are part of a nifR3-like-ntrB-ntrC operon and are negatively regulated.
                                                                                                      139495 #type fragment

Mypothetial protein 4 - Acospirillum brasilense (fragment)
#formal_name Acospirillum brasilense
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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J. Biol. Chem. (1994) 269:9319-9324
Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains leucine-rich repeats.
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CLASSIFICATION #superfamily leucine-rich alpha-2-glycoprotein repeat
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##molecule_type DNA
##residues
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Pred. No. 3.86e+00;
6; Mismatches 10; Indels
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                    42 ALQLLVYSDDHAVGMLEASIRYEYVNGTETSPVAFL 77
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Best Local Similarity 44.8%;
Matches 13; Conservative
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nes 8; Conservative
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139495; S49974
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Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conway, A.; Kurtz, D.; Oji, O.; Shen, Y.; Toriumi, M.; Vysotskaia, V.; Yu, G.; Davis, R.W.; Federspiel, N.A.; Theologis, A.; Ecker, J.R. submitted to the EMBL Data Library, April 1998 Genomic sequence for Arabidopsis thaliana BAC F22013.
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RNA polymerase sigma-factor, plastid - Arabidopsis thaliana
protein F22013.2
*formal_name Arabidopsis thaliana *common_name mouse-ear
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##residues 1-889 ##label BOW
##cross-references EMEL:247814; NID:9642294; PID:9642299; MIPS:YDR027c
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submitted to the EMBL Data Library, February 1996
Sequencing and analysis of a 35.4 kb region on the left ar
of Chromosome IV for Saccharomyces cerevisiae reveal 23
open reading frames.
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                                                                                                                                              12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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#submission submitted to the Protein Sequence Database, July 1996
#accession S67840
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##residues 1-572 ##label SHI
##cross-references EMBL:AC003981; NID:g3063438; PID:g3063440
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Pred. No. 3.86e+00;
12; Mismatches 13; Indels
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60 LHLRVFDPSTGALVDSKSYAFSTSNDTTSAA 90
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hypothetical protein ORF64 - saimiriine herpesvirus 1 (strain
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                                                        #authors Eide, L.G.; Sander, C.; Prydz, H.
#journal Yeast (1996) 12:1085-1090
#title Sequencing and analysis of a 35.4 kb region on the left of chromosome IV from Saccharomyces cerevisiae reveal open reading frames.
#cross-references MUID:97051598
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host Saimiri sciureus (common squirrel monkey)
16.oct-1992 #sequence_revision 16-oct-1992 #text_change
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#length 2469 #molecular-weight 280165 #checksum 4051
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#length 889 #molecular-weight 101519 #checksum 1524
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Pred. No. 3.86e+00;
8; Mismatches 12; Indels
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##residues 1-2469 ##label ALB
##cross-references GB:X64346; NID:g60320; PID:g60385
:NCE A37309
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##residues 1-86
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#note YDR027c
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#type complete

D69200

11

RESULT ENTRY

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#domain signal sequence #status predicted #label SIG\
#product hemagglutinin HA1 #status predicted #label HA1\
#product hemagglutinin HA2 #status predicted #label HA2\
#domain transmembrane #status predicted #label TM1\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:AE000854; GB:AE000666; NID:g2621839; PID:g2621840 ##exper1mental_source strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Sugita, S.; Yoshioka, Y.; Itamura, S.; Kanegae, Y.; Oguchi,
K.; Gojobori, T.; Nerome, K.; Oya, A.
#journal J. Mol. Evol. (1991) 32:16-23
#title Molecular evolution of hemagglutinin genes of HINI swine and human influenza A viruses.
#cross_references_MUID:91186408
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                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis
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glycoprotein; hemagglutinin; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *superfamily hypothetical protein MJ1374 *length 241 *molecular-weight 26734 *c.
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J. Bacteriol. (1997) 179:7135-7155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AGMNIHI-DPGPGALV--RSYQFDSDPRKLDAVMVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic actranslation not shown
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##cross-references EMBL:X57494
                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references MUID:98037514
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Best Local Similarity 38.9%;
Matches 14; Conservative
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#authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Shiroza, T.; Ueda, S.; Kuramitsu, H.K.
#journal J. Bacteriol. (1987) 169:4263-4270
#title Sequence analysis of the gtfB gene from Streptococcus mutans.
#across-references MUID:87308013
#accession C33135
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#product glucosytransferase #status predicted #label
MAT\
                                                                    *binding_site carbohydrate (Asn) (covalent) *status
                                                                                                                                                                                                                                                                                                                                                                         #formal_name Streptococcus mutans
31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
22-Nov-1996
JT0345; C33135
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*superfamily cpl repeat homology
duplication; glycosyltransferase; hexosyltransferase;
                                                                                      predicted
#length 566 #molecular-weight 63409 #checksum 2042
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#domain cpl repeat homology #label CP2\
#domain cpl repeat homology #label CP3
#length 1375 #molecular-weight 153021 #checksum
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Pred. No. 5.39e+00;
8; Mismatches 7; Indels
                                                                                                                                  Score 71; DB 2; Length 566;
Pred. No. 5.39e+00;
9; Mismatches 7; Indels
                                   #disulfide_bonds #status predicted\
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Gene (1988) 69:101-109
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sucrose 6-glucosyltransferase
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                                                                                                                                                                                                        259 FE-ATGNLVVPR-YAFAMNRDPGSGIIIS 285
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65 FDPSTGALVDSKSYAFSTSNDTTSAAFVS 93
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##residues 1-1375 ##label UED
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##cross-references GB:M17361
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*accession JT0345
                                                                                                                                    30.6%;
larity 37.9%;
Conservative
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NCE A33135
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Best Local Similarity 41.4%;
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                                                                                                                      Query Match
Best Local Similarity 3
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                                                  27,28,40,104,293,
304,498,557
21-481,59-292,
72-84,153-488,
296-320
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1253-1272
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#authors
#journal
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RESULT

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CGESSION
###Olecule_type DNA
##molecule_type DNA
##residues 1-1609 ##label FRO
##cross-references EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227;
##cross-references EMBL:X59789w
                                                                                                                                                                                              925345
Wilson, C.; Grisanti, P.; Frontali, L.
Yeast (1992) 8:569-575
The complete sequence of a 6146 bp fragment of Saccharomyces
cerevisiae chromosome III contains two new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
#journal Science (1992) 257:771-778
#title Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.
#cross-references MUID:92358234
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Escherichia coli
#formal_name Escherichia coli
02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
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Dhmori, H.
submitted to the EMBL Data Library, January 1993
Physical map of the cora region of the E.coli chromosome.
$25345 #type complete probable membrane protein YCR089w · yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain transmembrane #status predicted #label TMl\
                                                                         hypothetical protein YCR1102
#formal_name Saccharomyces cerevisiae
30.5ep-1993 #requence_revision 30-Sep-1993 #text_change
06-Feb-1998
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#length 1609 #molecular-weight 166047 #checksum 8346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Frontal1, L.; Grisanti, P.
#submission submitted to the Protein Sequence Database, March 1992
#accession S19504
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translation not shown
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Best Local Similarity 34.2%; Pred. No. 5.39e+00;
Matches 13; Conservative 12; Mismatches 12; Indels
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#tcross-references SGD:S0000685; MIPS:YCR089w
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                                                       cerevisiae)
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#submission
#description
                                                                         ALTERNATE_NAMES
ORGANISM
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##Accession S30745
##RACCESSION BOAD
##RACCESSION BOAD
##RACCESSION BOAD
##RACCESTOR BOAD
##ACOS-TEGETENCE BOAD
##ACOS-TEGETENCE BOAD
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 3.53 Seconds 296.202 Million cell updates/sec Wed Sep 1 16:23:45 1999; MPsrch_pp Run on:

1 SAGLHLRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS 37 (57-93) from PCTUS9913024.pep (9 of 12) 232 >PCT-US99-13024-2 Description: Perfect Score: Sequence:

Tabular output not generated.

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 Database:

1:swissprot

Mean 33.585; Variance 52.447; scale 0.640 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	7.18e-01	1.04e+00	1.50e+00	1.50e+00	2.16e+00	2.16e+00	3.10e+00	3.10e+00	3.10e+00	3.10e+00	4.42e+00	6.29e+00	6.29e+00	8.91e+00	8.91e+00	8.91e+00	8.91e+00	8.91e+00	8.91e+00	8.91e+00	8.91e+00	1.26e+01	1.26e+01
	Description	HYPOTHETICAL 136.3 KD	GTP CYCLOHYDROLASE II	NITROGEN REGULATION PR	PROBABLE LARGE TEGUMEN	GLUCOSYLTRANSFERASE-SI	FACTOR INDUCED GENE 2.	HYPOTHETICAL 15.8 KD P	HYPOTHETICAL 104.4 KD	IMMUNOGLOBULIN A1 PROT	HANSENULA MRAKII KILLE	DNA REPLICATION FORK B	PARVALBUMIN BETA.	HYPOTHETICAL PROTEIN M	17.3 KD CLASS I HEAT S	HYPOTHETICAL 27.2 KD P	MINOR CAPSID PROTEIN L	COLLAGEN ALPHA 1(XII)	ISOLEUCYL-TRNA SYNTHET	NONSTRUCTURAL POLYPROT	COLLAGEN ALPHA 1(XII)	COLLAGEN ALPHA 1(XII)	PARVALBUMIN BETA.	HYDROXYMETHYLGLUTARYL-
SUMMARIES	QI QI	YMH5_CAEEL	GCH2_YEAST	NTRY_AZOBR	TEGU_HSVSA	GTFC_STRMU	FIG2_YEAST	YIGG_ECOLI	YMB4_CAEEL	IGA3_HAEIN	HKR1_YEAST	FOB1_YEAST	PRVB_ESOLU	Y700_METJA	HS11_SOYBN	YO23_MYCTU	VL2_HPV09	CA1C_RABIT	SYL_TREPA	POLN_SFV	CA1C_HUMAN	CAIC_MOUSE	PRVB_MERBI	HMCS_DICDI
	DB	-	-	-	٦	H	-4	-	-	Н	-	~	Н	-	-	٦	-	 1	-	٦	~	ч	Н	٦
	Length DB	1222	345	300	2469	1375	1609	138	932	1545	1802	266	107	324	153	256	533	639	1091	2431	3063	3067	108	163
œ	Query	31.9	31.5	31.0	31.0	30.6	30.6	30.2	30.2	30.2	30.5	29.7	29.3	29.3	28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.9	28.4	28.4
	Score	74	73	72	72	71	71	70	70	70	70	69	89	89	29	67	29	29	29	67	67	67	99	99
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01 1.76e+01	2.47e+01 2.47e+01 2.47e+01
RIBOSOME-INACTIVATING T-COMPLEX PROTEIN 1, D T-COMPLEX PROTEIN 1, D PROLYL-TRNA SYNTHETASE METHYLMALONYL-COA WUTA GLUCOSYLTRANSFERASE-S PARYALBUMIN BETA. ATRIAL GLAND PEPTIDE A ATRIAL GLAND PEPTIDE A ATRIAL GLAND PEPTIDE A MOVEMENT PROTEIN (CELL MOVEMENT PROTEIN (LIL T-COMPLEX PROTEIN 1, D MINOR CAPSID PROTEIN 1, D MINOR CAPSI	ASPARAGINE SYNTHETASE HYPOTHETICAL 251.0 KD DYNEIN BETA CHAIN, CIL
RIPA_LUFCY TCPD_MOUSE SYP_HELPY WUTA_STRUM GTFD_STRUM GTFD_STRUM GTFD_STRUM MOVP_ANVIA MOVP_ANVIA PURA_THIFE TRAA_STRAM TRAA_STRAM TCPD_FUGRU VI2_HPV41 HENA_IAIN TCAA_CLODI CSPE_ECOLI CSPE_ECOLI	ASN1_LOTJA YCS2_YEAST DYHC_TRIGR
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277 5739 5739 108 108 108 108 108 108 108 108 108 108	585 2167 4466
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ALIGNMENTS

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RN STAIN-BRISTOL N2;

KATAIN-BRISTOL N2;

KATISON R., AINSCOUGH R., ANDERSON K., BAINES C., BERKS M.,

CRAZTON M., DEAR S., DU Z., DURBIN R., FRAFELLO A., FRASER A.,

BONFIGLUD L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,

JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,

LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPPA A., SAUNDERS D., SHOWNKEEN R.,

SINS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,

NA SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VANGHAN K.,

WOHLDMAN P.,

WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                  01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 136.3 KD PROTEIN FS8A4.5 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1222 AA; 136273 MW; 2F6802B7 CRC32;
                                                                    1222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEGAUS.
NATURE 368:32-38(1994).
-! SIMILARITY: TO REVERSE TRANSCRIPTASE.
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S4097/; S4097/; WORMPEP; F58A4.5; CE00221. PFAM; PF00078; rvt; 1. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 222179; E1347484; -.
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                             CAENORHABDITIS ELEGANS
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YMH5_CAEEL
P34472:
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                         RESULT
                                                                         SOW RRY RESERVE RESERVED BY READ BY RE
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31.9%; Score 74; DB 1; Length 1222;

Query Match

PCT-US99-13024-2-09.rsp

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TRANSMEM
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SEQUENCE
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TRANSMEM
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                                   ö
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKALA J., VAN DYCK L., PURNELLE B., GOFFEAU A.;
"The sequence of an 8.8 kb segment on the left arm of chromosome II from Saccharomyces cerevisiae reveals four new open reading frames including homologs of animal DNA polymerase alpha-primases and bacterial GTP cyclohydrolase II.";
YEAST 10:S13-S24(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SAIZ J.E., SANTOS M.A., PLAZA M.A., REVUELTA J.L.;
SUBMITTED (FEB-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYIT (ACTIVITY: GTP + 31 (2)0 = FORMATE + 2,5-DIAMINO-6-HYDROXY 4 (-5-PROSPHORIBOSYLAMINO)PYRIMIDINE + PYROPHOSPHATE.
-!- PATHWAY: RIBOFLAVIN BIOSYNTHESIS.
-!- SIMILARITY: SOME, TO BACTERIAL GTP CYCLOHYDROLASE II (RIBA).
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Pred. No. 1.04e+00;
4; Mismatches 9; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISION TO 181.
SKALA J., VAN DYCK L., PURNELLE B., GOFFEAU A.;
SUBMITTED (XXX-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
Best Local Similarity 37.5%; Pred. No. 7.18e-01;
Matches 9; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S45/0, September 1997; SGD; LO001634; RIB1.
PFAM; PF00925; GTP_cyclohydro2; 1.
RIBOFLAVIN BIOSYNTHESIS; HYDROLASE.
RIBOFLAVIN 345 AA; 38332 MW; C49A8442 CRC32;
                                                                                                                                                                                                                                                                                                                                        (REL. 30, CREATED)
(REL. 37, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                              345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 AA.
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(REL. 32, LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                               GTP CYCLOHYDROLASE II (EC 3.5.4.25). RIBI OR YBL033C OR YBL0417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
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                                                                                          788 LHLRTFSVKINKFVSSNAYPISSG 811
                                                                                                                                31.5%;
llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 235794; E1263937; -. EMBL; X74738; G511141; -. EMBL; Z21617; G642219; -. PIR; S45767; S45767.
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288C;
MEDLINE; 94378718.
                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998
15-DEC-1998
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01-NOV-1995
                                                                                                                                                                                                                                                                                                                                        01-0CT-1994
                                                                                                                                                                                                                                                                           GCH2_YEAST
P38066;
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P45675;
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DD4CB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 92333688.
ALBRECHT J.-C., NICHOLAS J., BILLER D., CAMERON K.R., BIESINGER B., NEWMAN C., WITTMANN S., CRAXTON M.A., COLEMAN H., FLECKENSTEIN B., HONESS R.W.;
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NITROGEN REGULATION PROTEIN NTRY HOMOLOG (EC 2.7.3.-) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NICHOLAS J., CAMERON K.R., COLEMAN H., NEWMAN C., HONESS R.W.; "Analysis of nucleotide sequence of the rightmost 43 kbp or herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
                                       AZOSPIRILLUM BRASILENSE.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHODOSPIRILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SENSORY TRANSDUCTION: TRANSFERASE; KINASE; PHOSPHORYLATION: NITROGEN FIXATION; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of the herpesvirus saimiri genome."; J. VIROL. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERPESVIRUS SAIMIRI (STRAIN 11).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 72; DB 1; L
Pred. No. 1.50e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32998 MW; 0775B134 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VFDPSTGALVDSKSYAFS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z37984; G599603; -.
                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SP7 / ATCC 29145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
127
222
300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
202
300
300
300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 92230228.
                                                                                  AZOSPIRILLUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
TEGU_HSVSA
Q01056:
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Thu Sep

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae chromosome III contains two new open reading frames."; YEAST 8:569-575(1992).
                                                                                           EMBL; M17361; G153641; -.
PIR; JT0345; JT0345.
PIR; JT0345; JT0345.
PIR; C33135; C33135.
PFAM; PF00128; alpha-amylase; 1.
TRANSFENSE; GLYCOSYLTRANSFENSE; SIGNAL; REPEAT; DENTAL CARIES.
SIGNAL 1 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 9337594.
WILSON C., GRISANI P., FRONTALI L.;
"The complete sequence of a 6146 bp fragment of Saccharomyces
                                                                                                                                                                                                                    CATALTIC (APPROXIMATE).
2.4 A. I C AND 1 AC REPEATS.
A REPEAT.
A REPEAT.
C REPEAT.
AC REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 1; Length 1609;
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.16e+00;
8; Mismatches 7; Indels
                                                                                                                                                                                                        GLUCOSYLTRANSFERASE-SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1609 AA; 166049 MW; DE974CE8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 SSSFELPVTAPSSSSLPSSTSLTFTSVNPSQSWTSFNS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.16e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
FACTOR INDUCED GENE 2.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- FUNCTION: REQUIRED FOR EFFICIENT MATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1609 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1093 SSVTGLVFDGKGYVYYSTSGNQAKNAFIS 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIG2 OR YCR089W OR YCR89W OR YCR1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- INDUCTION: BY MATING PHEROMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                   AA; 153022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (REL. 22, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.6%;
larity 34.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        30.68;
                                                                                                                                                                                                                                                                                                                                                                                                                         larity 41.4%;
Conservative
                                                                              EMBL; M22054; G153643; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59720; E264634; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                       1050
1375
1159
1159
1200
1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S19504; S19504.
PIR; S25345; S25345.
SGD; L0003312; FIG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIG2_YEAST
P25653;
                                                                                                                                                                                                                                                                                                                                                  REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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DOMAIN
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REPEAT
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Matches
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A SHIROZA T., UEDA S., KURANITSU H.K.;
SHIROZA T., UEDA S., KURANITSU H.K.;

"Sequence analysis of the giff gene from Streptococcus mutans.";

"L J. BACTERIOL. 169:4263-4270(1987).

-!- FUNCTION: PRODUCTION OF EXTRACELLUIAR GLUCANS, THAT ARE THOUGHT

TO PLAY A KEY ROLE IN THE DEVELORENT OF THE DEWTAL PLAQUE BECAUSE

OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE

AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-- CATALITY CATIVITY: SUCROSE + (1.6-ALPHA-D-GLUCOSYL) (N) -

D-FRUCTOSE + (1.6-ALPHA-D-GLUCOSYL) (N-1).

-- SUBCELLULAR LOCATION: SECRETED.

-- OTSELSES: DEWTAL CARIES.

-- OTSELSES: DEWTAL CARIES.

-- OTSELSES: DEWTAL CARIES.

-- OTSELSES: DEWTAL CARIES.

-- OTSELSES: MATER-INSOSIDIE GLUCANS (ALPHA 1,3-LINKED GLUCANS (ALPHA 1,6-LINKASES), GTF-SI SYNTHESIZES BOTH FORMS OF
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., KURAMITSU H.K.; of the gtfC gene from Streptococcus mutans GS-5.";
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCANBINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                           TOGETHER HSV-1 UL36,
                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                           Score 72; DB 1; Length 2469;
Pred. No. 1.50e+00;
8; Mismatches 10; Indels
organization between HVS and Epstein-Barr virus.";
VIROLOGY 188:296-310(1992).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELOMGS TO FAMILY THAT GROUPS TOGETHER HS
EHV-1 24, EBV BPLE1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (REL. 09, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
62UCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GTF-SI)
(DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                     EMBL; X64346; G60385; -.
EMBL; M86409; G330993; -.
PIR; H36612; H36812.
SEQUENCE 2469 AA: 280165 MW; 1B72F5F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   161 IFDPHSCPLVPNSPAHVFSTSNVNDAIEYLS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VFDPSTGALV-DSKSYAFSTSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           / Match 31.0%;
Local Similarity 38.7%;
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of
GENE 69:101-109(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREPTOCOCCUS MUTANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UEDA S., SHIROZA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-GS-5;
MEDLINE; 89137980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTFC_STRMU ST
P13470; P05427;
01-NOV-1988 (REL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GS-5
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                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONTIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-KIZ. 7 MG1655;
MREDLINE; 92358334.
DANIELS D.L., PLUNKETT G. III, BURLAND V.D., BLATTNER F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
SCIENCE 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA, METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                        BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
               Score 70; DB 1; Length 138;
Pred. No. 3.10e+00;
""." matches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.
                                                                                                                                                                      TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL PROTEIN.
SEQUENCE 138 AA; 15794 MW; C92E2E54 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000457; G1790251; -. PIR; S30745; S30745. PIR; S30708; ECGGENE; EG11465; YIGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LRIFIPTSNGKISRRYIFS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LRVFDPSTGALVDSKSYAFS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-574 FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                        EMBL; L02122; G145579; -. EMBL; M87049; G148217; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
                                                                                                                                                                      SUBMITTED (JAN-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                        SEQUENCE FROM N.A. STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94150718.
                                                                                                ESCHERICHIA COLI
                                                                                                                    ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YMB4_CAEEL
Q03601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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               RESULT
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                          PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SIMS M., SNALDON N., SMITH A., SONHAHAMER E., STADEN R., SULGYON J., THIERRY MIEG J., THOMAS K., VADDIN M., VAUGHAN K., WAIERSON R., WAISON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: SECRETED.
-!- DOMAIN: THE SIGNAL PEPTIDE GUIDES THE PRECURSOR TO THE PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
IMMUNOCLOBULIN A1 PROTEASE PRECURSOR (EC 3.4.21.72) (IGA1 PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                         Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOUTH ASSOCIATES WITH SOUTH ASSOCIATES WITH SOUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS SIMILARITY).
                                                                                                                                           WOHLDMAN P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN; ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 1; Length 932; Pred. No. 3.10e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         NATÜRE 368:32-38(1994).
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING 43 83 C3HC4-TYPE.
SEQUENCE 932 AA; 104438 MW; 45C877B4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1545 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 TEGLEYLRNFQPDADELFNRK-LRFSAGDDAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 SAGLH-LRVFDPSTGALVDSKSYAFSTSNDTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S28275; S28275.
WORNDER: F5468.4; CEO5942.
PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
PFAM; PF00097; zf-C3HC4; 1.
HSSP; P29590; LBOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.2%;
34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.2%;
Best Local Similarity 34.4%;
Matches 11; Conservative
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P45385;
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SER/THR ARCH.
12 X SA ANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-A-P-A-A-I-S-S-F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HANSENULA MRAKII KILLER TOXIN-RESISTANT
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-YNN 295,
MEDLINE: 9415687.
KASHARA S., YAMADA H., MIO T., SHIRATORI Y., MIYAMOTO C.,
YABE T., NAKAJIMA T., ICHISHIMA E., FURUICHI Y.;
Cloning of the Saccharomyes cerevisiae gene whose overexpression overcomes the effects of HM-1 killer toxin, which inhibits beta-glucan synthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. BACTERIOL. 176:1488-1499(1994).
-!- FUNCTION: COULD REGULATE BETA-GLUCAN SYNTHESIS. OVEREXPRESSION
-!- PROVIDES RESISTANCE TO HM-1 KILLER TOXIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE).
-!- PTM: COULD BE O-GLYCOSYLATED IN SERINE/THREONINE RICH DOMAIN.
-! SIMILARITY: SOME, TO YEAST MSB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                              ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                    HANSENULA MRAKII KILLER TOXIN-RESISTANT PROTEIN 1 PRECURSOR
                                                                                              EMBL; M87490; G148909; -.
HYDROLASE; SERINE PROTEASE; TRANSMEMBRANE; 2YMOGEN; SIGNAL
                                                                                                                                                                                                               Score 70; DB 1; Length 1545; Pred. No. 3.10e+00;
                                                                                                                                                                                                                                             6; Indels
                                                                                                                           POTENTIAL.
IMMUNOGLOBULIN AL PROTEASE.
HELPER PEPTIDE (POTENTIAL).
                                                                                                                                                                                     93EE4AD6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APPROXIMATE)
                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                               PRT; 1802 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                         336 KIYEQYSAGSLIGSKTDYSWSSNGKTSTIT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN 1.
                                                                                                                                                                                                                                                                                          Y-T-S-P-
                                                                                                                                                                        PROBABLE.
                                                                                                                                                                                    1545 AA; 170627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; S69101; G545660; -.
SGD; L0000788; HKR1.
GLYCOPROTEIN; TRANSMEMBRANE;
SIGNAL 1 21
                                                                                                                                                                                                                30.2%;
26.7%;
                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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508
536
564
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                       1013
292
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKR1 OR YDR420W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
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453
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481
509
537
                                                                                                                                                                                                                                                                                                                                          )LT 10
HKR1_YEAST
P41809;
                                                                                                                                                                      ACT_SITE
SEQUENCE
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                                                                                                                              SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 97233188.
KOBATSHI T., HORIUCHI T.,
A yeast gene product, Fobl protein, required for both replication fork blocking and recombinational hotspot activities.";
GENES CELLS 1:465-474(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ESSENTIAL FOR BOTH DNA REPLICATION FORK BLOCKING AND RECOMBINATIONAL HOTSPOT ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
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STRAIN-S288C / AB972;
MURPHY L., SHORE L., HARRIS D., BARRELL B., RAJANDREAM M.A.,
WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                    Score 70; DB 1; Length 1802;
                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 1; Leng
Pred. No. 4.42e+00;
8; Mismatches 5;
                                                                                                                                                                                                                                                                                           84B6C85F CRC32;
                                                                                                                                                                                                                                                                                                                                                         No. 3.10e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A -> T (IN REF. 2)
49D933EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOBL TEAST STANDARD; PRT; 566 AA. 13129; 004587; SC CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) FOBL OR YERLIGON OR YEAST STANDATION UPDATE FOBL OR YERLIGON OR YEAST STANDATE OF THE OR YEAR OR YEAST STANDATE OF THE OR YEAR OF THE OR YEA
                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
5.
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112.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                           AA; 188890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 IHIEVFEPFNGEAIEGK-YSY 242
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566 AA; 65288 MW;
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                                                                                                                                                                                                                                                                                                                                                         larity 31.0%;
Conservative
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Best Local Similarity 33.3%;
Matches 7; Conservative
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  592
620
648
648
732
760
788
788
11253
11342
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Best Local Similarity
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1252
1293
1342
1400
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REPEAT
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                      NEOPTERYGII;
ESOCIDAE;
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-!- THIS PARVALBUMIN HAS AN ISOELECTRIC POINT OF 4.10.
-!- SIMILARITY: TO OTHER EF HAND CALCIUM BINDING PROTEINS, BELONGS TO THE PARVALBUMINS SUBFAMILY.
                                                                                                                                                         "The primary structure of the parvalbumin II of pike (Esox lucius)."; EUR. J. BIOCHEM. 70:305-318(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (0.91 ANGSTROMS).
DECLERCO J.-P., EVRARD C., LAMZIN V., PARELLO J.;
SUBMITTED (COT-1998) TO THE PDB DATA BANK.
-!- FUNCTION: IN MUSCLE, THE CALCIUM-BINDING PROTEIN PARVALBUMIN IS
THOUGHT TO BE INVOLVED IN MUSCLE RELAXATION.
-!- THIS IS ONE OF TWO MAJOR PARVALBUMINS FOUND IN THE WHITE MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A03054; PVPK2.
PDB: 1PAL; 15-JAN-92.
PDB: 2PAL; 15-JAN-92.
PDB: 3PAL; 15-JAN-92.
PDB: 4PAL; 15-JAN-92.
PDB: 4PAL; 15-JAN-92.
PDB: 2PVB: 07-OCT-98.
PROSITE: PSO0018; EF_HAND; 2.
PROSITE: PSO0036; efhand; 2.
CALCIMY-BINDING; MUSCLE PROTEIN; REPEAT; ACETYLATION; 3D-STRUCTURE.
                                                                                                                                                                                                 MEDLINE; 84051312.
PERMYAKOV E.A., MEDVEDKIN V.N., KALINICHENKO L.P., BURSTEIN E.A.; "Comparative study of physiochemical properties of two pike parvalbumins by means of their intrinsic tyrosyl and phenylalanyl
                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
MEDLINE, 91350177.
DECLERCQ J.-P., TINANT B., PARELLO J., RAMBAUD J.;
"Ionic interactions with parvalbumins. Crystal structure determination of pike 4.10 parvalbumin in four different ionic puvironments.":
                                                                                                                                                                                                                                                                                               HUBER R.;
pike 4.10
                                                                           ESOX LUCIUS (NORTHERN PIKE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
TELEOSTEI; EUTELEOSTEI; PROTACANTHOPTERYGII; ESOCIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLATION.
SITE 1 (BY SIMILARITY).
SITE 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                  MEDLINE; 89011963.
DECLERCO J.-P., TINANT B., PARELLO J., ETIENNE G., I Crystal structure determination and refinement of parvalloumin (minor component from Esox lucius)."; J. MOL. BIOL. 202:349-353(1988).
                                             (REL. 01, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                 107 AA.
                                                                                                                                                                                                                                                     ARCH. BIOCHEM. BIOPHYS. 227:9-20(1983).
                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                       environments.";
J. MoL. BIOL. 220:1017-1039(1991).
(5)
                                    01, CREATED)
                 STANDARD;
                                                                                                                                                                                         CALCIUM-BINDING DATA.
                                                                                                                                      MEDLINE; 77090998.
GERDAY C.;
                                  21-JUL-1986 (REL.
                                                                  PARVALBUMIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
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117
117
117
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                                             21-JUL-1986
15-DEC-1998
               PRVB_ESOLU
P02619;
                                                                                                                             SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.F., ADDAS M.D., REICH C.I.,
OVERBEEK R., KIRNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.K., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIENCE 273:1058-1073(1996).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-1- SIMILARITY: SOME, TO THE UPF0003 FAMILY.
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                       Score 68; DB 1; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 1; Length 324;
Pred. No. 6.29e+00;
14; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                            Pred. No. 6.29e+00;
                                                                                                                                                                                                                  11390 MW; 1D1088D7 CRC32;
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POTENTIAL.
7055857F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROFEIN MJ0700.
                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 AA
                                                                                                                                                                                                                                                                                                                                   64 LFLQNFSPSARALTDAETKAFLADGDKDGDGMIG 97
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                         29.38;
32.48;
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larity 26.7%;
Conservative
                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67516; G1591415; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
57
63
64
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72
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105
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                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conser
  59
64
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96
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96
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Q58111:
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SEQUENCE
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SEQUENCE
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173 HLRALEATRGALLERMPTSLSARFDRACA 201
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                                                                                                                                                                                                                                                                                                                               Job time : 15 secs.
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                                                                                                                                                                                             EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH HARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS TO CLASS I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYCOBACTERIUM TUBERCULOSIS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
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                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 1; Length 153;
Pred. No. 8.91e+00;
10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-H37RV,
MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (SEP-1996) TO EMBL/GENBARK/DDBJ DATA BANKS.
-!- SIMILARITY: LOW, TO E.COLI YDCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01031; HSP20; 1.
PFAM; PF00011; HSP20; 1.
PFAM; PC0011; HSP20; 1.
SEQUENCE MULTIGENE FAMILY.
SEQUENCE 153 AA; 17347 MW; 7D3410AC CRC32;
                                                                                                                               17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3) HSP17.3-B OR HS6871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.2 KD PROTEIN CY10H4.23.
                                                                                  153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 AA
                                                                                                                           LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 VFDPFSLDVWDPFKDFPFPSSLSAENSAFVS 45
 175 FEPTGRVLIIPNSYIFTASIENLTKGSPYI 204
                |:|: |: ::|| |::|: |::::: | 65 FDPSTGALVDSKSYAFSTS-ND-TTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                  PRT;
                                                                                                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQ
01-FEB-1994 (REL. 28, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Match 28.9%;
Local Similarity 38.7%;
Nes 12; Conservative
                                                                                  STANDARD;
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                                                                                                                                                                               (SOYBEAN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A02922;
                                                                                                                                                                                 GLYCINE MAX
                                                                                HS11_SOYBN
P02519;
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P71593;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 1; Length 256; Pred. No. 8.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                     256 AA; 27187 MW; CB2E71C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                          28.9%;
Similarity 31.0%;
9; Conservative
                                                                                                                                                                                                                                       EMBL; 280233; E267389; -. HYPOTHETICAL PROTEIN.
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Best Local Similarity
Matches 9; Conser
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protein - protein database search, using Smith-Waterman algorithm Wed Sep 1 16:24:17 1999; MasPar time 6.41 Seconds 315.183 Million cell updates/sec MPsrch_pp Run on:

>PCT-US99.13024-2 (57-93) from PCTUS9913024.pep (9 of 12) 232 1 SAGLHLRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS 37 Tabular output not generated. Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

Januar 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 32.300; Variance 54.738; scale 0.590 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description Pred. No.			æ			SOFFIER		
88 37.9 1577 2 054178 GLUCOSYLTRANSFERASE. 80 34.5 3443 14 01979 POLYPROTEIN. 74 31.9 1449 2 068542 GLUCOSYLTRANSFERASE N 74 31.9 1449 2 068542 GLUCOSYLTRANSFERASE N 73 31.5 353 1 028918 HYDOTHEITCAL 39.3 KD p 73 31.5 34 2 045397 KYLANASE PRECURSOR. 72 31.0 145 2 044246 6 AAC(6')-IK. 72 31.0 420 4 013641 ST4 ONOSFETAL ANTIGEN 72 31.0 574 10 022056 SIGMA PACTOR 2. 72 31.0 574 10 022056 SIGMA PACTOR 2. 73 31.0 574 10 022056 SIGMA PACTOR 2. 74 30.6 351 14 012676 HEMAGGLUTININ (FRAMEN STATEMEN STA	Result No.	Score	Query	Length	DB	Q1	Description	
80 34.5 3443 14 011979 POLYPROTEIN. 74 31.9 1449 2 047628 TIEB PROTEIN. 74 31.9 1449 2 055264 GLUCOSYLTRANSFERASE N 73 31.5 353 1 028918 HYDOTHEITCAL 39.3 KD P 73 31.5 34.2 046397 XYLANASE PRECURSOR. 72 31.0 145 2 044246 6 AAC(6')-IK. 72 31.0 420 4 013641 574 0NOOFETAL ANTIGEN 72 31.0 574 10 022056 SIGMA PACTOR 2. 72 31.0 574 10 022056 SIGMA PACTOR 2. 73 31.0 574 10 022056 SIGMA PACTOR 2. 74 30.6 357 14 012676 HEMAGGLUTININ (FRAMEN PACTOR 2.) 75 31.0 6 351 14 012676 HEMAGGLUTININ (FRAMEN PACTOR 2.) 76 31.0 6 357 14 067091 HEMAGGLUTININ (FRAMEN PACTOR 2.) 71 30.6 1455 2 069381 GLUCOSYLTRANSFERASE-SI 30.6 1455 2 069381 GLUCOSYLTRANSFERASE-SI 30.6 1455 2 069397	П	88	37.9	1577	7	954178	GLUCOSYLTRANSFERASE	9.51e-03
76 32.8 424 2 047628 TIEB PROTEIN. 74 31.9 1449 2 068542 GUUCOSYLTRANSFERASE N 74 31.9 1449 2 068542 GLUCOSYLTRANSFERASE N 73 31.5 353 1 028918 HYPOTHETICAL 39.3 KD p 73 31.5 584 2 045397 XYLANASE PRECURSOR. 72 31.0 145 2 044246 6 AAC(6.) -IK. 72 31.0 572 10 022056 PLASTID RNA POLYMERASE 72 31.0 572 10 022056 PLASTID RNA POLYMERASE 73 31.0 574 10 022455 SIGNA FACTOR 2. 71 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 357 14 012076 HEMAGGLUTININ (FRAGMEN P 71 30.6 357 14 0407091 HEMAGGLUTININ (FRAGMEN P 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI S 71 30.2 253 2 P96151 DNA FOR AMINOPEPTINASE	7	80	34.5	3443	14	011979	POLYPROTEIN.	2.016-01
74 31.9 1449 2 068542 GLUCOSYLTRANSFERASE N 1419 1449 2 055264 GLUCOSYLTRANSFERASE N 1410 145 2 045397 XYLANASE PRECURSOR. 72 31.0 145 2 04534 5 AAC(6')-IK. 72 31.0 572 10 022056 PLASTID RNA POLYMERASE N 1510 1574 10 022455 SIGNA FACTOR 2. 71 30.6 241 1 022455 SIGNA FACTOR 2. 71 30.6 351 14 012676 HEMAGGLUTININ (FRAGMEN 1510 1510 1510 1510 1510 1510 1510 151	٣	9,6	32.8	424	~	047628	TIEB PROTEIN.	8.68e-01
74 31.9 1449 2 Q55264 GLUCOSYLTRANSFERASE PR 73 31.5 353 1 028918 HYDOTHETICAL 39.3 KD P 73 31.5 354 1 028918 HYDOTHETICAL 39.3 KD P 73 31.0 145 2 044246 6 AAC(6')-IK. 72 31.0 420 4 013641 574 0NOESTAL ANTIGEN 72 31.0 574 10 022056 SIGMA FACTOR 2. 72 31.0 574 10 022056 SIGMA FACTOR 2. 71 30.6 351 14 012676 HEMAGGLUTININ (FRACMEN FOLSOMEN FOR FOLSOMEN FOLSOMEN FOLSOMEN FOR FOLSOMEN FOLSOM	4	74	31.9	1449	7	068542	GLUCOSYLTRANSFERASE N	1.77e+00
73 31.5 353 1 028918 HYPOTHETICAL 39.3 KD P 73 31.5 584 2 045397 XYLANASE PRECURSOR. 72 31.0 420 4 013641 5 T4 ONCOFETAL ANTIGEN 72 31.0 420 4 013641 5 T4 ONCOFETAL ANTIGEN 72 31.0 572 10 022455 SIGMA FACTOR 2. 72 31.0 574 10 022455 SIGMA FACTOR 2. 73 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 351 14 012676 HEMAGGLUTININ PRECURSO 71 30.6 351 14 067091 HEMAGGLUTININ PRECURSO 71 30.6 1350 2 069385 GLUCOSYLTRANSFERASE-SI 71 30.6 1455 2 069381 GLUCOSYLTRANSFERASE-SI 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 72 30.2 253 2 P96151 DNA FOR AMINOPEPTINASE	S	74	31.9		7	055264	GLUCOSYLTRANSFERASE PR	1.77e+00
73 31.5 584 2 045397 XYLANASE PRECURSOR. 72 31.0 145 2 044246 6 AAC(6')-IK. 72 31.0 145 1 0.22056 PLASTID RNA POLYMERASE 72 31.0 572 10 022056 PLASTID RNA POLYMERASE 72 31.0 574 10 022455 SIGMA FACTOR 2. 71 30.6 241 1 0.2645 CONSERVED PROTEIN. 71 30.6 351 14 012676 HEMAGGLUTININ (FRAGMEN FOR SIGMA FROMEN FOR SIGMA	9	73	31.5		1	028918	HYPOTHETICAL 39.3 KD P	~
72 31.0 145 2 044246 6 AAC(6')-IK. 72 31.0 420 4 013641 5T4 ONCETAL ANTIGEN 72 31.0 420 1 022056 PLASTID RNA POLYMERASE 72 31.0 574 10 022455 SIGMA FACTOR 2. 71 30.6 351 14 012676 HEMAGGLUTININ (FRACMEN PROSENCE) 71 30.6 357 14 057091 HEMAGGLUTININ (FRACMEN PROSENCE) 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 72 31.0 1455 2 069397 GLUCOSYLTRANSFERASE-SI 73 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE	7	73	31.5		7	045397	XYLANASE PRECURSOR.	2.52e+00
72 31.0 420 4 013641 5T4 ONCOFETAL ANTIGEN 72 31.0 572 10 022055 PLASTID RNA POLYMERASE 72 31.0 572 10 022455 SIGMA FACTOR 2. 72 31.0 889 3 012071 ORF:PZF889. 71 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 351 14 012676 HEMAGGLUTININ (FRACHEN FOR EACH FO	80	72	31.0	145	7	044246	6 AAC(6')-IK.	3.58e+00
72 31.0 572 10 022056 PLASTID RNA POLYMERASE 31.0 574 10 022455 SIGMA FACTOR 2. 31.0 89 3 012071 ORF: PEPEB89. 71 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 357 14 012676 HEMAGGLUTININ PRECURSO 71 30.6 357 14 047091 HEMAGGLUTININ PRECURSO 71 30.6 357 30 059382 GLUCOSYLTRANSFERASE-SI 57 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 57 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 57 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 57 30.6 1455 2 069387 GLUCOSYLTRANSFERASE-SI 57 30.2 253 2 996151 DNA FOR AMINOPEPTIDASE 31 30.2 253 2 996151 DNA FOR AMINOPEPTIDASE 31 30.2 253 2 906151 DNA FOR AMINOPEPTIDASE 31 30.2	6	72	31.0	420	4	013641	514 ONCOFETAL ANTIGEN	3.58e+00
72 31.0 574 10 022455 SIGMA FACTOR 2. 71 30.0 889 3 012071 ORF:PZEB89. 71 30.6 351 14 012676 HEMAGGLUTININ (FRAGMEN 5) 71 30.6 357 14 067091 HEMAGGLUTININ (FRAGMEN 5) 71 30.6 1455 2 069385 GLUCOSYLTRANSFERASE-SI 5) 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5) 71 30.6 1455 2 069387 GLUCOSYLTRANSFERASE-SI 5) 71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5) 70 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE	10	72	31.0	572	10	022056	PLASTID RNA POLYMERASE	3.58e+00
72 31.0 889 3 012071 ORF:PZF889. 71 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 357 14 067091 HEMAGGLUTININ (FRAGMEN F.) 30.6 1390 2 069385 GLUCOSYLTRANSFERASE-SI F.) 30.6 1455 2 069381 GLUCOSYLTRANSFERASE-SI F.) 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI F.) 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI F.) 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI F.) 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE	11	72	31.0	574	10	022455	SIGMA FACTOR 2.	3.58e+00
71 30.6 241 1 026845 CONSERVED PROTEIN. 71 30.6 351 14 012676 HEMAGGLUTININ (FRACMEN 57 14 012676 HEMAGGLUTININ FRECURSO 57 14 067091 HEMAGGLUTININ PRECURSO 57 1 30.6 1390 2 069385 GLUCOSYLTRANSFERASE-SI 57 1 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 57 30.6 1455 2 069387 GLUCOSYLTRANSFERASE-SI 57 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	12	72	31.0	889	3	012071	ORF: PZF889.	3.58e+00
71 30.6 351 14 012676 HEMAGGLUTININ (FRAGMEN 5 1 30.6 357 14 067091 HEMAGGLUTININ PRECURSO 7 3 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5 3 3 2 605339 GLUCOSYLTRANSFERASE-SI 5 3 3 2 605337 GLUCOSYLTRANSFERASE-SI 5 3 2 605337 GLUCOSYLTRANSFERASE-SI 5 3 3 2 605337 GLUCOSYLTRANSFERASE-SI 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	13	71	30.6	241	7	026845	CONSERVED PROTEIN.	5.07e+00
71 30.6 357 14 067091 HEMAGGLUTININ PRECURSO 5 13 30.6 1390 2 069385 GLUCOSYLTRANSFERASE-SI 5 1 30.6 1455 2 069391 GLUCOSYLTRANSFERASE-SI 5 1 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5 1 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5 1 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	14	71	30.6	351	14	012676	HEMAGGLUTININ (FRAGMEN	5.07e+00
71 30.6 1390 2 069385 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069391 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5 70 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	15	71	30.6	357	14	067091	HEMAGGLUTININ PRECURSO	5.07e+00
71 30.6 1455 2 069391 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5 70 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	16	71	30.6	1390	7	069385	GLUCOSYLTRANSFERASE-SI	5.07e+00
71 30.6 1455 2 069382 GLUCOSYLTRANSFERASE-SI 5 71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5 70 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	17	71	30.6	1455	~	069391	GLUCOSYLIRANSFERASE-SI	5.07e+00
71 30.6 1455 2 069397 GLUCOSYLTRANSFERASE-SI 5 70 30.2 253 2 P96151 DNA FOR AMINOPEPTIDASE 7	18	71	30.6	1455	~	069382	GLUCOSYLTRANSFERASE-SI	5.07e+00
253 2 P96151 DNA FOR AMINOPEPTIDASE 7	19	7.1	30.6	1455	7	069397	GLUCOSYLTRANSFERASE-SI	5.07e+00
	20	70	30.2	253	7	P96151	DNA FOR AMINOPEPTIDASE	7.14e+00

7.14e+00 7.14e+00 7.14e+00	7.14e+00 7.14e+00 7.14e+00	1.00e+01	1.00e+01	1.00e+01	1.00e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.41e+01	1.96e+01	1.96e+01
⊃ H Ø	F54G8.4 PROTEIN. HKR1P.	THAUMATIN-LIKE PROTEIN	F57A10.3 PROTEIN.	NUCLEOPORIN NUP153 HOM	SCAFFOLDING PROTEIN PR HYPOTHETICAL 13.0 KD P	MULTICATALYTIC ENDOPEP	MULTICATALYTIC ENDOPEP	20S PROTEASOME BETA SU	T21C12.4 PROTEIN.	HYPOTHETICAL 37.3 KD P	HYPOTHETICAL 54.6 KD P	HYPOTHETICAL 54.0 KD P	REVERSE TRANSCRIPTASE.	HYPOTHETICAL 82.4 KD P	C34F6.10 PROTEIN.	NORTH AMERICAN SWINE I	HEMAGGLUTININ PRECURSO
P94412 023673 P77039	023510 004051 017575	024468	017895	073749	045996	023709	023710	081152	022635	053282	025326	007418	082894	P87122	017637	082486	980799
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486 642 820	974 1802 3036	245	733	1219	1546	218	273	273	287	360	477	515	574	743	1117	351	358
30.2	30.5	29.7		۲.	۲. ۳	m	m.	m.	۳.	29.3	۳.	٣.	٣.	m.	۳.	σ.	6.
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222	2 2 2 4	272	309	31	332	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

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Gaps
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     BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOCOCCUS SALIVARIUS.
BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 95122197.
SIMPSON C.L., GIFFARD P.M., JACQUES N.A.;
SIMPSON C.L., GIFFARD P.M., JACQUES N.A.;
Streptococcus salivarius ATCC 25975 possesses at least two genes coding for primer-independent glucosyltransferases.";
INFECT. IMMUN. 63:609-621(1995).
EMBL; L35495; 6662379; -.
PFAM; PRO0128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE: 98040343.
KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.
RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
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                                                                                                                                                                                                                                                                                                                                Query Match 31.9%; Score 74; DB 2; Length 1449; Best Local Similarity 38.5%; Pred. No. 1.77e+00; Matches 10; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1449;
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ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                     STRAIN-V1477;
JAFFE R. I.;
JAFFE R. I.;
EMBLTTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF049609; G2935546;
TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 39.3 KD PROTEIN.

        SIGNAL
        1
        35
        POTENTIAL.

        CHAIN
        36
        1449
        GLUCOSYLTRANSFERASE.

        SEQUENCE
        1449
        Aa;
        159984
        MW;
        E9A4BA87
        CRC32;

                                                                                                                                                                                                                                               NON_TER 1449 1449
SEQUENCE 1449 AA; 159895 WW; 2AE5FB6A CRC32;
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Pred. No. 1.77e+0
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1449 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           238 FNAETGELSNOKEYRFDKNGGTGSSA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 FNAETGELSNQKEYRFDKNGGTGSSA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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65 FDPSTGALVDSKSYAFSTSNDTTSAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 FDPSTGALVDSKSYAFSTSNDTTSAA 90
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Local Similarity 38.5%;
les 10; Conservative
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                                                                                   SEQUENCE FROM N.A.
                            STREPTOCOCCUS.
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Q55264
Q55264;
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028918
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     STARRAGO
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NATARO J., SERIWATANA J., FASANO A., MANEVAL D., GUERS L., NORIEGA M., DUBOVSKY F., LEVINE M. M., MORRIS J.G.;
"Identification and cloning of a novel plasmid-encoded enterotoxin of enteroinvasive Escherichia coli and Shigella strains.";
INFECT IMMUN. 63:4721-4728(1995).
EMBL; 254195; E198841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                      MATZE CHLOROTIC DWARF WAIKAVIRUS.
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; SEQUIVIRIDAE;
WAIKAVIRUS.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-TENNESSEE (TN);
MEDLINE, 9729698.
REDDICK B.B., HABERA L.F., LAW M.D.;
REDDICK B.B., HABERA L.F., LAW M.D.;
"Nucleotide sequence and taxonomy of maize chlorotic dwarf virus within the family Sequiviridae.";
J. GEN. VIROL. 78:1165-1174(1997).
EMBL: U67839; G2160664: -.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 14; Length 344
Pred. No. 2.01e-01;
10; Mismatches 13; Indels
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Pred. No. 8.68e-01;
9; Mismatches 10; Indels
                                                 (TREMBLREL. 04, CREATED)
(TREMBLREL. 04, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE N (FRAGMENT).
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3443 AA; 387659 MW; 7E60C323 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 AA; 47958 MW; 2366BD23 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 GGYLRIWHDPNGSLDEGVEFAMSTNLEPPPGAFV 1234
PRT; 3443 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 SASLRISMFDTPTGKLVRTSDRLSFKAGNAADS 183
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
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Best Local Similarity 39.4%;
Matches 13; Conservative
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Local Similarity 32.4%;
nes 11; Conservative
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STREPTOCOCCUS SALIVARIUS.
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PRELIMINARY;
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                                                 (TREMBLREL.
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STRAIN=ENTEROINVASIVE;
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                                                 01-JUL-1997 (
01-JUL-1997 (
01-NOV-1998 (
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                                                                                                                                  POLYPROTEIN.
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SEQUENCE 3
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047628
047628;
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MEDLINE; 95095028.
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SEQUENCE
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013641
013641;
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022056
022056;
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KIRKNESS E.F., DUGGHERTY B.A., MCKENBY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.L., MCNEIL L.K., BADGER J.H., GLODEK A., 2HOU L., OVERBEEK R., GCOAYNE J.D., WEIDHAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYRES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., CLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHITEHERD T.R.;

"Analyses of the gene and amino acid sequence of the Prevotella

"Analyses of the gene and amino acid sequence of the Prevotella

"Bacteroides) ruminicola 23 xylanase reveals unexpected homology with
endoqlucanases from other genera of bacteria.";

CURR. MICROBIOL. 27:27-33(1993).

EMBL; M83379; G419374; ...

PFAM: PFO0150; cellulase: 1.

SIGNAL: XXLAN DEGRADATION; HYDROLASE; GLYCOSIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
MORAXELLACEAE; ACINETOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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Pred. No. 2.52e+00;
12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 1; Length 353;
Pred. No. 2.52e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                          "The complete genome sequence of the hyperthermophilic, sulphare-reducing archaeon Archaeoglobus fulgidus."; NATURE 390.364-370(1997).
EMBL; AE001010; G2649225; -.
FIGR; AF1353; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 353 AA: 39283 MW; 27306BEF CRC32;
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01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PREVOTELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XYLANASE.; 7272FA75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 LQVKVYGDATGSSFKEAYYTLSANSKTTTVNF 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHLRVFDPSTGALVDSKSYAFSTSNDTTSAAF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 LRVYDLS-GNLVGEKEGYTFS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN 23 584 N
SEQUENCE 584 AA; 65740 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LRVFDPSTGALVDSK-SYAFS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,
08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   larity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 28.1%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     044246 PRELIMINARY;
044246;
01-NOV-1996 (TREMBLREL. 0]
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLREL. 01-NOV-1996 (TREMBLREL. 01-NOV-1998 (TREMBLREL. XYLANASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTEROIDES RUMINICOLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=23;
MEDLINE; 93291665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-CIP A165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Q45397
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DO 044
AC 045
DT 011
DD 01
DD 01
DD 02
DD 02
DD 02
DD 02
DD 03
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PLASTID RNA POLYMERASE SIGNA-SUBUNIT.
SIG1 OR SIG8 OR SIGB.
ARABIDOPSIS THALLANA (MOUSE-EAR CRESS).
EURARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen associated with metastasis contains leucine-rich repeats.";
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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STRAIN-COLUMBIA; TISSUE-LEAF;
STRAIN-COLUMBIA; TISSUE-LEAF;
SONO K., MASANORI S., YOSHIMOTO K., NIWA Y., SATOH K., YOKOTA A.,
KOBAYASHI H.;
"Leaf-specifically expressed genes for polypeptides destined for chloroplasts with domains of sigma70 factors of bacterial RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYERS K.A., RAHI-SAUND V., DAVISON M.D., YOUNG J.A., CHEATER A.J., STERN P.L.;
                      Ğ.
RUDANT E., BOURLIOUX P., COURVALIN P., LAMBERT T.;
"Characterization of the aac(6')-Ik gene of Acinetobacter sp.
FEMS MICROBIOL. LETT. 124:49-54(1994).
EMBL. L19910. G847647; -.
SPFAM: PF00583; Acetyltransf; 1.
SEQUENCE 145 Aa; 16638 MW; C824BA11 CRC32;
                                                                                                                                                                                  5
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                                                                                                                                      Score 72; DB 2; Length 145;
Pred. No. 3.58e+00;
10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 01, CREATED)
01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5T4 ONCOFETAL ANTIGEN,
43633112 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 4; L
Pred. No. 3.58e+00;
6; Mismatches 10
                                                                                                                                                                                                                                            42 ALQLLVYSDDHAVGMLEASIRYEYVNGTETSPVAFL 77
                                                                                                                                                                                                                                                                                                                                            420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 LRQLDLSHNPLADLSPFAFSGSNASVSAP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. BIOL. CHEM. 269:9319-9324(1994).
EMBL: 229083; G435655; -.
PFAM; PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 PO
420 5T
: 46031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                      Query Match
31.0%;
Best Local Similarity 30.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
32 4
420 AA;
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STRAIN-AB972;
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         DDT READ BY RE
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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                                                                                                                                                                          STRAIN-COLUMBIA:
MEDIINE: 97424381.
MEDIINE: 97424381.
MARARA K., TOZAMA I., MOCHIZUKI N., SHINOZAKI K., NAGATANI A.,
WAKASA K., TAKHASHI H.;
"Characterization of three cDNA species encoding plastid RNA
polymerase sigma factors in Arabidopsis thaliana: evidence for the
sigma factor heterogeneity in higher plant plastids.";
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SHINN P., BUEHLER E., DEWAR K., FENG J., KIM C., LI Y., SUN H.,
CONWAY A., CONWAY A., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
VYSOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
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Pred. No. 3.58e+00;
12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches 13; Indels
                                                                SEQUENCE FROM N.A.
HAKIMI A., PRIVAT I., LERBS-MACHE S.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-COLUMBIA; TISSUE-3 DAY-OLD SEEDLING HYPOCOTYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF015543; G2353173; -. PFAM; PF00140; sigma70; 1.
polymerases in Arabidopsis thaliana.";
PROC. NATL. ACAD. SCI. U.S.A. 94:14948-14953(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72; DB 10;
Pred. No. 3.58e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB004293; D1023292; -.
EMBL; AC003981; G3063440; -.
PFAM; PF00140; sigma70; 1.
SEQUENCE 572 As; 64054 MW; C0B0407E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64323 MW; 40F28766 CRC32;
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60 LHLRVFDPSTGALVDSKSYAFSTSNDTTSAA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 LRLPSFDTDSDSLISDRQWTYTRPDGPSTEA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05,
05,
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Local Similarity 19.4%;
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 31.0%;
Local Similarity 19.4%;
Hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB004820; D1025747;
EMBL; Y15362; E1169752; -
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022455 PRELIMINARY;
022455, 01-JAN-1998 (TREMBLREL. 0;
01-JAN-1998 (TREMBLREL. 0;
01-JAN-1998 (TREMBLREL. 0;
                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECKER J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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ID Q1
AC Q1
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889 AA

PRT;

PRELIMINARY;

LT 12 Q12071 Q12071;

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CTRAINDELTA H.

WEDLINE; 98037514.

MEDLINE; 98037514.

ALDREDGE T., BASHIRZADEH R., BLENGHERY C., LEE H.-M., DUBOLS J.,
ALDREDGE T., BASHIRZADEH R., BLENKELY D., COOK R., GILBERT K.,
ALDREDGE T., BASHIRZADEH R., BLENKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG I., KEAGLE P., LUMM W., POTHIER B., QIU D.,
SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
JIWANI N., CANGSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
ADINELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
of lath: functional analysis and comparative genomics.";
J. BACTERIOL. 179:7135-7155(1997).

EMBL: AEONOBS4; G2621840; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHANOBACTERIUM THERMOAUTOTROPHICUM.
ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
METHANOBACTERIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 3; Length 889;
Pred. No. 3.58e+00;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 241;
                                                                                                                                                             SEÓUENCE FROM N.A.
EIDE L.G., SANDER C., PRYDZ H.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                            SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                          BARRELL B., RAJANDREAM M.A.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
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SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889 AA; 101519 MW; 3C15605E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local Similarity 31.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 PRELIMINARY;
026845 PRELIMINARY;
01-3AN-1998 (TREMBLREL: 0
01-7AN-1998 (TREMBLREL: 0
01-AUG-1998 (TREMBLREL: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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EMBL; Z47814; G642299;
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SUBMITIED (JUL-1996)
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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STRAIN=A/SWINE/EHIME/1/80;
STRAIN=A/SWINE/EHIME/1/80;
STRAIN=A/SWINE/EHIME/1/80;
SUGITA S., YOSHIOKA Y., ITAMURA S., KANEGAE.Y., OGUCHI K.,
GOJOBORI T., NEROME K., OYA A.;
J. MOL. EVOL. 32.16-23(1994).
BEMBL: X57494; G516377; -.
PFAM: PF00509; Hemagglutinin; 1.
SIGNAL: HEMAGGLUTININ.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 34.5%; Score 71; DB 14; Length 351; Similarity 34.5%; Pred. No. 5.07e+00; 10; Conservative 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFLUENZA A VIRUS.
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHOMYXOVIRIDAE;
INFLUENZA VIRUS A AND B GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71; DB 14; Length 35/
Pred. No. 5.07e+00;
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Best Local Similarity 38.9%; Pred. No. 5.07e+00;
Matches 14; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHOMYXOVIRIDAE;
INFLUENZA VIRUS A AND B GROUP.
                                                                                                                                                                                                                                    LT 14 PRELIMINARY; PRT; 351 AA. 012676 0212676 01-301. 04, CREATED) 01-JUL-1997 (TREMBLREL: 04, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL: 08, LAST ANNOTATION UPDATE) HEMAGGLUTININ (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 15
067091 PRELIMINARY; PRT; 357 AA.
067091 067091 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HEMAGGLUTININ PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
HEMAGGLUTININ.
HEMAGGLUTININ.
7; 9C2D9A2F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A/SW/QUEBEC/3291/90;
STRAIN-A/SW/QUEBEC/3291/90;
ARORA D.J.S., W'DIAER M., DEA S.;
EMBL: U80449; G1754670; -.
PRAM; PF00509; Hemagglutinin; 1.
SEQUENCE 351 AA; 38678 MW; 1706B952 CRC32;
                                                                                    259 FE-ATGNLVAPR-YAFAMNRGSGSGIIIS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 FE-ATGNLVVPR-YAFAMNRDPGSGIIIS 285
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345 357 H
357 AA; 39544 MW;
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Best Local Similarity 37.9%;
Matches 11; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm

MasPar time 3.49 Seconds 48.772 Million cell updates/sec Wed Sep 1 16:28:14 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (57-54) from PCTUS9913024.pep (10 of 12) 56 Description: Perfect Score:

1 SAGLHLRV 8 Sequence:

Scoring table:

170751 seqs, 21266608 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35

Mean 15.625; Variance 42.633; scale 0.366 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		-														
Pred. No.	5.960+01	1.20e+02	1.20e+02	1.56e+02	1.56e+02	1.56e+02	1.56e+02	1.56e+02	1.56e+02	.56e+02	.56e+02	2.04e+02	2.04e+02	2.04e+02	2.66e+02	2.66e+02
14	. "		_	_	_	_		_	_	-			N	C		
Description	Domain 1 from integra	Human TNF receptor re	Human tumour necrosis	Glucocorticold induct	Rat Glucocorticoid in	Mutant SP6DNA polymer	Mutant SP6DNA polymer	SP6DNA polymerase.	Mutant SP6DNA polymer	Mutant SP6DNA polymer	Mutant SP6DNA polymer	NtrA gene product.	Platenolide synthase	Platenolide synthase	Staphylococcus aureus	Rhipicephalus appendi
	4															
£	R34572	W60046	W05810	W76426	W76427	R14924	R14927	R14922	R14923	R14925	R14926	P80674	W22610	W23720	W77578	R82811
88	7	32	7	36	36	ო	٣	٣	ო	m	m	-	56	56	34	16
Duery Match Length DB	28	: T85	240	467	467	843	844	849	849	849	849	523	1891	1891	112	172
Query Match	83.9	80.4	80.4	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	76.8	76.8	76.8	75.0	75.0
Score	47	45	45	44	44	44	44	44	44	44	44	43	43	43	42	42
Result No.	-1	2	m	4	S	9	7	&	6	10	11	12	13	14	15	16

17	42	'n.			Staphylococcus aureus	.66e+
18	42	'n			srmR polypeptide.	. 66e+
19	42	Š.	073		ST	•
20	42	'n.	073		receptor	.66e+
21	42	S.	075		•	
22	42	δ.			Human retinal degener	•
23	42	S.	422		Hepatitis GB virus (H	9
24	42	ď.	206			φ.
25	41	ω.			Amino acid sequence o	7
56	41	ë.			Amino acid sequence o	7.
27	41	ë.				7
28	41	ë.			Mouse G-CSF receptor	₹.
53	41	ω.			Ligand binding cytoki	3.45e+02
30	41	۵,			•	₹.
31	41	ω.			eptor	₹.
32	41	ω.				₹.
33	41	ë.			Ligand binding cytoki	₹.
34	41	ω.			Human heart lecithin-	7
32	41	ω.			Human kidney lecithin	4.
36	41	73.2	480 17	R85310	Cystathionine gamma s	3.45e+02
37	41	ë.				7.
38	41	m,			a	.45
39	40	ä			eta-like	.47
40	40	-			TGF-beta-like	47
41	40	ä				47
42	40	м			embryonal lung	47e+0
43	40	-			ed	0+0
44	40	н	303	R9030		47e+
45	40	71.4		R7591		ŧ.
				ALIGNMENTS		
SUI	T 1 R34572 stan	standard;	Protein	28 AA.		
0	-JUN-1993		(first entry	_		

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WPI; 93-152187/18.

Expression vector for expressing protein or polypeptide in mycobacterization vector for expressing protein or polypeptide in mycobacterization conto DNA sequences encoding lipoprotein flag. Secretion signal and peptide heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria protein protein fusion protein adomain 1 from the migrae of the protein 7n2603 ORF 3. The whole coding sequence of the enzyme could be included in an expression vector also includes at least the secretion into its host. The expression vector also includes at least the secretion signal of a lipoprotein and a second sequence encoding a heterologous protein and a mycobacterial promoter to control expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
O4-JUN-1993 (first entry)

Domain 1 from integrase like protein Tn2603 ORF3.

Cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG

Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV;

Pertussis; malaria; influenza vírus; CTL; herpes vírus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 6.96e+01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.9%;
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                              29-APR-1993.
21-OCT-1992; U09075.
21-OCT-1991; US-780261.
(MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heterológous protein.
Seguence 28 AA;
                                                                                                                                                                                                                                           Stover CK;
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64 | ||:||| 57 SAGLHLRV õ

15 seglqlrv 22

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RESULT 2 ID W60046 standard; Protein; 185 AA.

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Simplex infection

Claim 1; Fig 4; 151pp; English.

Claim 1; Fig 4; 151pp; English.

The human tumour necrosis factor (TNF) receptor related protein (TR2) is a member of the TNF family and displays considerable homology to murine CD40. It can be used in soluble forms to treat herpes simplex virus infection and TR2 proteins (or their agonists or antagonists) are used to be used to protect against the effects of radiation therapy and to stimulate lymphocyte proliferation and differentiation in patients infected by human immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                      Human TNF receptor related splice variant 1 (TR2-SV1) protein.
Human; tumour necrosis factor; TNF; herpes simplex virus;
aberrant cell survival; radiation therapy; lymphocyte proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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30-UN-1997 (first entry)
Human tumour necrosis factor receptor splice variant 1.
Human tumour necrosis factor; TNF; receptor; treatment;
Human; tumour necrosis factor; TNF; receptor; treatment;
activation; inhibition; identification; mediation; antagonist;
stimulation; T cell; differentiation; mediation; immune;
antiviral; response; regulation; growth; protection; HIV;
radiation; Chlamydia; infection; immunodeficiency; virus;
autoimmune disease; inflammation; septic shock; creatral;
cachexia; B cell; cancer; graft; host; reaction; refection;
prevention; apoptosis; cytotoxicity; hybridisation probe;
detection; antibody; reagent; splice variant 1; SVI.
                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-1996; U18540.
30-OCT-1996; WO-U18540.
(HUMA-) HUMAN GENOME SCI INC.
(SMIK ) SMITHKLINE BEENAM CORP.
Gentz RL, Hurle MR, Lyn SDP, Ni J, Rosen CA;
WPI: 98-272139/24.
N-PSDB; V34510.
Nucleic acid encoding TR2 tumour necrosis factor family receptor and its splice variants, useful for diagnosis and treatment of diseases involving abnormal cell survival or death, e.g. herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 1.20e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                           1..36
/note= "Signal peptide"
37..185
/note= "Mature peptide"
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/label= sig_peptide
39..240
/label= mat_peptide
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27-APR-1995.
27-APR-1995; WO-U05058.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               % Match 80.4%;
Local Similarity 100.0%;
nes 6; Conservative
                                                                                                                                                 deficiency syndrome
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WPI; 96-497627/49.
N-PSDB; T40049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 aglhlr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AGLHLR 63
                         25-SEP-1998
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      W09818824-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9634095-A1
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                                                                                                                                                    Lmmune
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PF 27-EB-1998.

03-52F-1998.

PF 27-FEB-1998.

28-FEB-1997. JP-062008.

A (CYTO-) INST CYTOSIGNAL RES INC.

Obtsuka T, Yoshida H;

WPI: 98-481142741.

DR WPSDB, v61810.

Protein inhibiting activation of interleukin-8 promoter in response

PT to extracellular stimulus - for use in diseases involving

Interleukin-8 expression, such as inflammatory disorders and asthma

T interleukin-8 expression, such as inflammatory disorders and asthma

CC Tals sequence represents the human glucocorticoid inducible suppressor

CC Trus sequence represents the human glucocorticoid inducible suppressor

CC Trus promoter activity in response to a specific extracellular signal

CC (IL-8) promoter activity in response to a specific extracellular simulus

CC (Sepecially by Interleukin-1 beta). The invention can be used in the

CC treatment and prevention of disorders in which IL-8 expression is

CC Involved, such as inflammatory diseases, bronchial asthma, allergy and
           The for drug screening to discuss the control of auto: immune diseases etc., in diagnosis and tor drug screening to discuss the control of auto: immune diseases etc., in diagnosis and Calaim in Pages 48.49; Inc. 2014 the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Glucocorticoid inducible suppressor protein.
Glucocorticoid inducible suppressor protein; interleukin-8; rheumatism; intracellular signal transmission inhibitor: IL-8 promoter; allergy; inflammatory disease; bronchial asthma; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Wew nucleic acid encoding a human tumour necrosis factor receptor
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Pred. No. 1.56+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 21; Length 240
Pred. No. 1.20e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 4
W76426 standard; Protein; 467 AA.
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W76427 standard; Protein; 467 AA.
W76427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein in the circulation.
Sequence 240 AA:
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Best Local Similarity 100.0%;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens.
WO9838213-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatism.
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SP6 phage.
J03232487-A.
           Exonuclease.
                                 SP6 phage.
J03232487-A.
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Best Local Si
Matches
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                                                                                                                                                                                                                                                                                         N-PSDB: V61811.
Protein inhibiting activation of interleukin-8 promoter in response
Protein inhibiting activation of interleukin-8 promoter in response
Interleukin-8 expression, such as inflammatory disorders and asthma
claim 3; Page 46-50; 72pp; Japanese.
This sequence represents the rat glucocorticoid inducible suppressor
protein (GISP) of the invention. The GISP is a intracellular signal
transmission inhibitor, and inhibits the activation of interleukin-8
(IL-8) promoter activity in response to a specific extracellular stimulus
(especially by interleukin-1 beta). The invention can be used in the
treatment and prevention of disorders in which IL-8 expression is
involved, such as inflammatory diseases, bronchial asthma, allergy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٠.;
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15-JAN-1999 (first entry)
Rat Glucocorticoid inducible suppressor protein.
Glucocorticoid inducible suppressor protein; interleukin-8; rheumatism; intracellular signal transmission inhibitor; IL-8 promoter; allergy; inflammatory disease; bronchial asthma; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            where
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP6DNA polymerase of defined sequence - and modified polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lacking 3',5'-exo-nuclease activity
Disclosure: Rage 8; 13pp; Japanese
The amino acid sequence is that of mutated SP6DNA polymerase,
amino acids His167-His172 have been deleted by site specific
mutation. This results in a mutant lacking 3',5'-exonuclease
activity. See also R14922-R14927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 36; Length 40,
Pred. No. 1.56e+02;
"...matches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 3; Length 843; Pred. No. 1.56e+02; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 6
R14924 standard; Protein; 843 AA.
R14924;
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                                                                                                                                                                              27-FEB-1998; JO0836.
28-FEB-1997; JP-062008.
(CYTO-) INST CYTOSIGNAL RES INC.
Ohtsuka T, Yoshida H;
WPI; 98-481142741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.6%;
ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant SP6DNA polymerase.
Exonuclease.
Sp6 nh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match
Local Similarity 75.0%;
les 6; Conservative
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11-FEB-1992 (first entry)
Mutant SP6DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1991.
06-FEB-1990; 025185.
06-FEB-1990; JP-025185.
(TAKA) TAKARA SHUZO KK.
WPI; 91-349003.48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467 AA;
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                                                                                                                                      WO9838213-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatism.
                                                                                                                                                                03-SEP-1998
                                                                                                                      Rattus sp.
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                                                                                                                                                                                                                                                                                  Gaps
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16-OCT-1991.
16-OCT-1991.
06-FEB-1990; 025185.
06-FEB-1990; JP-015185.
(TAKA-) TAKARA SHUZO KK.
TAKARA POLYMETASE OF GETING SPECIAL PROPRIATION ACID SEQUENCE SPECIAL OF MULTATED SPECIAL PROPRIATION. Sequence 1s that of mutated SPEDNA POLYMETASE, when multation. See also R14922-R14926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP6DNA polymerase of defined sequence - and modified polymerase lacking 3',5'-exo-nuclease activity
Claim 1; Fig 1: 13pp: Japanese
The amino acid sequence 1s that of SP6DNA polymerase and was obt
from the SP6 phage. It can be produced recombinantly and is of
property, superior to conventional polymerases. See also R14923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SP6DNA polymerase of defined sequence - and modified polymerase lacking 3',5'-exo-nuclease activity Disclosure; Page 8; 13pp; Japanese
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                                                                                                                                                                                                                                        Score 44; DB 3; Length 844; Pred. No. 1.56e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 3; LA Pred. No. 1.56e+02;
                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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R14923 standard; Protein; 849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              .r 8
R14922 standard; Protein; 849 AA.
R14922;
                                                                                                                                                                                                                                          78.6%;
Similarity 75.0%;
6; Conservative
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Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1992 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-FEB-1990; 025185.
06-FEB-1990; UP-025185.
(TAKA-) TAKARA SHUZO KK.
WPI; 91-349003/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1990; 025185.
06-FEB-1990; JP-025185.
(TAKA-) TAKARA SHUZO KK.
WPI; 91-349003/48.
                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                           844 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   849 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP6DNA polymerase.
                                                                                                                                                                                                                                                                                                                    566 gaglelrv 573
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EP-791655-A2
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                                       T 12
P80674 st
P80674;
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lacking 3',5'-exo-nuclease activity
Disclosure: Page 8: 13pp; Japanese
The amino acid sequence is that of mutated SP6DNA polymerase, where
the His at position 167 has been changed by site specific mutation
to Glu, Glu170 to Lys and His172 to Asp. See also R14922-R14927.
Sequence 849 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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The amino acid sequence is that of mutated SP6DNA polymerase, where the Asp at position 101 has been changed by site specific mutation to Ala. See also R14922-R14927.
Sequence 849 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-1990: D25185.
06-FEB-1990: JP-025185.
(TAKA-) TAKARA SHUZO KK.
WPI; 91-349003148.
SP6DNA polymerase of defined sequence - and modified polymerase lacking 3', 5'-exo-nuclease activity
Discling 3', 5'-exo-nuclease activity
Disclosure; Page 8: 13pp; Japanese
The amino acid sequence is that of mutated SP6DNA polymerase, where the His at postition 167 has been changed by site specific mutation to Gin and Series to Asn. See also R14922-R14927.
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                                                                                                                                                                     Score 44; DB 3; Length 849;
Pred. No. 1.56e+02;
1; Mismatches 1; Indels
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ilarity 75.0%;
Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Exonuclease.
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06-FEB-1990; JP-025185.
(TAKA-) TAKARA SHUZO KK.
WPI; 91-349003/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant SP6DNA polymerase
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57 SAGLHLRV 64
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57 SAGLHLRV 64
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57 SAGLHLRV 64
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SP6 phage.
J03232487-A.
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J03232487-A.
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Best Local
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OS SPO 106
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DIA encoding Streptomyces fradiae tylactone synthase domain - for production of tylosin-related polyketide compounds
Example 2; Pages 172-178; 220pp; English.
W12606-W12510 represent proteins encoded by the platenolide synthase gene Cluster. The gene cluster is also referred to as the srmG gene, and was isolated from Streptomyces ambofaciens. These sequences are multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide
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                                                                                                                                                                                                                                                                              cloned rhizobium meliloti ntrA gene - for use in C4-dicarboxylate transport, nitrate assimilation, symbiotic nitrogen fixation and identifying pathogenic genes.

Claim 1, Page 12, 19pp; English.

The ntrA gene product is a transcriptional activator. It controls the processes of nitrate assimilation, symbiotic nitrogen fixation and C4-dicarboxylate transport, working in conjunction with NrCC, NifA and DCtD resp. It can also be used to identify genes involved in
                                                    NtrA gene product.

NtrA; sigma factor; transcriptional activation; nitrogen assimilation; fixation; nif operon; C4-dicarboxylate transport.

Rhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-1998 (first entry)
Platenolide synthase ORF5 protein.
Tylactone synthase gene cluster; tylG gene; multifunctional protein;
polyketide; tylactone synthesis; antibiotic; tylosin.
Streptomyces ambofaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 523;
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1233..1418
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1502..1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; L
Pred. No. 2.04e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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19-FEB-1997; 301056.
22-FEB-1996; US-012078.
(ELIL ) LILLY & CO ELI.
Dehoff BS, Kuhstoss SA, Rosteck PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W22610 standard; Protein; 1891 AA.
   Š
standard; protein; 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.8%;
llarity 85.7%;
Conservative
                                     (first entry)
                                                                                                                                                  30-NOV-1988.
27-MAY-1988; 108482.
29-MAY-1987; US-055228.
(GEHO-) Gen Hospital Corp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35..458 /note= "]
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                                                                                                                                                                                                                       Ronson C, Ausubel F;
WPI; 88-339561/48.
N-PSDB; N81266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
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N-PSDB; T80414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             pathogenesis.
See also P82126.
Sequence 523 AA
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1007 taglhyrv 1014

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64

57 SAGLHLRV

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for production of spiramycin-related polyketide antibiotics usualing production of spiramycin-related polyketide antibiotics.

Claim 8; Pages 71-77; Bipp; English.

W23116-W23720 represent proteins encoded by the platenolide synthase gene cluster of the invention. The gene cluster is also referred to as the same gene, and was isolated from Streptomyces ambofaciens. These sequences are multi-functional proteins which direct the synthesis of the polyketide platenolide. Platenolide is the basic building block of the macrolide antibiotic spiramycin. The DNA can be used to produce compounds exhibiting antibiotic spiramycin. The DNA can be used to produce compounds including specifically the macrolide antibiotic spiramycin and spiramycin analogues and derivatives. Modifications of the platenolide synthase DNA sequence can be made so as to change the number and type of carboxylic acids incorporated into the growing polyketide chain and to change the common of the chain and to change the consumer.
        along with
se T80415).
                                                                                                                                                                                                                                                                                                                                                    ö
antibiotic spiramycin. The DNA encoding this sequence was used along wit the tylG gene (see T80413) to create a hybrid ORF1 sequence (see T80415) The tylG gene is the tylactone synthase gene cluster of the invention. The tylG gene is the tylactone synthase gene cluster of the invention. The tylG sequence was isolated from Streptomyces fradiae, and encodes multifunctional proteins which direct the synthesis of the polyketide tylactone. Tylactone is the basic building block of the antibiotic tylosin. The hybrid sequence can be used to transform S. ambofaciens lacking the srmG ORF1 sequence, or S. fradiae lacking the tylG ORF1 sequence, so that they can produce polyketides. The DNA sequence can be modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated, the reactions performed, thereby resulting in novel tylosin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Platenolide synthase ORF5 protein.
Platenolide synthase gene cluster; platenolide production; srmG gene; multi-functional protein; macrolide antibiotic; spiramycin.
Streptomyces ambdgaciens.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                        Length 1891;
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1715..1747
                                                                                                                                                                                                                                                                                                      Score 43; DB 26; Length 189
Pred. No. 2.04e+02;
1; Mismatches 1; Indels
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1233..1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "ketoreductase domain, KR7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
synthase ORF5 protein.
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ilarity 75.0%;
Conservative
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Burgett SG, Kuhstoss SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1997; 301066.
22-FEB-1996; US-012050.
                                                                                                                                                                                                                                                                1891 AA;
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N-PSDB; T78508.
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                                                                                                                                                                                                                                               polyketides
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Gaps

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1; Indels

Length 1891;

Score 43; DB 26; 1 Pred. No. 2.04e+02; 1; Mismatches 1:

76.8%; 75.0%;

Query Match Best Local Similarity

Matches

6; Conservative

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PR N-PSDB; V3376.

New nucleic acid sequences from Staphylococcus aureus WCHU29 -
useful in vaccines and for treatment of bacterial infections of e.g.

Tespiratory tract and central nervous system

respiratory tract and central nervous system

PS Claim 11; Page 263; 390pp; English.

C This sequence represents a Staphylococcus aureus protein of unknown function, and is encoded by a DNA sequence of the invention.

C The DNA sequences were isolated from Staphylococcus aureus WCHU29

(WCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides.

C Conditions which may be treated include bacterial infections, especially crespiratory, cardiac, gastrointestinal, central nervous, ege, kidney, curlnary tract, skin, bones and joints. The proteins can also be used to dentify antimicrobial compounds which are broad spectrum antibiotics, commence of the page of the proteins.
                                                                                                                                                    Staphylococcus aureus protein of unknown function.
Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; bacterial infection; central nervous system; kidney infection; uninary tract infection; antimicrobial compound identification; broad spectrum antibiotic;
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Misc_difference 1..112
/note= "residues designated X are unspecified, ar
represented as Xaa in the specification"
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(SMIK ) SMITHKLINE BEECHAM CORP.

(SMIK ) SMITHKLINE BEECHAM PLC.

Black MT, Burnham MKR, Hodgson JE, Knowles DJC,

Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,

Ward JM,

N-DSPR. "15-2240/23.
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Pred. No. 2.66e+02;
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Job time : 25 secs.
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W77578 standard; Protein; 112 AA.
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57 SAGLHLRV 64
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Wed Sep 1 16:27:45 1999; MasPar time 3.59 Seconds 89.384 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (57-64) from PCTUS9913024.pep (10 of 12) 56 1 SAGLHLRV 8 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 21.865; Variance 24.608; scale 0.889

Statistics:

SUMMARIES

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Score	Query Match	Length	DB	Ω	Description	Pred. No.
48	85.7	415	5	T02145	hypothetical protein	3.05e+00
47	83.9	303	~	S10927	integrase-like protei	5.12e+00
47	83.9	337	~	C26839	integrase - Escherich	5.12e+00
47	83.9	337	~	139499	•	5.12e+00
47	83.9	337	~	S32184	•	5.12e+00
47	83.9	337	~	A42646	٠	5.12e+00
47	83.9	337	~	JQ0300	hypothetical 38.4K pr	5.12e+00
45	80.4	499	7	F69833	monooxygenase homolog	1.40e+01
44	78.6	147	~	D27733	hypothetical protein	2.29e+01
44	78.6	461	7	S52408	•	2.296+01
44	78.6	572	-	VEHULC		2.29e+01
44	78.6	574	7	504333	lamin C - mouse	2.29e+01
44	78.6	657	7	S05517	C)	2.29e+01
44	78.6	664	н	VEHULA	lamin A - human	2.29e+01
44	78.6	665	7	S28182	lamin A - mouse	2.29e+01
44	78.6	665	~	S27267	lamin A - rat	2.29e+01
43	76.8	341	-	H69401	probable radical-form	3.71e+01
43	76.8	373	7	A27817	liquin peroxidase (EC	
43	76.8	513	ď	A33966	- Rhi	3.71e+01
43	76.8	525	7	A36130	_	3.71e+01
43	76.8	1117	~	S38673	•	3.71e+01
43	75.0	211	~	S65049	low molecular weight	5.97e+01
42	75.0	218	0	T01412		5.97e+01
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42 75.0 42 75.	42 75.0 42 75.	2 JN0148 E70640 2 JE0309 2 JE0309 2 S54543 2 S69027 2 A40100 2 F70579 2 BH7203 2 A47203 2 A47203 2 JC4397 1 OYRUHX 1 OYRUHX 2 J6835 2 A41685 2 J70492 3 T029422 2 T03454	Arable Ar	a NG hads .
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Nucleic Acids Res. (1987) 15:7491-7501
The region of the IncN plasmid R46 coding for resistance to beta-lactam antibiotics, streptomycin/spectinomycin and sulphonamides is closely related to antibiotic resistance segments found in IncW plasmids and in Tn21-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sundstroem, L.: Swedberg, G.: Skold, O. submitted to the EMBL Data Library, March 1991 Characterization of the transposon Tn5086, and its site-specifically inserted gene dhfrVII, which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sundstroem, L.; Radstroem, P.; Swedberg, G.; Skoeld, O. Mol. Gen. Genet. (1988) 213:191-201
Site-specific recombination promotes linkage between trimethoprim- and sulfonamide resistance genes. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heikkila, E.: Skurnik, M.; Sundstrom, L.; Huovinen, P. submitted to the EMBL Data Library, February 1993 Another dihydrofolate reductase cassette, inserted in an integron, borne on a Tn21-like element.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change
Nature (1990) 345:739-743
Transposition of an antibiotic resistance element in
                                                                                                                                                                                             ##residues 1-303 ##label NAT ##residues ##re
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##experimental_source transposon Tn5086
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##molecule_type DNA
##residues 1-337 ##label HAL
##cross-references GB:X06046; NID:g42204; PID:g42207
##experimental_source plasmid R46
##genetics PLA
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                                                       #cross-references MUID:90294910
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##molecule_type DNA
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#authors Radstrom, P.; Skold, O.; Swedberg, G.; Flensburg, J.; Roy,
P.H.; Sundstrom, L.
#journal J. Bacteriol. (1994) 176:3257-3268
#title Transposon Tn5090 of plasmid R751, which carries an integron,
is related to Tn7, Mu, and the retroelements.
#cross-references MUID:94252994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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# submission
# submitted to the EMBL Data Library, August 1995
# description
# authorofolde sequence of the cassette-borne type XIII
# accession
# south Africa.
characterization of dhfrV and sull and a recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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integrase - Acinetobacter baumannii
*formal_name Acinetobacter baumannii
19-Jul-1996 *sequence_revision 19-Jul-1996 *text_change
16-Feb-1997
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                                                                                          ##residues
##cross-references EMBL:X12868; NID:g45672; PID:g45673
##experimental_source plasmid pLMO20, Tn21
                                                                                                                                                                                                                                                                                                         Score 47; DB 2; LA Pred. No. 5.12e+00;
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Elisha, B.G.; Steyn, L.M.
Curr. Microbiol. (1991) 22:259-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                  translation not shown
             active locus of Th21.
*cross-references MUID:89039710
*accession S04809
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Skold, O. submitted to the EMBL Data Library, March 1993
The integrons of R751 and Tn21 are transposons related to the
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#journal J. Bacteriol. (1992) 174:1248-1257
#title Characterization of InO of Pseudomonas aeruginosa plasmid
pvS1, an ancestor of integrons of multiresistance plasmids
and transposons of gram-negative bacteria.
#cross-references MUID:92138617
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sequence extracted from NCBI backbone (NCBIN:79394,
NCBIP:79395)
Cloning of AAC(3) and AAD(2') genes from Acinetobacter: differential expression in the host strain.
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integrase - Klebsiella pneumoniae
#formal_name (Alebsiella pneumoniae
06-Jan-1995_#sequence_revision 06-Jan-1995 #text_change
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#formal_name Pseudomonas aeruginosa
04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
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                                                preliminary; translated from GB/EMBL/DDBJ
                                                                            ##residues 1-337 ##label RES ##cross-references EMBL:U17586; NID:9596249; PID:9596251
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Pred. No. 5.12e+00;
1; Mismatches 1; Indels
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#length 337 #molecular-weight 38381
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Best Local Similarity 75.0%;
Matches 6 Conservative
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##residues 1-3
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Borriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
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Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Foulger, D.; Fritz, C.; Fujita,
S.Y.; Glaser, P.; Goffeau, A.; Golightiy, E.J.; Grandi, G.;
Gliseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,
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Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Rlaerr-Blanchard, M.; Klein, C.; Kobayashi,
Y.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.;
Kurita, K.; Lapidus, A.; Lavine, A.; Liu, H.; Masuda, S.;
Lazarevic, V.; Lee, S.W.; Levine, A.; Liu, H.; Masuda, S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Wohlleben, W.; Arnold, W.; Bissonnette, L.; Pelletier, A.; Tanguay, A.; Roy, P.H.; Gamboa, G.C.; Barry, G.F.; Aubert, E.; Davies, J.; Ragan, S.A.
#journal Mol. Gen. Genet. (1989) 217:202-208
#title On the evolution of Tn21-like multiresistance transposons: sequence analysis of the gene (aacCl) for gentamicin accetyltransferase-3-I(AAC(3)-I), another member of the Tn21-based expression cassette.
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                                                                                                                                                                                                                                                         JQ0300 *type complete
hypothetical 38.4K protein - Pseudomonas aeruginosa
#formal_name Pseudomonas aeruginosa
07.5ep-1990 #sequence_revision 07-Sep-1990 #text_change
05-Dec-1997
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monooxygenase homolog yhjG - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24.Sep-1998
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##cross-references GB:X15852; NDD:945766; GB:U12338;
##cross-references GB:X15852; ND:945766; GB:U12338;
##note this sequence is encoded by transposon In1696
     #molecular-weight 38381 #checksum 9946
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Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogdwa, K.; Oglwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.W.; Portetelle, D.; Porwolik, S.; Prescott, A.M.; Persecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reyonlds, S.; Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Schoeiter, R.; Takanashi, H.; Takananu, K.; Takanashi, H.; Terpstra, P.; Tognoni, A.; Toasaco, V.; Ochiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.; Winter, P.; Vassarotti, A.; Vasumott, R.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winter, P.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.; Voshikawa, H. E.; Zumstein, E.; Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium
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Nucleotide sequence and genetic analysis of the nifB-nifQ region from Azotobacter vinelandii.
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#formal_name Azotobacter vinelandii
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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Pred. No. 1.40e+01;
0; Mismatches 0; Indels
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##experimental_source strain 168
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Best Local Similarity 100.0%;
Matches 6; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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*type complete

S52408

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RESULT ENTRY

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Fisher, D.2.; Chaudhary, N.; Blobel, G.
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6450-6454
CDNA sequencing of nuclear lamins A and C reveals primary and
secondary structural homology to intermediate filament
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        # authors McKeon, F.D.; Kirschner, M.W.; Caput, D.
# journal Nature (1986) 319.463-468
#title Homologies in both primary and secondary structure between muclear envelope and intermediate filament proteins.
#cross-references MUD:86118697
#accession A02962
                                                                                                                         Ponce, M.R.; Micol, J.L.; Davidson, E.H. submitted to the EMBL Data Library, February 1995 SpDVRI, a member of the transforming growth factor-beta superfamily expressed in the sea urchin embryo. $52408
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#formal_name Homo sapiens #common_name man
28-May-1986 #sequence_revision 28-May-1986 #text_change
                 #formal_name Strongylocentrotus purpuratus #common_name
purple urchin
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                                                  08-May-1995 #sequence_revision 21-Jul-1995 #text_change
09-Sep-1997
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                                                                                                                                                                                                                                                   #fresidues 1.461 ##label PON
##cross-references EMBL:Z48313; NID:g673496; PID:g673497
##cross-references EMBL:Z48313; NID:g673496; PID:g673497
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##residues 1-572 ##label MCK
##cross-references GB:X03445; NID:934235; PID:934236
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|larity 62.5%;
|Conservative
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*superfamily cytoskeletal keratin
alternative splicing; coiled coil; heptad repeat; membrane
protein; nuclear membrane; phosphoprotein; structural
protein
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#journal FEBS Lett. (1989) 257:411-414
#title Maturation of nuclear lamin A involves a specific carboxy-terminal trimming, which removes the polyisoprenylation site from the precursor; implications for the structure of the nuclear lamina.
#cross-references MUID:90060368
#accession S09704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #formal_name Mus musculus #common_name house mouse
28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
17-Mar-1999
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#journal FEBS Lett. (1995) 365:108-114
#title Genomic structure of the mouse A-type lamin gene locus encoding somatic and germ cell-specific lamins.
#cross-references MUID:95300954
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                                                                                            #product lamin C #status predicted #label MAT\
#domain head #label HED\
#domain rod #label ROD\
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FFICATION #superfamily cytoskeletal keratin
alternative splicing; coiled coil; heptad repeat;
intermediate filament; nucleus; phosphoprotein
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#domain rod #status predicted #label RODN
#region coiled coil 1\
#region coiled coil 2\
                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; Length 572; Pred. No. 2.29e+01; 3; Mismatches 0; Indels
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#region coil 2\
#region heptad change of phase\
#region heptad change of phase\
#region heptad change of phase\
#domain tail #label END\
#region nuclear location signal
#length 572 #molecular-weight 65134 #c
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##residues 521-574 ##label WEB
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Best Local Similarity 62.5%;
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'LWLFCLQCHGHSQLPQCGGQWGWQLRGQSG',
'HPLLPPGCLQPPNPEPPELQHHVIWDLPGR',
'HPLLPPGCLQPPNPEPPELQHHVIWDLPGR',
'GGGGGFLRPPHLMPTPCPARHGRGLBAREK' ##label MCK
GGGGGFLRPPHLMPTPCPARHGRGLBAREK' ##label MCK
GGGGGFLRPPHLMPTPCPARHGRGLBAREK' ##label MCK
HFCross-references GB:X03444; NID:934227; PID:934228
##note this sequence has been corrected in reference A94121; an
omitted nucleotide caused a reading frame error
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tauthors    Peter, M.; Kitten, G.T.; Lehner, C.F.; Vorburger, K.; Bailer,
S.M.; Maridor, G.; Migy, E.A.
tjournal    J. Mol. Biol. (1989) 208:393-404
title    Cloning and sequencing of cDNA clones encoding chicken lamins
A and B(1) and comparison of the primary structures of
tcross-references MUID:90012208
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#journal Nature (1986) 319:463-468
#title Homologies in both primary and secondary structure between
#cross-references MUD:86118697
#accession A02961
                                                                                                                                                                                                    Gaps
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28 May-1966 #sequence_revision 04-Dec-1986 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                      #formal_name Gallus gallus #common_name chicken
21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change
#region heptad change of phase\
fregion stutter\
fregion heptad change of phase\
fregion heptad change predicted #label END\
fregion nuclear location signal
#length 574  #molecular-weight 65405  #checksum 7573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X16879; NID:g63555; PID:g63556
FICATION #superfamily cytoskeletal keratin
nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 2; Lo
Pred. No. 2.29e+01;
3; Mismatches 0
                                                                                                                                                         Score 44; DB 2; I
Pred. No. 2.29e+01;
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lamin A - human
70kDa lamin
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stmolecule_type mrnA
stresidues
                                                                                                                                                      Query Match 78.6%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5%;
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S05517
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##residues 1-582
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57 SAGLHLRV 64
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57 SAGLHLRV 64
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KEYWORDS
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ORGANISM
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417-420
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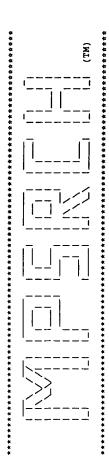
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REFERENCE
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                                                                 primary and
                                                                                                                                                                                                                                                                                                                                             ##Cross-references GB.M13122; NID:9186838; PID:9386856
##note
submitted sequence extracted from GenBank
NI Lamins A and C (see PIR:VEHULC) are products of alternative
splicing of the same gene.

NI The lamins (A, B, and C) contains several alpha-helical domains
capable of forming coiled coils.

NI The association of lamins, dependent upon ionic interactions, is
interrupted by hyperphosphorylation during the
interruptace-metaphase period of the cell cycle. The nuclear
envelope disintegrates with lamin dissociation; it does not
reform until telophase, when the lamins are dephosphorylated t
interphase levels and then reassociate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *superfamily cytoskeletal keratin
alternative splicing; coiled coil; heptad repeat;
lipoprotein; membrane protein; methylated carboxyl end;
nuclear membrane; phosphoprotein; prenylated cysteine;
                Fisher, D.Z.; Chaudhary, N.; Blobel, G. Proc. Natl. Acad. Sci. US.A. (1986) 83:6450-6454 CDNA sequencing of nuclear lamins A and C reveals primary secondary structural homology to intermediate filament
                                                                                                                           #cross-references MUID:86313596
#note parts of sequences from rat lamins, but not human, were
determined by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lamin A - mouse
#formal_name Mus musculus #common_name house mouse
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural component of the nuclear lamina, a fibrous meshwork on the nucleoplasmic surface of the nuclear
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#binding_site farnesyl (Cys) (covalent) #status
predicted\
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#domain head *label HED\
#domain rod *label ROD\
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mature form) #status predicted
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##residues 537-664 ##label FIS
##note sequence fragment shown in publication
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Pred. No. 2.29e+01;
3; Mismatches 0
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#domain tail #label END\
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#region coil 1B\
#region coil 2\
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S28182; S06662; S65931
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larity 62.5%;
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57 SAGLHLRV 64
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#authors Nakajima, N.; Sado, T.
#journal Biochim. Blophys. Acta (1993) 1171:311-314
#title Nuclectide sequence of a mouse lamin A cDNA and its deduced anino anino acid sequence.
#cross_references_MUID:93144345
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                      #authors Nakajima, N.; Abe, K.
#journal FEBS Lett. (1995) 365:108-114
#title Genomic structure of the mouse A-type lamin gene locus encoding somatic and germ cell-specific lamins.
#cross-references MUID:95300954
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#Commain rod *status predicted #label ROD\
#region coiled coil 1\
#region heptad change of phase\
#region stutter\
#region heptad change of phase\
#region heptad change of phase\
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##residues
##cross-references EMBL:D49732; NID:gl100724
##cross-references EMBL:D49732; NID:gl100724

IRICATION #superfamily cytoskeletal keratin
RDS alternative splicing; coiled coil; heptad repeat;
intermediate filament; lipoprotein; nucleus;
phosphoprotein; prenylated cysteine
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#length 665 #molecular-weight 74184
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                                                                                                                               ##molecule_type mRNA
##residues 1-665 ##label NAK
                                                                                                            preliminary
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Similarity 62.5%;
5; Conservative
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##residues 1-11
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Best Local Similarity
Matches 5; Conser
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protein . protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 2.52 Seconds 89.698 Million cell updates/sec Wed Sep 1 16:26:37 1999; Run on:

Tabular output not generated.

(57-64) from PCTUS9913024.pep (10 of 12) 56 >PCT-US99-13024-2 Description: Perfect Score:

1 SAGLHLRV 8 PAM 150 Gap 11 Scoring table: Sequence:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 22.517; Variance 22.845; scale 0.986 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	No.	: 8	01	01	010	01	010	01	5	01	01	10	01	01	01	010	10	01	01	01	01	01	01	5
	Pred. N	2.316+00	1.16e+0	1.16e+0	1.16e+0	1.16e+0	1.16e+0	1.16e+0	1.16e+0	1.16e+0	1.94e+0	1.94e+0]	1.94e+0	1.94e+0	1.94e+0]	1.94e+0	3.23e+0	3.23e+01	3.23e+01	3.23e+01	3.23e+01	3.23e+0	3.23e+01	3 230101
	Description	INTEGRASE/RECOMBINASE	RIBULOSE BISPHOSPHATE	DVR-1 PROTEIN HOMOLOG	LAMIN C.	LAMINS C AND C2.	LAMIN A.	LAMIN A (70 KD LAMIN).	LAMIN A.	LAMIN A.	PHTHALATE 4,5-DIOXYGEN	RNA POLYMERASE SIGMA-5	RNA POLYMERASE SIGMA-5	RNA POLYMERASE SIGMA-5	DESMOGLEIN 2 PRECURSOR	VITELLOGENIN 6 PRECURS	MITOCHONDRIAL HEAT SHO	NECDIN.	AMMONIUM TRANSPORTER M	NEURONAL ACETYLCHOLINE	CYTOCHROME P450 4E5 PR	HYPOTHETICAL 56.3 KD F	HEMOCYANIN D CHAIN.	PROTETY-CLITTAMINE CANN
SUMMAKIES	ID	INTRECOLI	RBL_PTEVI	DVR1_STRPU	LAMC_HUMAN	LAMC_MOUSE	LAMA_CHICK	LAMA_HUMAN	LAMA_MOUSE	LAMA_RAT	PHT2_PSEPU	RP55_RHIME	RP54_RHIME	RP54_RHISN	DSG2_HUMAN	VIT6_OSCBR	HS2M_SOYBN	NECD_MOUSE	MEP3_YEAST	ACH2_RAT	C4E5_DROMT	FTWH_MYCTU	HCYD_EURCA	TGLC CHICK
	DB	-	-	-	-	٦	٦	-	-	-	-	-	-	-	-	Н	М	ч	П	Н	r-4	~	Н	-
	Query Match Length DB	337	440	461	572	574	657	664	665	665	324	513	523	525	1117	1660	211	325	489	511	522	524	627	697
œ	Query Match	83.9	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	76.8	76.8	8.92	76.8	76.8	76.8	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
	Score	47	44	44	44	44	44	44	44	44	43	43	43	43	43	43	42	42	42	42	42	42	42	42
	Result No.	7	7	3	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.23e+01 3.23e+01	3.23e+01	3.23e+01	3.23e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01	5.31e+01
HYPOTHETICAL 78.9 KD P DNA MISMATCH REPAIR PR	HEAT-STABLE ENTEROTOXI		HEAT-STABLE ENTEROTOXI	HYPOTHETICAL 8.5 KD PR	HYPOTHETICAL FROTEIN M	60S RIBOSOMAL PROTEIN	60S RIBOSOMAL PROTEIN	OOCYTE ZINC FINGER PRO	HYPOTHETICAL PROTEIN H	HYPOTHETICAL 37.2 KD P	FRUCTOSE-1,6-BISPHOSPH	SLS1 PROTEIN PRECURSOR	HOMOSERINE DEHYDROGENA	CYSTATHIONINE GAMMA-SY	HYPOTHETICAL 67.2 KD P	HYPOTHETICAL 131.5 KD	TRANSPOSON TX1 HYPOTHE	RNA REPLICATION PROTEI	SUCRASE-ISOMALTASE, IN
YCBY_ECOLI	HSER_RAT	HSER HUMAN	HSER_CAVPO	YCX1_OENBE	Y213_METJA	RL10_CAEEL	RL10_PINTA	ZO20_XENLA	Y052_HAEIN	YOBN_MYCTU	F16P_XANFL	SLS1_YARLI	DHOM_SYNY3	METB_ARATH	YX45_MYCTU	YL17_CAEEL	YTX2_XENLA	RRPO_PMV	SUIS_RAT
		·	-	-	Ч	-	Н	Н		-	-	-	Н	-	-	٦	Н	ч	-
702 862	1072	1073	1076	72	149	214	228	247	328	340	364	426	433	563	611	1130	1308	1547	1841
75.0	75.0	75.0	75.0	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2
4 4 2 2 2	4 4 2 2	4	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
24 25	26 27	78	29	30	31	32	33	34	32	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

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PLASMID-INCN R46;
MEDLINE, 88015510.

HALL R.M., VOCKLER C.;
The region of the IncN plasmid R46 coding for resistance to beta-lactam antibiotics, streptomycin/spectinomycin and sulphonamides is closely related to antibiotic resistance segments found in incw plasmids and in Tallike transposons.";

NUCLEIC ACIDS RES. 15:7491-7501(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "SITESTROEM L., RADSTROEM P., SWEDBERG G., SKOELD O.;
"Site-specific recombination promotes linkage between trimethoprim-
and sulfonamide resistance genes. Sequence characterization of dhfrv
and sulf and a recombination active locus of Tn21.";

MOL. GEN. GENET. 213:191-201(1988).
                                                                                                                                   ESCHERICHIA COLI, AND PSEUDOMONAS AERUGINOSA.
PLASMID INCN R46, PLASMID RGN238, PLASMID R1033, PLASMID PLMO20,
PLASMID PLMO27, PLASMID PLMO180, PLASMID PLMO229, AND PLASMID PVS1.
BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                              PLASMID-RGN338;
MEDLINE; 88041110.
OUELLETTE M., BISSONNETTE L., ROY P.H.;
Precise insertion of antibiotic resistance determinants into In21-like transposons: nucleotide sequence of the OXA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OUELLETTE M.;
SUBMITTED (DEC-1987) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-lactamase gene.";
PROC. NATL. ACAD. SCI. U.S.A. 84:7378-7382(1987)
INTR ECOLI STANDARD; PRT; 337 AA. 109999; P11743; CREATED) 10-MAR-1989 (REL. 10, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) INTEGRASE/RECOMBINASE (E2 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGRATION: PLASMID; TRANSPOSABLE ELEMENT.

R -> P (IN PLMO150).

A -> P (IN PLMO20).

A -> P (IN PLMO20).

S -> T (IN R1033).

E -> Q (IN RGN238).

PROBABLE TRANSIENT COVALENT LINKAGE TO DNA DURA GYRANSIENT CLAVAGE AND REJOINING.
SEQUENCE FROM N.A.
SPECIES-P.AERUGINOSA; PLASMID-R1033; TRANSPOSON-TN1696;
MEDLINE; 89364699.
MOHLLEBEN W., ARNOLD W., BISSONNETTE L., PALLETIER A., TANGUAY A.,
ROY P.H., GAMBOA G.C., BARRY G.F., AUBERT E., DAVIES J., KAGAN S.A.;
"On the evolution of Tn21-like multiresistance transposons: sequence analysis of the gene (aacc1) for gentamicin acetyltransferase-3-
I(AAC(3)-1), another member of the Tn21-based expression cassette.";
MOL. GEN. GENET. 217:202-208(1989).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-P.AERUGINOSA; PLASMID-PVS1;
MEDLINE; 92138617.
BISSONNETTE L., ROY P.H.;
"Characterization of In0 of Pseudomonas aeruginosa plasmid pVS1, an ancestor of integrons of multiresistance plasmids and transposons of gram-negative bacteria.";
                                                                                                                                                                                                                                                                                                          be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-145 FROM N.A.
SPECIES-E.COLI; PLASMID-PIMO77; TRANSPOSON-TN5086;
SUNDSTROEM L., SWEDBERG G., SKOLD O.,
SUBMITTED (MAR-1991) TO EMBL/GENBARK/DDBJ DATA BANKS.
-!- FUNCTION: PUTATIVE INTEGRASE BELIEVED TO BE INVOLVED IN INSERTIONS OF ANTIBIOTIC RESISTANCE GENES INTO PLASMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND TRANSPOSONS.
-!- THE SEQUENCE SHOWN IS THAT OF PLASMID R46.
-!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                             SUNDSTROEM L., SKOELD O.; The dhirt trimethoprim resistance gene of Tn7 can specific sites in other genetic surroundings."; ANTIMICROB. AGENTS CHEMOTHER. 34:642-650(1990);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTEGRATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIOL. 174:1248-1257(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00589; Phage_integrase; 1.
HSSP; P21891; 1A0P.
                                                                                                                                                                                                                  SEQUENCE OF 1-145 FROM N.A. PLASMID-PLMO150, AND PLMO229; MEDLINE; 90262183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X06046; G42207; EMBL; X06046; G42207; EMBL; J02967; G151817; EMBL; X12868; G45678; EMBL; X12869; G45766; EMBL; X17479; G48206; EMBL; X17479; G4579; EMBL; X17479; G4579; EMBL; X3819; G151300; PIR; C46839; C26839; C268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U12338; G530804; -. EMBL; U49101; G530814; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA;
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DB 1; Length 337;

Score 47;

83.98;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOLF P.G., SOLTIS P.S., SOLTIS D.E.;
"Phylogenetic relationships of dennstaedtioid ferns: evidence from the aguences";
MOL. PHYLOGENET. EVOL. 3:383-392(1994).

-1. FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF THE PRATOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
LARGE SUBUNIT) (FRAGMENT).
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTA; FILICOPHYTA; FILICOPSIDA; FILICALES; PTERIDACEAE;
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-!- CATALITIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SUBJULIT: 8 LARGE CHAINS + 8 MALL CHAINS.
-!- SUBGELLULAR LOCATION: CHLOROPLAST.
-!- SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U05941; G463542; -.
PROSITE; PS00157; RUBISCO_LARGE; 1.
PRAM; PF00016; RuBlsCO_large; 1.
MENDEL; 3802; PTEV1; TbCL; 1.
HSSP; P00875; PAGS.
PHOTOSYNTHESIS; CARBON DIOXIDE FIXATION; PHOTORESPIRATION; LYASE; OXIDOREDGTASE; MONOOXYGENASE; CHLOROPLAST.
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 440;
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Pred. No. 2.31e+00;
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Pred. No. 1.16e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTERIS VITTATA (CHINESE BRAKE).
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llarity 83.3%;
Conservative
                                                       6; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
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MEDLINE; 95211278.
WOLF P.G., SOLTIS P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                    148 SEGLQLRV 155
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                                                                                                                                                       57 SAGLHLRV
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RBL_PTEVI
Q33015;
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    MEDLINE;
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                              STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).
EUKARYOTA; METAZOA; ECHINODERWATA; ECHINOZOA; ECHINOIDEA;
EUECHINOIDEA; ECHINACEA; ECHINOIDA; STRONGYLOCENTROTIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).
                                                                                                                              SEQUENCE FROM N.A.
PONCE M.R., MICOL J.L., DAVIDSON E.H.;
SUBMITTED (# 1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBMITTE: HOWOOIMER, DISULFIDE-LINKED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                         DVR-1 PROTEIN HOMOLOG.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; DB 1; LANO. 1.16e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
57C7CBA0 CRC32;
                                                                                                                                                                                                                                                                                                                 HSSP; P18075; 1BMP. GYTOKINE; GLYCOPROTEIN; SIGNAL.
                                      01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DVR-1 PROTEIN HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
           461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.16e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 AA.
                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 86118697.
MCKEON F.D., KIRSCHNER M.W., CAPUT D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
           PRT;
                                                                                                                                                                                                                                                                   EMBL; 248313; G673497; -. PROSITE: PS00250; TGF_BETA; 1. PFAM; PF00019; TGF_beta; 1. PFAM; PF00688; TGFb_propeptide; 1. HSSP; P18075; 1BMP.
                              (REL. 33, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                               51881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         envelope and intermediate NATURE 319:463-468(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Rest Local Similarity
                                                                                                            STRONGY LOCENTROTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                             01-FEB-1996 (REL. 01-FEB-1996 (REL. 01-FEB-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 NVGLQLRV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 SAGLHLRV 64
          DVR1_STRPU
P48969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMC_HUMAN
P02546;
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CARBOHYD
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RESULT
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                                                                                                                                                                                                                                                                                       LAMIN ASSOCIATIONS.
THERE ARE THEE TYPES OF LAMINS IN HUMAN CELLS: A, B, AND C.
THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY CONTROLLED BY
THE CELL CYCLE, AS SEEN BY THE DISINTEGRATION AND FORMATION OF
THE NUCLEAR ENVELOPE IN PROPHASE AND TELOPHASE, RESPECTIVELY.
ALTERNATIVE PRODUCTS: LAMINS A AND C ARE THE PRODUCTS OF ALTERNATE
SPLICING OF THE SAME GENE. THEY ARE PRESENT IN EQUAL AMOUNTS IN
FISHER D.Z., CHAUDHARY N., BLOBEL G.,
"CDNA sequencing of nuclear lamins A and C reveals primary and
secondary structural homology to intermediate filament proteins.";
PROC. NATL. ACAD. SCI. U.S.A. 83:6450-6454(1986).
-I- FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS
LLAYER OW THE NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR MEMBRANE,
WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR ENVELOPE
AND MAY ALSO INTERACT WITH CHROMATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEPTAD CHANGE OF PHASE.
HEPTAD CHANGE OF PHASE.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
6F0AZODO CRC32;
                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR.
PTM: INCREASED PHOSPHORYLATION OF THE LAMINS OCCURS BEFORE
ENVELOPE DISINTEGRATION AND PROBABLY PLAYS A ROLE IN REGULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REMBL, M13451, G307108; -.

REMBL, X03445; G34236; -.

REMBL, X03445; G34236; -.

REMBL, X03645; VEHULC.

REMBL, X03962; VEHULC.

REMBL, R03962; IF, 1.

DR PRAM; PF00038; filament; 1.

DR PFAM; PF00932; IF_tail; 1.

RW INTERMEDIATE FILAMENT; HEPTAD REPEAT PATTERN; COILED COIL;

KW NUCLEAR PROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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LANI OR LANA.
MUS MUSCULUS (MOUSE).
EURANYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKER 2.
COIL 2.
STUTTER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; LA Pred. No. 1.16e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAIL.
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
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llarity 62.5%;
Conservative
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(REL. 33,
(REL. 35,
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572 AA;
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Best Local Similarity
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57 SAGLHLRV 64
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34
71
81
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P11516;
01-OCT-1989 (
01-FEB-1996 (
01-NOV-1997 (
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PROSITE; PS00226; IF; 1.
PFAM; PF00038; filament; 1.
PFAM; PF00932; IF_tail; 1.
INTERNEDIATE FILAMENT; HEPTAD REPEAT PATTERN; COLLED COIL;
NUCLEAR PROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING.
1 33 HEAD.

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*** Identification of phosphorylation sites on murine nuclear lamin C by RP-PLC and microsequencing ***

*** Identification of phosphorylation sites on murine nuclear lamin C by RP-PLC and microsequencing ***

*** Identification of phosphorylation sites on murine nuclear lamin C by RP-PLC and microsequencing ***

*** Identification of phosphorylation of THE NUCLEAR LAMINA, A FIBROUS CONTROL AND NUCLEAR LAMINA, A FIBROUS CONTROL AND NUCLEAR MEMBRANE, AND MAY ALSO INTERACT WITH CHROMATIN.

*** IDENTIFICATION NUCLEAR READINARY OF THE NUCLEAR ENVELOPE CONTROL SPECIFICALLY EXPRESSED IN GERM CELLS. THIS SPECIFIC EXPRESSION AND UNIQUE STRUCTURE SUGGESTS AND CHARM CELLS. THIS SPECIFIC EXPRESSION AND UNIQUE STRUCTURE SUGGESTS AND CHARM CELLS. THIS SPECIFIC SPERMATOGENESIS.

*** CHARMACOMAL STRUCTURES DIFFING SPERMATOGENESIS.**

*** CHARMACOMAL STRUCTURE SPERMATOGENESIS.**

*** CHARMACOMAL STRUCTURE SPERMATOGENESIS.**

*** CHARMACOMAL STRUCTURE SPERMATOGENESIS.**

*** CHARMACOMACOM
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                                                                                                                                   "Nucleotide sequence of the full-length mouse lamin C cDNA and its deduced amino-acid sequence."; BIOCHIM. BIOPHYS. ACTA 1008:119-122(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \label{eq:national_point} \text{NAKAJIMA} \text{ N., SADO T.;} \\ \text{"Nucleotide sequence of a mouse lamin A cDNA and its deduced amino}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95300954.
NAKAJIMA N., ABE K.;
Genomic structure of the mouse A-type lamin gene locus encoding somatic and gene cell specific lamins.";
FEBS LETT. 365:108-114(1995).
                                                                                                                                                                                                                                                                                                                                  FURUKAWA K., INAGAKI H., HOTTA Y.;
"Identification and cloning of an mRNA coding for a germ
"cell-specific A-type lamin in mice.";
EXP. CELL RES. 212:426-430(1994).
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BICCHIM, BIOPHYS, ACTA 1171:311-314(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE, AND PHOSPHORYLATION.
                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A. (LAMIN C2).
CTRAIN-DDY: TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 235-568 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-119 FROM N.A.
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EMBL; D14050; G505027; -.
EMBL; D49732; E212319; -.
EMBL; D49733; G1794160; -.
EMBL; D49733; G1794161; -.
                                                                             MEDLINE; 89247440.
RIEDEL W., WERNER D.;
                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93144345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92070490.
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY CDC2) (PARTIAL,
AT INTERPHASE).
PHOSPHORYLATION (PARTIAL, AT INTERPHASE).
PHOSPHORYLATION (PARTIAL, AT INTERPHASE).
MISSING (IN LAMIN C2).
FKELKA -> MGNAEG (IN LAMIN C2).
AR -> VC (IN REF. 1).
R -> P (IN REF. 1).

COIL 2. STUTTER (BY SIMILARITY). HEPTAD CHANGE OF PHASE HEPTAD CHANGE OF PHASE

LINKER 2.

LINKER 1 TAIL. COIL 1A. COIL 1B.

DOMAIN DOMAIN DOMAIN

DOMAIN DOMAIN ö

Gaps

;; 0

Score 44; DB 1; Length 574; Pred. No. 1.16e+01; 3; Mismatches 0; Indels

78.6%; Similarity 62.5%; 5; Conservative

Best Local Similarity

Matches

Query Match

56 NAGLRLRI 63

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V -> WL (IN REF. 1). 3C8AD85A CRC32;

RV -> WL

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65446

407 409 112 118 119 401

MOD_RES VARSPLIC

MOD_RES

MOD_RES

DOMAIN

VARSPLIC CONFLICT

113 113 118 401 439 574 AA;

CONFLICT CONFLICT SEQUENCE

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                                                                                                                                                                                                                                                                                                                          MARIDOR G., NIGG E.A.;

Cloning and sequencing of cDNA clones encoding chicken lamins A and and sequencing of cDNA clones encoding chicken lamins A and Bl and comparison of the primary structures of vertebrate A- and B-type lamins.;

J. MOL. BIOL. 208:393-404(1989).

-I- FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS LAYER ON THE NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR MEMBRANE, WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR ENVELOPE AND MAY ALSO INTERACT WITH CHROMATIN.

-I- SUBCELLULAR LOCATION: NUCLEAR.

-I- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHÓKDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                               01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                657 AA
                                                                                              PRT;
                                                                                              STANDARD;
                                                                                                                                                                                                             GALLUS GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 90012208.
:|||:||:
57 SAGLHLRV 64
                                                         6
LAMA_CHICK
P13648;
01-7-
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EMBL; X16879; G63556; -.

S18324; S18324. MGI:96794; LMNA. S04333; S04333.

PIR; PIR; MGD;

PIR; S05517; S05517

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5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 AA;
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Best Local Similarity
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57 SAGLHLRV 64
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384
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                                                                                                                                                                                                                                                                                                                                                             MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 86313596.

T. CDNA sequencing of nuclear lamins A and C reveals primary and secondary structural homology to intermediate filament proteins.";

PROC. NATL. ACAD. SCI. U.S.A. 83:6450-6454(1986).

IL PROC. NATL. ACAD. SCI. U.S.A. 83:6450-6454(1986).

IL PROC. NATL. ACAD. SCI. U.S.A. 83:6450-6454(1986).

MICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR MEMBRANE, WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR BUYELOPE C.:

AND MAY ALSO INTEREACT WITH CHROMATIN.

C.I. SUBCELLULAR LOCATION: NUCLEAR.

C.I. PTM: INCREASED PHOSPHORYLATION OF THE LAMINS OCCURS BEFORE

ENVELOPE DISTINEERRATION AND PROBABLY PLAYS A ROLE IN REGULATING
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--- THERE ARE THREE TYPES OF LAMINS IN HUMAN CELLS: A, B, AND C.
--- THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY CONTROLLED BY
THE CELL CYCLE, AS SEEN BY THE DISINTEGRATION AND FORMATION OF
THE NUCLEAR ENVELOPE IN PROPHASE AND TELOPHASE, RESPECTIVELY.
--- ALTERNATIVE PRODUCTS: LAMINS A AND C ARE THE PRODUCTS OF ALTERNATE
SPLICING OF THE SAME GENE. THEY ARE PRESENT IN EQUAL AMOUNTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
-:- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 582 ONWARD AND IS LONGER (702 AA) DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 86118697.
MCKEON F.D., KIRSCHNER M.W., CAPUT D.;
"Homologies in both primary and secondary structure between nuclear envelope and intermediate filament proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKĀRYOTĀ, METĀZOA; CHORDĀTĀ, VERTĒBRĀTĀ; MAMMĀLIĀ; EUTHĒRIĀ;
PRIMĀTĒS; CATĀRRHINI; HOMINIDĀĒ; HOMO.
                  PFAM; PF00038; filament; 1.
PFAM; PF00932; IF_tail; 1.
INTERMEDIATE FILAMENT; HEPTAD REPEAT PATTERN; COILED COIL;
NUCLEAR PROTEIN: LIPOPROTEIN; PRENYLATION; PHOSPHORYLATION;
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                             Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                    COIL 2. FARNESYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                      44; DB 1; LANO. 1.16e+01;
                                                                                                                                                                                                                                                                                                                               3E7C5858 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                             COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                               LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                             Score 44;
                                                                                                                                                                                                                                           COIL 1B.
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                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                               73164 MW:
                                                                                                                                                                                                                                                                                                                                                                      78.6%;
Similarity 62.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE LAMINA OF MAMMALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 319:463-468(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
PS00226; IF; 1
                                                                                                                                                  382
657
69
79
217
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LMN1 OR LMNA.
HOMO SAPIENS (HUMAN).
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70
80
218
242
654
657 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 NAGLRLRI 62
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57 SAGLHLRV 64
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383
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P02545;
PROSITE;
                                                                                                                                                                                                                                                                                                                               SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  LINKER 2.
COIL 2.
COIL 2.
STUTTER (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FARNESYL (BY SIMILARITY).
31F253EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOCHIM, BIOCHYS. ACTA 1171:311-314(1993).
-I- FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS
LAYER ON THE NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR MEMBRANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93144345. NARAJIMA N., SADO T.; "Nucleotide sequence of a mouse lamin A cDNA and its deduced amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKAJIMA N., ABE K.;
"Genomic structure of the mouse A-type lamin gene locus encoding somatic and germ cell-specific lamins.";
FEBS LETT. 365:108-114(1995).
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ROBENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                 PFAN; PF00932; IF_tail; 1.
INTERMEDIATE FILAMENT; HEPTAD REPEAT PATTERN; COILED COIL;
NUCLEAR PROTEIN; LIPOPROTEIN; PRENYLATION; PHOSPHORYLATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1; LA
Pred. No. 1.16e+01;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAMA_MOUSE STANDARD; PRT; 665 AA. P48678; p97859; 01-FEB-1996 (REL. 33, CREATED) 01-FEB-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deduced amino-acid sequence."; BIOCHIM. BIOPHYS. ACTA 1008:119-122(1989)
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COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                             BLOCKED.
                                                                                                                                                                                                                                                                                                              HEAD.
                                                                                       EMBL; X03444; G34228; ALT_FRAME.
EMBL; M13452; G386B56; -
PIR; A02961; VEHULA.
PIR; B24249; B24249.
MIM; 150330; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74139 MW;
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                                                                                                                                                                                                PFAM; PF00038; filament; 1.
PFAM; PF00932; IF_tail; 1.
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62.5%;
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[1]
SEQUENCE FROM N.A.
MEDLINE; 93050186.
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STUTTER (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FARNESYL (BY SIMILARITY).
AR -> VC (IN REF. 2).
R -> P (IN REF. 2).
R -> W (IN REF. 2).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
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                                                                                   THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY CONTROLLED BY THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY CONTROLLED BY THE CELL CYCLE, AS SEEN BY THE DISINTEGRATION AND FORMATION OF THE NUCLEAR ENVELOPE IN PROPHASE AND TELOPHASE, RESPECTIVELY ALTERNATIVE PRODUCTS: LAMINS A, C AND C2 ARE THE PRODUCTS OF ALTERNATIVE SPLICTING OF THE SAME GENE. LAMINS A AND C ARE PRESENT IN EQUAL AMOUNTS IN THE LAMINA OF MAMMALS.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 582
ONWARD AND IS LONGER (702 AA) DUE TO A FRAMESHIFT.
WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR ENVELOPE AND MAY ALSO INTERACT WITH CHROMATIN.
SUBCELLULAR LOCATION: NUCLEAR.
PTW: INCREASED PHOSPHORYLATION OF THE LAMINS OCCURS BEFORE ENVELOPE DISINTEGRATION AND PROBABLY PLAYS A ROLE IN REGULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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R EMBL; D49733; G1794159; JOINED.
R EMBL; D49732; G1794159; JOINED.
R EMBL; D49732; E1294159; JOINED.
R EMBL; D49732; E12319; --
R EMBL; D49732; E12319; --
R EMBL; D13181; G220474; --
R MGD; MGI196794; LMNA.
R PFAM; PF00138; filament; 1.
R PFAM; PF0038; filament; 1.
R PF0038; filament; 1.
R PF0038; filament; 1.
R PF0038; filament; 1.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 665; Pred. No. 1.16e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
10-FUOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LAMIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIL 1A.
LINKER 1.
COIL 1B.
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similarity 62.5%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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RATTUS NORVEGICUS (RAT).
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70
80
218
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325
422
662
1119
401
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665 AA;
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SAGLHLRV 64
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P48679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
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Matches
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STUTTER (BY SIMILARITY).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FARNESYL (BY SIMILARITY).
K -> R (IN REF. 1).
T -> S (IN REF. 1).
R -> P (IN REF. 1).
A -> P (IN REF. 1).
A -> P (IN REF. 1).
A -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMIN ASSOCIATIONS.

-1 THE STRUCTURAL INTEGRITY OF THE LAMINA IS STRICTLY CONTROLLED BY THE STRUCTURAL INTEGRATION OF THE STRUCTURAL INTEGRATION OF THE STRUCTURAL INTEGRATION OF THE NUCLEAR ENVELOPE IN PROPHASE AND TELOPHASE, RESPECTIVELY.

-1 ALTERNATIVE PRODUCTS: LAMINS A AND C ARE THE PRODUCTS OF ALTERNATE SPLICING OF THE SAME GENE. THEY ARE PRESENT IN EQUAL AMOUNTS IN THE LAMINA OF NAMMALS.

-1 SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

-1 CAUTION: REF. I SEQUENCE DIFFERS FROM THAT SHOWN IN THE N- AND C-TERMINAL DUE TO FRAMESHIFTS.
                                                                                                                                        SEQUENCE OF 26-663 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
JONNALAGADDA V.S., PARNAIK V.K.,
JONNALAGADDA V.S., PARNAIK V.K.,
SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I-FUNCTION: LAMINS ARE COMPONENTS OF THE NUCLEAR LAMINA, A FIBROUS
LAYER ON THE NUCLEOPLASMIC SIDE OF THE INNER NUCLEAR MEMBRANE,
WHICH IS THOUGHT TO PROVIDE A FRAMEWORK FOR THE NUCLEAR ENVELOPE
AND MAY ALSO INTERACT WITH CHROMATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PTM: INCREASED PHOSPHORYLATION OF THE LAMINS OCCURS BEFORE ENVELOPE DISINTEGRATION AND PROBABLY PLAYS A ROLE IN REGULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X66870; G56551; ALT_FRAME.
EMBL; X76297; G453180; -.
PROSITE; PS00226; IF; 1.
PFAM; PF00038; filament; 1.
PFAM; PF00932; IF_tall; 1.
INTERMEDIATE FILAMENT; HEPTAD REPEAT PATTERN; COILED COIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 665;
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OGAKI T., SAKIYAMA S.;
"Lamin A gene expression is specifically suppressed in V-src-transformed cells.";
FEBS LETT. 312.165-168(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Lenc
Pred. No. 1.16e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74323 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584
606
665 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 NAGLRLRI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||:||:
57 SAGLHLRV 64
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D13229; G295709; -.

R PRAM; PRO0175; ZFEZS_FERREDOXIN; 1.

DR PFAM; PF00111; fer2; 1.

DR PFAM; PF00115; oxidored_fad; 1.

DR PFAM; PF00111; fer2; 1.

DR PFAM; PF00115; oxidored_fad; 1.

DR PFAM; PF00115; oxidored_fad; 1.

DR PFAM; PF00115; oxidored_fad; 1.

DR PFAM; PF00175; oxidored_fad; 1.

DR PFAM; PF00175; oxidored_fad; 1.

TANDSMIDARITY).

FT NF_BIND 115 229 NAD (BY SIMILARITY).

FT METAL 280 280 IRON-SULFUR (ZFE-2S) (BY SIMILARITY).

FT METAL 283 283 IRON-SULFUR (ZFE-2S) (BY SIMILARITY).

THON-SULFUR (ZFE-2S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                      15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEDUNCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHTHALATE 4,5-DIOXYGENASE OXYGENASE REDUCTASE SUBUNIT (EC 1.14.12.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                         PHTHALATE OXYGENASE AND PHTHALATE OXYGENASE REDUCTASE.
INDUCTION: INDUCED BY PHTHALATE AND REPRESSED BY GLUCOSE.
SIMILARITY: IN THE C-TERMINAL, BELONGS TO THE 2FE2S PLANT-TYPE
FERREDOXIN FAMILY.
                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA; PROTEGBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP; RHIZOBIACEAE; SINORHIZOBIUM.
                                                                                                                 BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                             NOMURA Y., NAKAGAWA M., OGAWA N., HARASHIMA S., OSHIMA Y.;
"Genes in PHT plasmid encoding the initial degradation pathway
phthallate in Pseudomonas putida.";
J. FERMENT. BIORNG. 1333-344(1992).
-i- CATALYTIC ACTIVITY: PHTHALATE + NADH + O(2) =CIS-4,5-
DIHYDROXYCYCLOHEXA-1(6),2-DIENE-1,2-DICARBOXYLATE + NAD(+)
                                                                                                                                                                                                                                                                     PATHWAY: FIRST STEP OF PHTHALATE DEGRADATION.
COFACTOR: FMN (BY SIMILARITY).
SUBUNIT: THIS DIOXYGENASE SYSTEM CONSISTS OF TWO PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 1; Lot
Pred. No. 1.94e+01;
                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE PDR/VANB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA-54 FRACTOR (VERSION 2).
 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                        PSEUDOMONAS PUTIDA.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPON OR NTRA. RHIZOBIUM MELILOTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 TAGAHLRV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-NMH102-2
                                                                                                                              SEUDOMONAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
ن
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P33985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                          104A14.";
J. BACTERIOL. 171:5087-5094(1989).
-1. EUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES
AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 87222158.
RONSON C.W., NIXON B.T., ALBRIGHT L.M., AUSUBEL F.M.;
ROADOLIN HELILOIT INTA (IPON) gene is required for diverse metabolic functions.";
J. BACTERIOL. 169:2424-2431(1987).
-i- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                       MEDLINE; 89359151.
SHATTERS R.G., SOMERVILLE J.E., KAHN M.L.;
"Regulation of glutamine synthetase II activity in Rhizobium meliloti
                                                                                                                                                                                                               THEN IS RELEASED.

-I- FUNCTION: THIS SIGMA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF THE NITROGEN FIXATION PROTEINS (NIF OPERON), GLNA AND DCTA FOR DICARBOXILATE TRANSPORT. THE OPEN COMPLEX (SIGMA-54 AND CORE RNA POLYMERASE) SERVES AS THE RECEPTOR FOR RECEIPT OF THE MELTING SIGNAL FROM THE REMOTELY BOUND ACTIVATOR PROTEINS NIFA, NIRC, OR DCTD FOR THE EXPRESSION OF THE REGULATED PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A33966; A33966.
PROSITE; PS00717; SIGMA54_1; 1.
PROSITE; PS00718; SIGMA54_2; 1.
PROSITE; PS50044; SIGMA54_3; 1.
PROSITE; PS50044; SIGMA54_3; 1.
PRAME, PF00309; Sigma54_factors; 1.
DRANCEIPTION REGULATION: SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE; DNA-BINDING; NITROGEN FIXATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: THIS SIGNA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF THE NITROGEN FIXATION PROTEINS (NIF OPERON), GLNA AND DCTA FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 513;
Pred. No. 1.94e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUCINE-ZIPPER (POTENTIAL).
LEUCINE-ZIPPER (POTENTIAL).
H-T-H MOTIF (POTENTIAL).
RPON BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F3DE59C4 CRC32;
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01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA-54 FACTOR (VERSION 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHIZOBIACEAE; SINORHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.8%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M28846; G152147; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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394
483
513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHIZOBIUM MELILOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SASLHLR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
STRAIN-104A14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:||||
57 SAGLHLR
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P17263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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PROSITE; PS00232; CADHERIN;
                 EMBL; M58481; G152432; -. PIR; A36130; A36130.
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
                                                                                                                                        11
21
191 2
393 4
484 4
525 AA;
                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 4 SASLHLR 10
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57 SAGLHLR 63
                                                                                                                        DNA-BINDING.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          LT 14
DSG2_HUMAN
Q14126;
                                                                                                                                                                       DOMAIN
DNA_BIND
SITE
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    SFFFFF WAR DOR SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS SIGMA FACTOR IS RESPONSIBLE FOR THE EXPRESSION OF THE NITROGEN FIXATION PROTEINS (NIF OPERON), GLNA, AND DCTA FOR INCARBOXYLATE TRANSPORT. THE OPEN COMPLEX (SIGMA-54 AND CORE RNA POLYMERASE) SERVES AS THE RECEPTOR FOR RECEIPT OF THE MELLING SIGNAL FROM THE REMOTELY BOUND ACTIVATOR PROTEINS NIFA, MTRC, OR DCTD FOR THE EXPRESSION OF THE REGULATED PROTEINS.
DICARBOXYLATE TRANSPORT. THE OPEN COMPLEX (SIGMA-54 AND CORE RNA POLYMERASE) SERVES AS THE RECEPTOR FOR RECEIPT OF THE MELTING SIGNAL FROM THE REMOTELY BOUND ACTIVATOR PROTEINS NIFA, NTRC, OR DCTD FOR THE EXPRESSION OF THE REGULATED PROTEINS. SIMILARITY: BELONGS TO THE SIGMA-54 FACTOR FAMILY.
                                                                                                                                                                                                                 EMBL; MI6513; G152390; -.
PROSITE; PS00717; SIGMA54_1; 1.
PROSITE; PS00718; SIGMA54_2; 1.
PROSITE; PS50044; SIGMA54_3; 1.
PROSITE; PS50049; SIGMA54_3; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHIZOBIUM SP. (STRAIN NGR234).
BACTERIA: PROTEOBACTERIA: ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1; Length 523;
Pred. No. 1.94e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           GEN-RICH.
LEUCINE-ZIPPER (POTENTIAL).
LEUCINE-ZIPPER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         2EB5FCD7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-EB-1994 (REL. 28, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA-54 FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AA.
                                                                                                                                                                                                                                                                                                                                                                                            RPON BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                 DNA-BINDING; NITROGEN FIXATION.
                                                                                                                                                                                                                                                                                                                                                                                                           57815 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                            210
412
490
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            189 2
393 4
482 4
523 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 91008923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SASLHLR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPON OR NTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP54_RHISN
P22881;
                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
SITE
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                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                               NIAMOC
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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PROSITE; PS00718; SIGMA54_2; 1.
PROSITE; PS0044; SIGMA54_2; 1.
PROSITE; PS0044; SIGMA54_2; 1.
PRAMSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-COLON CARCINOMA;
MEDLINE; 94192736.
SCHARFER S., KOCH P.J., FRANKE W.W.;
"Identification of the ubiquitous human desmoglein, Dsg2, and the expression catalogue of the desmoglein subfamily of desmosomal cadherins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO THE CADHERIN FAMILY. BELONGS TO THE DESMOSOMAL SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                     Score 43; DB 1; Length 525;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                               LEUCINE-ZIPPER (POTENTIAL).
LEUCINE-ZIPPER (POTENTIAL).
H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     Pred. No. 1.94e+01;
                                                                                                                                                                                                                                                          6691BDA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                            GLN-RICH
                                                                                                                                                                                                                                  RPON BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXP. CELL RES. 211:391-399(1994).
                                                                                                                                       29 GI
42 LE
212 LE
412 H-
492 RP
57800 MW;
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                                                                                                                                                                                                                                                                                                     76.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z26317; G416178; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNATE CENT;
MEDLINE; 96212989.
WINTER C.E., PENHA C., BLUMENTHAL T.;
"Comparison of a vitellogenin gene between two distantly related
rhabditid nematode species."
MOL. BLOL. EVOL. 13:674-684(1996).
-i- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES OF
NUTRIENTS DURING EMBRYONIC DEVELOPMENT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSCHEIUS BREVESOPHAGA.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; RHABDITINAE; OSCHEIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
PFAM; PF00028; cadherin; 4.
MSSP; PI3116; 1NCI.
CELL ADHESION: GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL;
CYTOSKELETON; CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; Length 1117;
Pred. No. 1.94e+01;
3; Mismatches 0; Indels
                                                                                                                                                     DESMOGLEIN 2.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
                                                                                                                                                                                                                                                                             CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
DESMOCLEIN REPEAT 1.
DESMOCLEIN REPEAT 2.
DESMOCLEIN REPEAT 3.
DESMOCLEIN REPEAT 4.
DESMOCLEIN REPEAT 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84D3B898 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
VITELLOGENIN 6 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STORAGE PROTEIN: MULTIGENE FAMILY; SIGNAL.
SIGNAL
1 15 POTENTIAL.
CHAIN 16 1660 VITELLOGENIN 6.
CARBOHYD 237 237 POTENTIAL.
CARBOHYD 383 383 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%;
similarity 62.5%;
5; Conservative
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VIT6_OSCBR . STANDARD;
Q94637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
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57 SAGLHLRV 64
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                                                                                                                                                     CHAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
CARBOHYD
CARBOHYD
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                                                                                                     SIGNAL
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REPEAT
REPEAT
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REPEAT
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FT CARBOHYD 695 695 POTENTIAL.
FT CARBOHYD 1307 POTENTIAL.
FT CARBOHYD 1596 1596 POTENTIAL.
FT CARBOHYD 1629 1629 POTENTIAL.
SQ SEQUENCE 1660 AA: 192108 MW; 9AA62413 CRC32;

Query Match
Best Local Similarity 71.4%; Pred. No. 1.94e+01;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 887 TGLRLNV 893
:||:|||
Qy 58 AGLHLRV 64

Search Completed: Wed Sep 1 16:26:45 1999
JOb time: 8 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 5.10 Seconds 85.590 Million cell updates/sec Wed Sep 1 16:27:02 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (57-64) from PCTUS9913024.pep (10 of 12) 56 1 SAGLHLRV 8 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Post-processing:

179066 seqs, 54579741 residues

Searched:

Minimum Match 0% Listing first 45 summaries

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 21.702; Variance 24.925; scale 0.871 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	1.66e+00	4.68e+00	4.68e+00	4.68e+00	7.77e+00	7.77e+00	7.77e+00		7.77e+00	7.77e+00	7.77e+00	7.77e+00	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	3.41e+01	3.41e+01	3.41e+01
	Description	POLYCYSTIC KIDNEY DISE	F8K4.20 PROTEIN.	SIMILAR TO GLUTAMATE R	SAFRAMYCIN MX1 SYNTHET	INTEGRASE (FRAGMENT).	INTEGRASE (FRAGMENT).	INTEGRASE.	INTEGRASE (FRAGMENT).	INTEGRASE.	HYPOTHETICAL 38.4 KD P	INTEGRASE.	INTEGRASE.	REPLICATION-RELATED PR		HYPOTHETICAL 54.4 KD P	SCVP86.	MC035R.	RIBULOSE BISPHOSPHATE	RIBULOSE BISPHOSPHATE	RIBULOSE BISPHOSPHATE
SUMMARIES	đ	008852	080705	017697	050858	P97168	005288	049186	051431	056438	Q56440	048337	050324	P90337	966890	007561	P89107	098203	080030	032141	078589
	DB	11	10	Ŋ	~	~	~	~	~	~	~	~	~	14	ď	~	14	14	œ	ω	œ
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ф	Query Match	89.3	85.7	85.7	85.7	83.9	83.9	83.9	83.9	83.9	83.9	83.9	83.9	80.4	80.4	80.4	80.4	80.4	78.6	78.6	78.6
	Score	20	48	48	48	47	47	47	47	47	47	47	47	45	45	45	45	45	44	44	44
	Result No.	7	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20

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Gaps

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TEXAIN-DM504-15;

XX MEDLINE;

XX MEDLINE;

XY POSPIECH A., SCHUPP T.;

YOUNG MULTIfunctional peptide synthetases and an O-methyltransferase are involved in the blosynthesis of the DNA-binding antibiotic and an antitumour agent saframycin MX from MXCCOCCUS Xanthus.";

XI MICROBIOLOGY 142:741-746(1996).

XI MICROBIOLOGY 142:741-746(1996).

XI MICROBIOLOGY 142:741-746(1996).

XI PREL; PSO0455; AMP_BINDING; 2.

XI PRAM; PFO0550; PP-binding; 2.

XI PRAM; PFO0560; PP-binding; 2.

XI PRAM; PFO0681; AMP-binding; 2.

XI PRAM; PFO0681; DNE4; 2.

XI MICROBIOLOGY 165: AMP-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
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MEDLINE; 96032006.
MEDLINE; 96032006.
*A new MYXCOCCUE B., BIETENHADER J., SCHUPP T.;
*A new MYXCOCCUE Xanthus gene cluster for the biosynthesis antiblotic saframycin MX1 encoding a peptide synthetase.";
MICROBIOLOGY 141:1793-1803(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYXOCOCCUS XANTHUS.
BACTERIA; PROTEOBACTERIA; DELTA SUBDIVISION; MYXOBACTERIA;
MYXOCOCCALES; CYSTOBACTERINEAE; MYXOCOCCACEAE; MYXOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 2; Length 2605;
Pred. No. 4.68e+00;
0; Mismatches 0; Indels
                                                                                                                                                                               Length 479.
                                                                                                                                                                                                                           0; Indels
                                   SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL: U39849; G1055049; -. PPAM; PF00060; 11g_chan; 2. SEQUENCE 479 AA; 54976 MW; 604C46C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 01, LAST SEÓUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SAFRAMYCIN MX1 SYNTHETASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                            Score 48; DB 5; Louis Bred. No. 4.68e+00; 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                          2605 AA
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03,
07,
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Local Similarity 100.0%;
les 6; Conservative
                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P97168 PRELIMINARY;
P97168, P97168, 01-8AY-1997 (TREMBLREL. 0 01-8AY-1997 (TREMBLREL. 0 01-8UG-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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  [3]
SEQUENCE FROM N.A.
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050858
050858;
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Matches
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ABOUTE FROM N.A.

ABOUTE 94150118.

ABOUTELD J., BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,

RA GARTON R., AINSCOUGH R., BAINES C., BERKS M.,

RA GRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA LIGHTNING J., LLOYD C., MCHORRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA LIGHTNING J., LLOYD C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R.,

RA MALDON N., SMITH A., SONNHAMMER E., STADEN R., SAUNDERS D., SHOWNKEEN R.,

RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., MATERSTON J.,

RA MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.)

RT "2.2 MG CONTIGUOUS NUCLECTION SEQUENCE from Chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                       STRAIN-CV. COLUMBIA:
VYSOTSKAIA V.S., SCHWARTZ J.R., TORIUMI M., KWAN A., YU G., OJI O.,
VYSOTSKAIA V.S., SCHWARTZ J.R., TRRIDEL V., BUEHLER E., COMMAY A.B.,
CONWAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI Y., PALM C.J.,
SHINN P., SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A.,
THEOLOGIS A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; META2OA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITIOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 10; Length 415
Pred. No. 4.68e+00;
0; Mismatches 0; Indels
                                                                                                                                                                          "Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.";
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
THEOLOGIS;
SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
THEOLOGIS A ;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
THEOLOGIS A.;
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
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SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
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SEQUENCE FROM N.A.
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STRAIN-CV. COLUMBIA;
THEOLOGIS;
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| 59 GLHLRV 64
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FLING M.E., KOPF J., RICHARDS C.;
"Nuclectide sequence of the transposon Tn7 gene encoding an aminoglycoside-modifying enzyme, 3"(9)-0-nuclectidyltransferase.";
NUCLEIC ACIDS RES. 13:7095-7106(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPOSON-TN2426;
MADLINE, 8706673.

CAMERON F. H., GROOT OBEINK D.J., ACKERMAN V.P., HALL R.M.;
"Nucleotide sequence of the AAD(2") aminoglycoside
adenylyltransferase determinant aads. Evolutionary relationship of
this region with those surrounding aada in R538-1 and dhfrII in
R388.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHIGELLA SONNEI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP; PSEUDOMONAS.
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                     Indels
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LARAKI N., ROSSOLINI G., GALLENI M., FRERE J.M.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X98393; E248569; -.
PFAM; PF00589; Phage_integrase; 1.
                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
   Pred. No. 7.77e+00;
1; Mismatches 1;
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TRANSPOSON-TN2426;
WIEDEMANN B.;
ANTIMICROB. AGENTS CHEMOTHER. 0:85-92(1986).
                                                                                                                                                        336 AA
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801,
801,
 Best Local Similarity 75.0%;
Matches 6; Conservative
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Similarity 75.0%;
6; Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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Best Local Similarity
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TRANSPOSON-TN2426;
MEDLINE; 86041899.
                                                  148 SECLQLRV 155
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                                                                                    64
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57 SAGLHLRV 64
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57 SAGLHLRV
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Q51431
Q51431;
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Q56438;
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MEDLINE; 90294910.
MARTIN C., TIMM J. RAUZIER J., GOMEZ-LUS R., DAVIES J., GICQUEL B.;
"Transposition of an antibiotic resistance element in mycobacteria.";
"ATABLE 345:739-743(1990).
EMBL: X53635; G44286; --
PFAM; PF00589; Phage_integrase; I.
SEQUENCE 303 AA; 34884 MW; IC45D6BB CRC32;
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ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                               01-10U-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
101-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
INTECRASE (FRAGMENT).
KLEBSIELLA OXYTOCA.
PLASMID PACMI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
KLEBSIELLA.
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EMBL: U90945; G1906652; -.

PFAM; PF00589; Phage_integrase; 1.
                                                                                                                                   Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 284;
                                                                                                                                                                 1; Indels
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              STRAIN-RA33.2;
ADRIAN P.V., THOMSON C.J., KLUGMAN K.P., AMYES S.GB.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z50802; G950043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          049186 PRELIMINARY; PRT; 303 AA. 049186 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                              Score 47; DB 2; L4
Pred. No. 7.77e+00;
1; Mismatches 1
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Pred. No. 7.77e+00;
1; Mismatches 1.
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284 AA; 32632 MW;
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ilarity 75.0%;
Conservative
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6; Conservative
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SEQUENCE FROM N.A.
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57 SAGLHLRV 64
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57 SAGLHLRV 64
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"Functional and physiological characterization of the Tn21 cassette for resistance genes in Tn2426.";
J. GEN. MICROBIOL.
J. GEN. MICROBIOL.
PEMBL: M86913; G155024;
PFAM; PF00589; Phage_integrase; 1.
SEQUENCE 337 AA; 38415 MW; 093D245D CRC32;
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MERCIER J., LACHAPELLE J., COUTURE F., LAFOND M., VEZINA G.,
MERCIER J., LACHAPELLE J., COUTURE F., LAFOND M., VEZINA G.,
MERCIER J., LACKAPELLE J., COUTURE F., LAFOND M., VEZINA G.,
Structural and functional characterization of tnpl, a recombinase
locus in Tn21 and related beta-lactamase transposons.";
J. BACTERIOL. 172:3745-3757(1990).
FEMBL, M33633; G1197009;
PFAM; PF00589; Phage_integrase; I.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                   MEDLINE; 90299796.
MERCIER J., LACHAPELLE J., COUTURE F., LAFOND M., VEZINA G.,
BDISSINOT M., LEVESQUE R.C.;
"Structural and functional characterization of tnpI, a recombinase
locus in Tn21 and related beta-lactamase transposons.";
J. BACTERIOL, 172:3745-3757(1990).
                                            TENOVER F.C., FILPULA D., PHILLIPS K.L., PLORDE J.J.;
"Cloning and sequencing of a gene encoding an aminoglycoside
6'-N-acetyltransferase from an R factor of Citrobacter diversus.";
J. BACTERIOL. 170:471-473(1988).
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LAST ANNOTATION UPDATE)
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Pred. No. 7.77e+00;
1; Mismatches 1;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
HYPOTHETICAL 38.4 KD PROTEIN.
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01-NOV-1996 (TREMBLREL. 01,
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 75.0%;
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TRANSPOSON-TN2426;
MEDLINE; 93329367.
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                                    MEDLINE; 88086917
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57 SAGLHLRV 64
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MEDLINE; 88015610.
HAALL R., VOCKLER C.;
HTALL R., VOCKLER C.
The region of the IncN plasmid R46 coding for resistance to beta-lactam antibiotics, streptomycin/spectinomycin and sulphonamides is closely related to antibiotic resistance segments found in IncW plasmids and in Th21-like transposons.",
NUCLEIC ACIDS RES. 15:7491-7501(1987).
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"Comparison of the nucleotide sequences of the vegetative replication origins of broad host range Incp plasmids R751 and RK2 reveals conserved features of probable functional importance.";
NUCLEIC ACIDS RES. 13:557-572(1985).
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                                                                                                                      ESCHERICHIA COLI, AND KLEBSIELLA AEROGENES.
PLASHID PGGO100, AND PLASHID INCP-BETA R751.
BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92206862.
PARSONS Y., HALL R.M., STOKES H.W.;
"A new trimethoprim resistance gene, dhfrX, in the In7 integron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUNDSTROM L.;
SUNDSTROM L.;
"Transposon Tn5090 of plasmid R751, which carries an integron, related to Tn7, Mu, and the retroelements.";
J. BACTERIOL. 176:3257-3268(1994).
EMBL: L06418; G149117; -.
EMBL: U67194; G157256; -.
EMBL: X72585; G288634; -.
PFAM: PF00589; Phage_integrase; 1.
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RADSTROM P., SKOLD O., SWEDBERG G., FLENSBURG J., ROY P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93391548.
STOKES H.W., TOWARAS C., PARSONS Y., HALL R.M.;
"The partial 3'-conserved segment duplications in the from pSa and In7 from pDG0100 have a common origin.";
PLASMID 30:39-50(1993).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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   (TREMBLREL.
(TREMBLREL.
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38358 MW; D25371F2 CRC32;

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337

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PRELIMINARY;
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SEQUENCE FROM N.A.
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57 SAGLHLRV 64
                                                                                                                                     STRAIN-2151;
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01-JUL-1997
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007561;
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOMBUSVIRIDAE;
CARMOVIRUS.
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                                                                                                                                                                                                                                                                            IYOBE S., MINAMI S., YAMADA H.;
"Insertion of a carbapenemase gene cassette into an integron of Pseudomonas aeruginosa plasmid published erratum appears in J Antimicrob Chemother 1997 Jun;39(6):845].";
J. ANTIMICROB. CHEMOTHER. 38:1114-1115(1996).
EMBL: D78374; D1024672; -
SEQUENCE 337 AA: 38298 MW; 753AD743 CRC32;
                                                                                                                                                                                                  PLASMID PMS350.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
PSEUDOMONAS.
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Pred. No. 2.10e+01;
2; Mismatches 0; Indels
  Length 337;
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                     1; Indels
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SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U72332; G1685120; -.
                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
REPLICATION-RELATED PROTEIN.
Score 47; DB 2; L. Pred. No. 7.77e+00;
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Pred. No. 7.77e+00;
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                     1; Mismatches
                                                                                                            337 AA
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Match 83.9%;
Local Similarity 75.0%;
tes 6; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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J. GEN. VIROL. 0:0-0(0).
[2]
                                                                                                            PRELIMINARY;
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                                                                                                                                                                                        PSEUDOMONAS AERUGINOSA.
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                                           148 SEGLOLRV 155
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57 SAGLHLRV 64
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57 SAGLHLRV 64
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AGLHLRV 64
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Query Match
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050324;
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RA TUBERT H., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS K., BOURSTER L., BRANS A., BRANN M., BRICHELL S.C., BRON S.,
RA BORNISS K., BOURSTER L., CAPURELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL S., CAPURON V.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUPMINGS N.J., DANIEL R.A.,
RA CHOI S.K., DEVIRE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
A GHIMS Y., CLASER P., GOFFENU A., GOLIGHTLY E.J., GRANDI G.
A GUISEPPI G., GUY B.J., HARGA K., HAIECH J., HARWOOD C. R., HENAUT A.,
A CUBISEPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C. R., KINANO M.,
A KOBATASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUHANO M.,
A KOBATASHI Y., KORETTER P., LARDINOIS S., LAULEO R., KEDRE C., MEDIGGE C.,
A KOBATASHI Y., KONINGSTEIN G., KROGH S., KROH S.,
A KURITA K., LAPIDUS A., LARDINOIS S., LAULEO R., MENAI S., NOBACK M.,
A NOONE D., O'REILLY M., OGANA K., OGINARA A., OUDEGA B., PARK S.H.,
RRA RESECAN E., PUJIC P., PURNELLE D., PORMOLLIK S., PRESCOTT A.M.,
RRESECAN E., RIVOLT C., ROCHA E., ROCH B., SADAIE Y.,
RRA RIEGER M., RIVOLT C., ROCHA E., ROCH B., SADAIE Y.,
RRA SATO T., SCANLAN E., SCHLEICH B., SACHROEP P., SHIN B.S., SOLDO B.,
RA SERIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDO B.,
RA SERIGUCHI J., TAKAHASHI H., TAKEMARU K.,
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                                                                                                                                                                       BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.4%; Score 45; DB 2; Length 260; 75.0%; Pred. No. 2.10e+01; Arive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          ECKSTEIN T.M., SILBAQ F.S., INAMINE I.M., BELISLE J.T.; SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF060182; 63170647; -
HYPOTHETICAL PROTEIN
SEQUENCE 260 AA; 27809 WW, 882DB702 CRC32;
                                         01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
HYPOTHETICAL 27.8 KD PROTEIN.
MYCOBACTERIUM AVIUM.
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(TREMBLREL. 04, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
260 AA
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PRT;
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HYPOTHETICAL 54.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WELTZENEGGER T.,
WINTERS P., WIPAT A., YAMANOTO H., YAMANE K., YASUMOTO K., YATA K.,
YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
"The complete genome sequence of the gram-positive bacterium Bacillus
subtilis:",
                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2; Length 499;
Pred. No. 2.10e+01;
0; Mismatches 0; Indels
                                                                                                                                                                  STRAIN-168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
EMBL: Y14081; E324980; --
EMBL: Z9109; E1183052; --
EMBL: Z9109; E1183052; --
EMBL: Z9109; E1183052; --
EMBL: Z99109; A1183052; --
SEQUENCE 499 AA; 54356 MW; 86F6D7E9 CRC32;
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Best Local Similarity 100.0%;
Matches 6; Conservative
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| 58 AGLHLR 63
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 1 16:30:31 1999; MasPar time 4.42 Seconds 67.410 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (66-79) from PCTUS9913024.pep (11 of 12) 86 1 DPSTGALVDSKSYA 14 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-genesed35 Database:

1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part14 15:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part28 23:part28 22:part29 22:part29 23:part29 23:part29 33:part39 33:part39 33:part39 33:part39 33:part39 33:part39

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Mean 17.858; Variance 46.416; scale 0.385 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.71e+01	4.90e+01	6.45e+01	6.45e+01	8.49e+01											
Description	Excitatory amino acid	Bacterial periplasmic	Human EAA3d excitator	Human EAA3c excitator	Glutamate receptor 6.	Human EAA3 receptor (Human EAA3b excitator	Human EAA3a excitator	Human EAA4 receptor (Excitatory amino acid	Excitatory amino acid	Glutamate receptor 5-	Excitatory amino acid	Sequence of oncodene	N. meningitidis alpha	Pseudorabies virus gp
9	R45368	W76238	R63070	R63069	R11994	R75883	R63068	R60112	R75884	R45367	R50179	R11993	R45369	P60011	W41513	P70646
DB	6	32	11	11	~	16	ij	Ξ	16	σ	10	~	σ	٣	53	7
Query Match Length DB	20	146	849	865	901	905	905	905	806	806	919	920	20	259	371	577
Query Match	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	. 60.5	60.5	60.5	59.3	58.1	58.1	57.0
Score	52	25	52	. 52	25	52	52	52	52	. 25	52	52	51	20	20	49
Result No.	1	2	m	4	S	9	7	80	თ	10	11	12	13	14	15	16

4444	8.49e+01 8.49e+01 8.49e+01 8.49e+01		1.46e+02 1.46e+02 1.46e+02 1.46e+02 1.46e+02	, 4 4 4 4 4	7 7 7 7
0 6 6 4	SERP antigen. SERA protein encoded The SERA protein of P Mouse INS-2. Curvularia verruculos	SCX phosphotyrosine b Human ShCB protein. Curvularia verruculos Nitrate reductase.	Chimeric restriction H. pylori secreted or Foki insertion mutant Influenza A/Johannesb Influenza A/Shandong/ Foki amino acid come	fied en insert	insertion -3 FRhl cp4 -3 JS isola
R63144 R27529 R68837 P80550	R22247 R60164 R05526 R96994	R97242 W23247 W12042 R90987	W08956 W20951 R96300 W01676 W01673	R72810 R72810 R88595 R88596	R88598 W48712 W48711
577 12 984 5 984 13 984 13	32008		303 20 377 22 570 17 571 22 571 22		3333
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118 198 209	5 5 3 5 T	3555 36876	> # # # # # # # # # # # # # # # # # # #	2 K W W 4 4	4444 10640

ALIGNMENTS

The excitatory animo acid receptor (See R45367) can be used to screen ligands. The ligands can be assayed for interaction by incubating them with cells, preferably occytes, expressing the receptor or with membrane preparations from these cells, and assessing any interaction by determining receptor-ligand binding or ligand-mediated ion channel activation. This method is useful in the identification of the activation. This method is useful in humans. Fragments of the receptor are useful for structural investigations and to raise antibodies. This fragment of the receptor 50 AA; 07-JUL-1994 (first entry)
Excitatory amino acid receptor (EAA4a) fragment.
Excitatory amino acid receptor; EAA4a; screening; detection;
identification; CNS; nervous disorders; antibody; oocyte; membrane protein; ion-channel; therapeutics.
Ep-578409-A. 12-JAN-1994.
12-JAN-1995.
24-JUN-1995; 304961.
24-JUN-1995; 01-903456.
(ELLI) ELLIOTT C E.
(KAMBA) RABOJ R.
(NUTY) NUTL S L.
(NUTY) NUTL S L.
(NUTY) NUTL S L.
(NUTY) NUTL S L.
(NUTY) S Elliott CE;
WPI; 94-010248/02.
WPI; 94-010248/02.
USEd to test 11gands for CNS receptor interaction to identify cpds. useful against CNS disorders
Disclosure; Figure 3a; 37pp: English. standard; Protein; 50 AA

Gaps ö 0; Indels Score 52; DB 9; Length 50; Pred. No. 3.71e+01; 4; Mismatches 0; Indels 60.5%; imilarity 60.0%; 6; Conservative Query Match Best Local Similarity Matches 6; Conserv

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gglidskgyg 35 |:|:|||:| 26

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08-DEC-1993; 110933.
11-DEC-1992; US-989793.
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                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure: Page 215-216; 218pp; English.

Disclosure: Page 215-216; 218pp; English.

M76226-W76250 are protein fragments used in the design of a model of a protein-ligand binding pocket (PLBP) of a blinding protein. A model is constructed based on typographic similarity to the binding pocket of a bacterial periplasmic binding protein. The model is refined by energy minimisation, with a high affinity ligand in the binding pocket.

Interaction energies of basis set molecules (BEW) are obtained by calculating energy of the models for the binding pocket BP and BSM individually (Er and Em) and total energy (Erm) of bound complexes individually (Er and Em) and total energy (Erm) of bound complexes inguitied ligand for a set of related PLBP's, specifically inoncropic glutamate receptor binding and activity and as modulators of receptor activity or receptor binding and activity and as modulators of receptor activity or receptor binding and activity and as modulators of receptor activity or shouland in the rapmentically, e.g. as neuroprotectants during neuropathic pain etc. The method allows affinity of ligands to be estimated withhout having to prepare them and then test them, in vitro. Ligands with high selectivity for particular glutamate receptors should have fewer side effects than known receptor antagonists.
                                                                                              02-DEC-1998 (first entry)
Bacterial periplesmic binding protein fragment #13.
Brotein-ligand binding pocket; PLBP; binding protein; ligand; modulator; bacterial periplesmic binding protein; interaction energies; ischaemia; basis set molecules; BSM; ionotropic glutamate receptors; treatment; neuroprotectant; stroke; epilepsy; neuropathic pain.
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                                                                                                                                                                                                                                                                                                               Well; 98-495386/42.
Designing a model for a ligand-binding pocket in a protein and its use for assessing ligand affinity - without the need to prepare test ligand, for identifying selective antagonists for identifying selective antagonists for identifying selective antagonists for identifying selective antagonists with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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excitatory amino acid receptor; human EAA3 receptor; kainate-type;
EAA3d receptor; central nervous system receptor; CNS.
Homo sapiens.
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Pred. No. 3.71e+
4; Mismatches
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/label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R63070 standard; Protein; 849 AA.
                                                               W76238 standard; protein; 146 AA
                                                                                                                                                                                                Prokaryota.
W09838208-A2.
03-SEP-1998.
27-FEB-1998: U03951.
28-FEB-1997: US-808804.
(BEAR-) BEARSDEN BIO INC.
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Local Similarity 60.0%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        reduced side effects
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70 GALVDSKSYA 79
GALVDSKSYA 79
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The human EAA3a receptor (R60112) and its variants EAA3b, EAA3c and EAA3d (R63068-R63070) occur naturally in human brain. They are all members of the EAA3 receptor family, having extracellular N° and C-termini and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
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excitatory amino acid receptor; human EAA3 receptor; kainate-type;
EAA3c receptor; central nervous system receptor; CNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors.

N.B. The CDNA and corresp, amino acid sequences for EAA3b, 3c and 3d do not appear in full in the specification; the sequences have been compiled by combining sequences in Figures 1 and 4 according to the description given in the disclosure.
                                                                                                                                                                                                         Polynucleotide encoding a human excitatory amino acid 3 receptor or fragment - used to assay test ligands for their interaction with a human CBS receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 11; Length 849;
Pred. No. 3.71e+01;
4; Mismatches 0; Indels
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/label= mature_EAA3c_receptor
/label= mature_Eda3c_receptor
which 40 amino acids have been eliminated
from the C-terminus and in which the last
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563..5bel-
7.label- TM-1
*** "transmembrane domain"
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/note- "transmembrane domain"
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/label= TM-3
/note= "transmembrane domain"
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/label- TM-2
/note- "transmembrane domain"
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/note= "extracellular"
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/label- signal_peptide
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                                                                                                               Nutt SL;
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Best Local Similarity 60.0%;
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563..840
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/label- C
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(KAME) KAMBOJ R.
(ELLI/) ELLIOT C E.
(NUTT,) NUTT S L.
Elliot CE. Kamboj R,
WPI; 94-25829/32.
N-PSDB; 081158.
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70 GALVDSKSYA 79
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Identification of human CNS receptor ligand - and identification of agents that modulate editing of human CNS receptors claim 4, Fig 5, 59pp; English.

The amino acid sequence (R75883) of human EAA3 receptor deduced from a genomic DNA sequence (Q91231) differed from that deduced from EAA3 cDNA at position 591 of the mature protein; the genomic sequence coded for glutamine at this position, and the cDNA sequence for arginine. This was due to a single nucleotide change of A to G at position 2279 as a result of RNA editing. The edited and unedited positions were functionally distinct and appeared to be selectively expressed. CNS receptors subject to such editing (see also R75882 and R75884) have value in screening cpds. for potential therapeutic
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Human EAA3b excitatory amino acid receptor.

excitatory amino acid receptor; human EAA3 receptor; kainate-type;

EAA3a receptor; central nervous system receptor; CNS.
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31..905
/label- mature_EAA3b_receptor
/note- "differs from EAA3a by one amino acid,
1.e. Asp at position +639 of mature
EAA3a is replaced by Asn in EAA3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 16; Length 9U5;
Pred. No. 3.71e+01;
......+rhes 0; Indels
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Human EAA3 receptor (Q-591).
Glutamate receptor; EAA3 receptor; excitatory amino acid;
CNS receptor; RNA editing.
Homo sapiens.
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/label= TM-1
/note= "transmembrane domain"
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/note- "transmembrane domain"
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/note= "transmembrane domain"
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/label- hydrophobic_region
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/label- N-terminal_domain
                                                                                                                                                                                                                                                                                        21-DEC-1994; CA0705.
23-DEC-1993; US-172188.
(ALLX.) ALLELLX BIOPHARMACEUTICALS INC. KAMDOJ R. Nutt S; WPI; 95-24670/31.
N-PSDB; Q91231.
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31..905
/label= Mat_protein
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R63068 standard; Protein; 905 AA.
R63068;
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60.0%;
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/label- TM-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Claim 13; Fig 1 and Fig 4B; 35pp; English.

The human EAA3a receptor (R60112) and its variants EAA3b, EAA3c and EAA3d (R63068-R63070) occur naturally in human brain. They are all members of the EAA3 receptor family, having extracellular N- and C-termini and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors.

N.B. The cDNA and corresp. amino acid sequences for EAA3b, 3c and 3d do not appear in full in the specification; the sequences have been compiled by combining sequences in Figures 1 and 4 according to the description given in the disclosure.
                                                                                                                                                                                                                              Polynucleotide encoding a human excitatory amino acid 3 receptor or fragment - used to assay test ligands for their interaction with a human CBS receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutamate receptors - used to screen for functional ligands and identify and isolate further receptors Disclosure; Fig 11: 109pp; English. GluK6 has a Mr of 100,000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-0CT-1990; U06153.
27-0CT-1989; US-428116.
(SALK ) SALK INST FOR BIOL STUD.
Helnemann SF, Boulter JR, Hollmann M, Bettler B, Jensen JE;
WPI; 91-164197/22.
N-PSDB; Q11854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 865;
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Glutamate receptor 6; probe; ligand; drug screening.
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Pred. No. 3.71e+01;
4; Mismatches 0;
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R75883 standard; Protein; 905 AA.
R75883;
10-JUL-1996 (first entry)
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R11994 standard; Protein; 901 AA.
                                                                                                                                                            Nutt SL;
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Similarity 60.0%;
6; Conservative
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60.0%;
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       12-JUN-1994.
08-DEC-1993; 110933.
11-DEC-1992; US-989793.
                                                                                                                              WPI; 94-255829/32.
                                                                               (KAMB/) KAMBOJ R.
(ELLI/) ELLIOT C E.
(NUTI/) NUTI S L.
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Matches 6; Conserv
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Best Local Similarity
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| GALVDSKSYA 79
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21-DEC-1993; CA0705.
RALELY BIOPHARMACEUTICALS INC.
RAMBOJ R, Nutt S;
RAMBOJ R, Nutt S;
RAMBOJ R, Nutt S;
RPI: 95-240670/31.
RP
                                                                                                                                                                                                                                                                                or fragment - used to assay test ligands for their interaction with a human CBS receptor.
Claim 13: Fig 1: 35pp; English.
The sequence cooling for the EAA3a receptor was isolated by probing a human foetal brain cDNA library. The EAA3a receptor and naturally occurring variants of it (i.e. EAA3b, EAA3c and EAA3d) are members of the EAA3 receptor family; they all have extracellular N- and C-termin and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
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Polynucleotide encoding a human excitatory amino acid 3 receptor
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10-JUL-1996 (first entry)
Human EAA4 receptor (1532, X536, Q586).
Glutamate receptor; EAA4 receptor; excitatory amino acid;
CNS receptor; RNA editing.
Homo sapiens.
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Pred. No. 3.71e+01;
4; Mismatches 0; Indels
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/label= Sig_peptide
32..908
/label= Mat_protein
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Best Local Similarity 60.0%;
Matches 6; Conservative
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                                                                                                  (KAMBA) KAMBOJ R.
(ELLI/) ELLIOT C E.
(NUTT.) NUTT S L.
Elliot CE, Kamboj R, 19
                                                  08-DEC-1993; 110933.
11-DEC-1992; US-989793.
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Matches 6; Conserv
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70 GALVDSKSYA 79
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The human EAA3a receptor (R60112) and its variants EAA3b, EAA3c and EAA3d (R63068-R63070) occur naturally in human brain. They are all members of the EAA3 receptor family, having extracellular N- and C-termini and 4 internal hydrophobic domains which anchor the receptor within the cell surface membrane. The receptors bind glutamate and also exhibit binding properties characteristic of kainate-type EAA
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12-MAR-1995 (first entry)
Human EAA3a excitatory amino acid receptor.
EAA3a receptor; kainate-type;
EAA3a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptors.

N.B. The CDNA and corresp, amino acid sequences for EAA3b, 3c and 3d do not appear in full in the specification; the sequences have been compiled by combining sequences in Figures 1 and 4 according to the description given in the disclosure.

Sequence 905 AA;
                                                                                                                                                                                                                                                                                                                             N-PSDB; 081156.
Polynuclectide encoding a human excitatory amino acid 3 receptor or fragment - used to assay test ligands for their interaction with a human CBS receptor.
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/label= signal_peptide
31.905
/label= mature_EAA3a_receptor
31.562
/label= N-terminal_domain
/note= "extracellular"
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604..624
/label- TM-2
/~^te= "transmembrane domain"
  "transmembrane domain"
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/label- TM-4
/note= "transmembrane domain"
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/note= "transmembrane domain"
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/note= "transmembrane domain"
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/label- hydrophobic_region
/note= "transmembrane doma
841..905
/label= C-terminal_domain
/note= "extracellular"
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R60112 standard; Protein; 905 AA.
R60112;
                                                                                                                                                                                                                                                                                Nutt SL;
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Best Local Similarity 60.0%;
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                                                                                                                                                  08-DEC-1993; 110933.
11-DEC-1992; US-989793.
                                                                                                                                                                                                                        (ELLI/) ELLIOT C E. (NUTT/) NUTT S L. Elliot CE, Kamboj R, WPI; 94-255829/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Excitatory aminoacid for receptors with kainate binding activity used to test ligands for CNS receptor interaction to identify cpds. useful against CNS disorders

Trougs. useful against CNS disorders
Claim 13: Figure 1: 37pp; English.
The excitatory amino acid receptor can be used to screen ligands.
The ligands can be assayed for interaction by incubating them with cells, preferably occytes, expressing the receptor or with membrane preparations from these cells, and assessing any interaction by determining receptor-ligand binding or ligand-mediated ion channel cativation. This method is useful in the identification of the receptor are useful for structural investigations and to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human excitatory aminoacid receptors - used for producing receptors and in assays for test ligands for binding to human CNS receptors.

Claim 12; Page 16-19; 34eppic. Bnglish.

Nucleotides which encode the excitatory amino acid receptors (EAA's)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                07-JUL-1994 (first entry)

Excitatory amino acid receptor (EAA4a receptor).

Excitatory amino acid receptor; EAA4a; screening; detection; identification; CNS; nervous disorders; antibody; oocyte; membrane protein; ion-channel; therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Excitatory amino acid receptor (EAA5).
Excitatory amino acid receptor; EAA; identification; detection;
CNS; central nervous system; therapeutic; antibody; ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.71e+01;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.JAN-1994.
24.JUN-1993: 304961.
24.JUN-1992: US-903456.
(ELLI/) ELLIOTT C E.
(KAMB/) KAMBOJ R.
(KAMB/) NUTT S L.
KAMBOJ R. NUTT S L.
KAMBOJ R. NUTE SL.
WPI: 94-010248/02.
                                                                                                                                                                                                     R45367 standard; Protein; 908 AA. R45367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R50179 standard; Protein; 919 AA. R50179; 17-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nutt SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1993; 307325.
17-SEP-1992; US-945210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELLI/) ELLIOTT C E.
(KAMB/) KAMBOJ R.
(NUTT/) NUTT S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                      756 gglidskgyg 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 gglidskgyg 765
                                                       1:1:11:1:
70 GALVDSKSYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
EP-578409-A.
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                                                                                                                                                                                                        NAME OF THE PROPERTY OF THE PR
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can be used for the production of the receptors, to identify sequence related genes or for locating the receptor encoding DNA in a specimen. Recombinant cells which produce the receptors, or their membrane preparations, can be used for assaying a test ligand for binding to a human CNS receptor to develop therapeutics. The receptors can themselves be used in the production of antibodies for use in detection methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          distributed the control of the contr
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Excitatory amino acid receptor (EAA4b) fragment.
Excitatory amino acid receptor; EAA4a; screening; detection;
Identification: CNS; nervous disorders; antibody; oocyte; membrane protein; ion-channel; therapeutics.
EP-578409-A.
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27-071-1989; US-428116.
(SALK ) SALK INST FOR BIOL STUD.
Helnemann SF, Boulter JR, Hollmann M, Bettler B, Jensen JE;
WPI; 91-164197/22.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 10; Length 919;
Pred. No. 3.71e+01;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 2; Length 920;
Pred. No. 3.71e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Glutamate receptor 5-1.
Glutamate receptor 5-1; probe; ligand; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402..416
/label- insertion
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R11993 standard; Protein; 920 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                   60.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757 gglidskgyg 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 gglidskgyg 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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70 GALVDSKSYA 79
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                                                                                                                                                                                                                                                                                                                              919 AA;
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Rambol R. Nutt SL.

Rambol R. Nutt SL.

Rambol R. Nutt SL.

Rapic 94-010248/02.

Excitatory aminoadd for receptors with kainate binding activity

used to test ligands for CNS receptor interaction to identify

reds. useful against CNS disorders

Disclosure: Figure 3a: 7pp: English.

The excitatory amino acid receptor EAA4a can be used to screen

ligands. The ligands can be assayed for interaction by incubating

the with cells, preferably occytes, expressing the receptor or with

membrane preparations from these cells, and assessing any

interaction by determining receptor-ligand binding or

ligand-mediated ion channel activation. This method is useful in

the identification of therapeutics useful to treat CNS disorders in

humans. Fragments of the receptor are useful for structural

investigations and to raise antibodies. This fragment of the

receptor EAA4b corresponds to amino acid residues 700 to 750 and has

caparitic acid at position in receptor EAA4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example: Fig 5: 62pp; English.

A mutant IR is claimed which may have a mutated alpha-chain, esp.
the precursor processing site. The beta-chain may be mutated, e.g.
by deletion of the transmembrane sequence; the tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity may be inactivated. Fig. 5 is a comparison of oncogene a human EGF receptor sequences with that of HIR in the cytoplasmic domain of the insulin receptor beta subunit.

Sequence 259 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis of receptor and mutants for therapeutic and diagnostic
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Bell JR, Ulrich A, Ramachandran J;
WPI; 86-226966/35.
New DNA encoding insulin receptor or its fragments - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 9; Leuy...
Pred. No. 4.90e+01;
......rches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 259;
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W41513 standard; Protein; 371 AA.
W41513;
17-JUN-1998 (first entry)
N. meningitidis alpha-2,3-sialyltransferase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P60011 standard; Protein; 259 AA
24-JUN-1993; 304961.
24-JUN-1992: US-903456.
(ELLI/) ELLIOTT C E.
(KME/) KAMBOJ R.
(NUTT/) NUTT S L.
KAMDOJ R. NUTT SE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1991 (first entry)
Sequence of oncogene v-fms.
Therapy; diagnosis; insulin.
EP-192392-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%;
ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 59.3%;
Local Similarity 60.0%;
les 6; Conservative
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10-FEB-1986; 300894.
12-FEB-1985; US-700776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 npypgilvnskfy 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |:|||:|:
70 GALVDSKSYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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This sequence represents an alpha-2,3-sialyltransferase which has been isolated from Neisseria meningitidis. The protein can be used as a reagent for adding a slalic acid residue to an acceptor having a terminal galactose residue, e.g. in synthesis of biologically active oligosaccharides or sialyl-modified proteins or lipids. The nucleic acid sequence can be used for the recombinant production of sequence 371 AA,
                                                                                                                                                                                                             Nucleic acid sequence encoding Neisseria alpha-2,3-sialyl:transferase - useful to add sialic acid to acceptor with terminal galactose residue for synthesis of biologically active cliquasaccharide cliquas 38; 50pp; English.
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Alpha-2,3-sialyltransferase; sialic acid; acceptor; lipid;
biologically active oligosaccharide; sialyl-modified protein.
Nelsseria meningitidis.
W09477745-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 29; Length 371
Pred. No. 6.45e+01;
3; Mismatches 3; Indels
                                                     10-JUN-1997; CA0390.
10-JUN-1997; US-872485.
10-JUN-1996; US-019520.
(CANA ) NAT RES COUNCIL CANADA.
Glibert M, Jennings MP, Wakarchuk WW, Young NM; WPI; 98-052313/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Wed Sep 1 16:30:56 1999 Job time: 25 secs.
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53.8%;
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Best Local Similarity
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 3.68 Seconds 152.280 Million cell updates/sec Wed Sep 1 16:30:02 1999; Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Tabular output not generated.

>PCT-US99-13024-2 (66-79) from PCTUS9913024.pep (11 of 12) 86 Description: Perfect Score: Sequence: Title:

1 DPSTGALVDSKSYA 14 PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 24.770; Variance 28.525; scale 0.868 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Fred. No.	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	4.06e+00	6.60e+00	6.60e+00	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.06e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01
10	000000	nesci ibrion	glutamate receptor be	glutamate receptor Gl	receptor		glutamate receptor -		kainate receptor - ra	glutamate receptor Gl	crtJ protein - Rhodob	mutL protein - Vibrio	glutamin-(asparagin-)	monocarboxylate trans	protein-tyrosine kina	macrophage colony-st1	macrophage colony-sti	hypothetical protein	hypothetical protein	adhesion protein homo	serine-repeat antigen	parasitophorous vacuo	glycoprotein E - suid	5-aminolevulinate syn	hypothetical protein
SUMMARIES	£	77	A43954	S35792	A54260	S19098	158178	S19810	153474	S19808	S17813	S04886	A28063	JC5507	TVMVMD	TVHUMD	TVCTMD	T01757	S48382	A69756	A54512	A54639	VGBEGI	SYCHAL	G69189
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\$35792 *type complete glutamate receptor GluR6C - mouse #formal_name Mus musculus #common_name house mouse 13.4an-1995 #sequence_revision 13.Jan-1995 #text_change 08.Sep-1997

ACCESSIONS

RESULT ENTRY TITLE ORGANISM DATE

49 57.0 989 2 A54505 serine-repeat antigen 1.70e 48 55.8 427 2 B71617 SERA antigen/papain-1 1.70e 48 55.8 437 2 B71617 SERA antigen/papain-1 1.70e 48 55.8 434 2 B7323 SLR2 protein (56 alse 2.70e 48 55.8 434 2 B7323 SLR2 protein (52 alse 2.70e 48 55.8 643 2 B5323 SLR2 protein (52 alse 2.70e 48 55.8 643 2 B5323 SLR2 protein (52 alse 2.70e 48 55.8 643 2 B5323 SLR2 protein (52 alse 2.70e 48 55.8 648 2 P50047 Serine protein 2.70e 48 55.8 663 2 S69781 outer membrane protei 2.70e 48 55.8 663 2 S69781 outer membrane protei 2.70e 48 55.8 663 2 S69781 outer membrane protein 4.25e 47 54.7 257 2 A71068 hypothetical protein 4.25e 47 54.7 257 2 A71068 hypothetical protein 4.25e 47 54.7 359 2 B71086 hypothetical protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 2.70e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 2 S69781 outer membrane protein 4.25e 47 54.7 350 1 S78749 splicing factor S736 6.25e 47 54.7 501 2 S53783 splicing factor S736 6.25e 47 54.7 501 2 S53783 splicing factor S736 6.25e 47 54.7 2233 1 ZLNEP3 splicing factor S736 6.25e 47 54.7 2233 1 ZLNEP3 sequence_revision 31-bcc.1993 *text_change 60-Sep-1996 47 54.7 2233 1 ZLNEP3 sequence_revision 31-bcc.1993 *text_change 60-Sep-1996 48 555 4 M3154 143.143.146 49 555 4 M3154 M31	#domain glutamate receptor #length 864 #molecular-weight	<pre>neurotransmitter receptor; transmembrane pr #domain glutamate receptor homology #1 #length 864 #molecular-weight 97353 #chec</pre>	Similari 6; Con IDSKGYG	
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                                                                                                               ##residues 1-869 ##label GRE ##cross-references EMBL:X66117; NID:g312493; PID:g312494 ##cross-references EMBL:X66117; NID:g312493; PID:g312494 IFICATION #superfamily glutamate receptor; glutamate receptor homology neurotransmitter receptor; transmembrane protein
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#map_position 6q16.3-6q21
CLASSIFICATION #superfamily glutamate receptor; glutamate receptor homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Paschen, W.: Blackstone, C.D.; Huganir, R.L.; Ross, C.A.
#journal Genomics (1994) 20:435-440
#title Human GluR6 kainate receptor (GRIK2): molecular cloning,
expression, polymorphism, and chromosomal assignment.
#cross-references MUD:94307730
#accession A54260
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#formal_name Rattus norvegicus #common_name Norway rat
04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
08-Sep-1997
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submitted to the EMBL Data Library, December 1991
S19098
                                                                                                                                                                                                                    #domain glutamate receptor homology #label #length 869 #molecular-weight 97807 #checksum
Gregor, P.
submitted to the EMBL Data Library, June 1992
S35792
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Pred. No. 4.06e+00;
4; Mismatches 0; Indels
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Pred. No. 4.06e+00;
4; Mismatches 0; Indels
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glutamate receptor GluR6 precursor - rat
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##residues 1-908 ##label BET
                                                                            preliminary
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ilarity 60.0%;
Conservative
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Best Local Similarity 60.0%;
Matches 6; Conservative
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##residues 1-90
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                                                                                                 ##molecule_type mRNA
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                      #authors
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#journal Nature (1991) 351:745-748
#fitle Cloning of a cDNA for a glutamate receptor subunit activated
by kainate but not AMPA.
#cross-references MUID:91287799
                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
#fresidues 1-620,0',622-908 ##label SEE
#fcross-references EMBL:211715; NID:956279; PID:956280
FICATION #superfamily glutamate receptor; glutamate receptor homology
IDS neurotransmitter receptor; transmembrane protein
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*length 918 *molecular-weight 103980 *checksum 1748
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                                       Egebjerg, J.; Bettler, B.; Hermans-Borgmeyer, I.; Heinemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gregor, P.; O'Hara, B.F.; Yang, X.; Uhl, G.R.
Neuroreport (1993) 4:1343-1346
Expression and novel subunit isoforms of glutamate receptor
genes GluRS and GluR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain signal sequence #status predicted #label SIG\
#product glutamate receptor GluR6 #status predicted
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain glutamate receptor homology #label GRH\
#domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TMZ\
#domain transmembrane #status predicted #label TM3\
#domain transmembrane #status predicted #label TM3\
#length 908 #molecular-weight 102423 #checksum 3737
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Pred. No. 4.06e+00;
4; Mismatches 0; Indels
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##cross-references EMBL:211548; NID:956281; PID:956282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158178 #type complete
glutamate receptor - human
02-Jul-1996 #sequence_revision 02-Jul-1996
28-Aug-1998
158178
                                                                                                                                                                              nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 2; Le
Pred. No. 4.06e+00;
4; Mismatches 0;
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#map_position 21q22.1-21q22.2
CLASSIFICATION #superfamily glutamate receptor;
REYMORDS heurotransmitter receptor
#length 918 #molecular-weight 1
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larity 60.0%; 1
Conservative
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larity 60.0%;
Conservative
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70 GALVDSKSYA 79
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#Journal FEBS Lett. (1992) 307:139-143
#title High-affinity kainate and domoate receptors in #cross-references MUID:92354697
#accession 153474
                                                                                                                                                       Score 52; DB 2; Len
Pred. No. 4.06e+00;
4; Mismatches 0;
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Best Local Similarity 60.0%;
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Hermans-Borgmeyer, I.; Moll, C.; Stevens, C.F.; Heinemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title Cloning of a putative glutamate receptor: a low affinity
kainate-binding subunit.
#cross-references MUID:92153417
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#domain transmembrane #status predicted #label TM3,
#domain transmembrane #status predicted #label TM4,
#domain transmembrane #status predicted #label TM4,
#domain transmembrane #status predicted #label TM4,
#domain transmembrane #status predicted #label TM5,
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#langth 919 #molecular-weight 103991 #checksum 9539
                                                                                                                              S19810 *type complete
glutamate receptor GluR7 - rat
kainate receptor
#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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*formal_name Rattus norvegicus *common_name Norway rat
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submitted to the EMBL Data Library, February 1992
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4; Mismatches 0; Indels
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JH0312
Bettler, B.; Boulter, J.; Hermans-Borgmeyer, I.;
O'Shea-Greenfield, A.; Deneris, E.S.; Moll, C.; Borgmeyer,
U.; Hollmann, M.; Heinemann, S.
Neuron (1990) 5:583-595
Cloning of a novel glutamate receptor subunit, GluR5:
expression in the nervous system during development.
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1-21, 'L', 283-353, 'WR', 356-476,'G', 478-602,'G', 604-869, 899-949 ##label BET # superfamily glutamate receptor; glutamate receptor homology neurotransmitter receptor; phosphoprotein; transmembrane
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30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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Query Match 60.5%; Score 52; DB 2; Length 949; Best Local Similarity 60.0%; Pred. No. 4.06e+00; Matches 6; Conservative 4; Mismatches 0; Indels
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#fresidues 1-869,899-949 ##label SE2
#cross-references EMBL:211713; NID:956275; PID:956276
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ffresidues 1-869,'HY' ##label SE3
ftross-references EMBL:211712; NID:956273; PID:956274
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#journal Nucleic Acids Res. (1989) 17:6241-6251

#title Cloning and characterization of mutL and mutS genes of Vibrio cholerae: nucleotide sequence of the mutL gene.
                                                                                                                                                                                                  Burke, D.H.; Alberti, M.; Armstrong, G.A.; Hearst, J.E. submitted to the EMBL Data Library, November 1991
The complete nucleotide sequence of the 46 kb photosynthesis gene cluster of Rhodobacter capsulatus.
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crtJ protein - Rhodobacter capsulatus
#formal_name Rhodobacter capsulatus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutL protein - Vibrio cholerae
#formal_name Vibrio cholerae
28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
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glutaminase-asparaginase
#formal_name Acinetobacter calcoaceticus
28-Aug-1989 #sequence_revision 28-Aug-1993
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glutamin-(asparagin-)ase (EC 3.5.1.38) - Acinetobacter
                                                                                                                                                                                                                                                                                                                                                     #length 469 #molecular-weight 51331 #checksum 8204
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                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.3%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.3%;
Similarity 63.6%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          308 DAGSAALVQGRSFA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 DPSTGALVDSKSYA 79
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          771 GGLIDSKGYG 780
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S04886
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|GALVDSKSYA 79
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Best Local Similarity
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#submission
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Tanaka, S.; Robinson, E.A.; Appella, E.; Miller, M.; Ammon, H.L.; Roberts, J.; Weber, I.T.; Wlodawer, A.
H.D.; Roberts, J.; Weber, I.T.; Wlodawer, A.

#title Structures of amidohydrolases. Amino acid sequence of a glutaminase-asparaginase from Acinecobacter glutaminase-asparaginase from Acinecobacter an asparaginase from Erwinia chrysanthemi.
#cross-references MUID:88243706
#accession A28063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Yoon, H.; Fanelli, A.; Grollman, E.F.; Philp, N.J.
#journal Blochem. Blophys. Res. Commun. (1997) 234:90-94
#title Identification of a unique monocarboxylate transporter (MCT3)
#cross-references MUID:97312526
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*binding_site phosphate (Thr) (covalent) (by cAMP- an cGMP-dependent kinases) *status predicted\
*binding_site phosphate (Ser) (covalent) (by casein kinase II) *status predicted\
*binding_site phosphate (Ser) (covalent) (by casein kinase II) *status predicted\
*binding_site phosphate (Ser) (covalent) (by protein kinase C) *status predicted
*linase C) *status predicted
*length 542 *molecular-weight 58085 *checksum 7501
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This protein regulates lactate levels in the interphotoreceptor
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#formal_name Gallus gallus #common_name chicken
02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change
18-Sep-1998
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#length 331 #molecular-weight 35485 #checksum
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the source is designated as Acinetobacter
glutaminasificans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Len
Pred. No. 1.06e+01;
4; Mismatches 0;
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Pred. No. 1.06e+01;
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##residues 1-542 ##label YOO
##cross-references GB:U15685
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61.5%;
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nucleic acid sequence not shown; translation not shown

FMS proto-oncogene. #cross-references MUID:89239490 #accession S08123

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protein-tyrosine kinase (EC 2.7.1.112) fms precursor - feline
    sarcoma virus (strain McDonough)
    #formal_name feline sarcoma virus
                                                                                                                                                                                                                                                                                                                                                                                         *Superfamily macrophage colony-stimulating factor I receptor; immunoglobulin homology; protein kinase homology ATF: autophosphorylation; glycoprotein; kinase-related transforming protein; magnesium; oncogene; phosphoprotein; phosphotransferase; receptor; transmembrane protein; tyrosine-specific protein kinase
                                                                                                      *dutnors Hampe, A.; Gobet, M.; Sherr, C.J.; Galibert, F.

#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:85-89

#title Nuclectide sequence of the feline retroviral oncogene v-fms shows unexpected homology with oncogenes encoding tyrosine-specific protein kinases.

#cross-references MUD:84119469
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Nucleotide sequence and structural organization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain signal sequence #status predicted #label SIG\
#product protein-tyrosine kinase fms #status predicted
#label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVHUMD #type complete macrophage colony-stimulating factor 1 receptor precursor human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain extracellular #status predicted #label EXT\
                                                              host Felis sp. (cat)
27-Nov-1985 #sequence_revision 31-Dec-1991 #text_change
13-Jnn-1997
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#formal_name Homo sapiens #common_name man
28-Dec-1987 #sequence_revision 31-Dec-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                    This protein is synthesized as a gag-fms polyprotein.
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#region protein kinase ATP-binding motif\
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2; Mismatches 4
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larity 53.8%;
Conservative
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                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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45,73,94,153,275,
286,302,335,410,
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535-941
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#authors Wheeler, E.F.; Roussel, M.F.; Hampe, A.; Walker, M.H.; Fried, V.A.; Look, A.T.; Rettenmier, C.W.; Sherr, C.J.

"Variol. (1986) 59:224-233

#title The amino-terminal domain of the v-fms oncogene product includes a functional signal peptide that directs synthesis of a transforming glycoprotein in the absence of feline leukemia virus gag sequences.

#accession 156672
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W.G.; O'Brien, S.
Cell (1985) 42:421-428
Expression of the human c-fms proto-oncogene in hematopoietic cells and its deletion in the 5q- syndrome.
                                                                                           #journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:7800-7804
#title Replacement' of COOH-terminal truncation of v-fms with c-fms sequences markedly reduces transformation potential.
#cross references MUID:87017034
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the authors translated the codon GCA for residue 54
                                                                                                                                                                                                                                                                                                                                                                                                                                        **cross-references GB:M14002; NID:9182676; PID:9553292
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##residues 874-972 ##label RE3
##cross-references GB:M14193; NID:9182521; PID:9182522
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ftresidues 1-53,'A',55-972 ##label COU
ftcross-references GB:J03149
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Paccession I52772
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completed: Wed Sep 1 16:30:13 1999
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                                                                                                            *superfamily macrophage colony-stimulating factor 1 receptor; immunoglobulin homology; protein kinase homology
ATP; autophosphorylation; glycoprotein; kinase-related
transforming protein; magnesium; phosphoprotein;
phosphotransferase; prote-oncogene; receptor; transmembrane
protein; tyrosine-specific protein kinase
                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label SIG\
#product macrophage colony-stimulating factor 1 receptor #status predicted #label MAT\
#comain extracellular #status predicted #label EXT\
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                      #map_position 5q33.2-5q33.3
#introns 17/1: 103/1: 198/1: 243/3: 297/1: 361/2; 400/1: 440/2; 504/1:
#542/3: 585/1: 620/1: 657/1: 711/2: 741/1: 773/3: 814/3:
852/1: 885/2: 921/3
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Activation of the feline c-fms proto-oncogene: multiple alterations are required to generate a fully transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine kinase (EC 2.7.1.112) csflr/fms
#formal_name Felis sllvestris catus #common_name domestic (
31. Dec-1989 #sequence_revision 31-Dec-1989 #text_change
13-Jun-1997
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#domain intracellular #status predicted #label INTN
#domain protein kinase homology #label KINN
#region protein kinase ATP-binding motif\
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Pred. No. 1.06e+01;
2; Mismatches 4; Indels
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##cross-references GDB:120600; OMIM:164770
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##cross-references EMBL:X03663
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*cross-references MUID:89077553
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Best Local Similarity 53.8%;
Matches 7; Conservative
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66 DPSTGALVDSKSY 78
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224-278,419-485
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302,335,353,412,
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ORGANISM
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ENTRY
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#domain signal sequence #status predicted #label SIG\
#product macrophage colony-stimulating factor 1 receptor #status predicted #label MAT\
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                                                             #domain extracellular #status predicted #label EXT\
#domain immunoglobulin homology #label IMM1\
#domain immunoglobulin homology #label IMM2\
#domain immunoglobulin homology #label IMM3\
#domain immunoglobulin homology #label IMM4\
#domain immunoglobulin homology #label IMM5\
#domain transmenbrane #status predicted #label IMM>
#domain intracellular #status predicted #label IMM>
#domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
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Pred. No. 1.06e+01;
2; Mismatches 4; Indels
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similarity 53.8%;
7; Conservative
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224-278,417-482
45,73,94,153,275,
302,335,410,477,
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781,794
SUMMARY
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535-980
577-915
585-593
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PCT-US99-13024-2-11.rsp

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:28:57 1999; MasPar time 2.70 Seconds 146.747 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (66-79) from PCTUS9913024.pep (11 of 12) 86 1 DPSTGALVDSKSYA 14

Description: Perfect Score: Sequence:

77977 seqs, 28268293 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot37 1:swissprot

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 25.367; Variance 25.400; scale 0.999 Statistics:

	Pred. No.	1.22e+00	1.22e+00	1,22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	1.22e+00	2.10e+00	2.10e+00	3.57e+00	3.57e+00	3.57e+00	3.57e+00	6.03e+00	6.03e+00	6.03e+00	6.03e+00	6.03e+00	6.03e+00	1.01e+01	1.01e+01	1.67e+01
	Description	GLUTAMATE RECEPTOR, IO	GLUTAMATE RECEPTOR, IO	GLUTAMATE RECEPTOR, IO			GLUTAMATE RECEPTOR, IO	GLUTAMATE RECEPTOR, 10	GLUTAMATE RECEPTOR, 10	CRIJ PROTEIN.	PROTEIN MUTL.	GLUTAMINASE-ASPARAGINA	MACROPHAGE COLONY STIM	FMS TYROSINE KINASE TR	MACROPHAGE COLONY STIM	HYPOTHETICAL 27.2 KD P	GLYCOPROTEIN GI PRECUR	5-AMINOLEVULINIC ACID	5-AMINOLEVULINIC ACID	SERINE-REPEAT ANTIGEN	INSULIN RECEPTOR SUBST	PROTEIN SCK (FRAGMENT)	EXTRACELLULAR SERINE P	CRYPTIC PLASMID PROTEI
SUMMARIES	QI	GLK2_XENLA	GLK2_MOUSE	GLK2_HUMAN	GLK2_RAT	GLK1_HUMAN	GLK3_RAT	GLK3_HUMAN	GLK1_RAT	CRTJ_RHOCA	MUTL_VIBCH	ASPQ_ACIGL	KFMS_HUMAN	KFMS_FSVMD	KFMS_FELCA	YIP2_YEAST	VGLE_PRVRI	HEM1_OPSTA	HEM1_CHICK	SERA_PLAFG	IRS2_MOUSE	SCK_HUMAN	PRTE_BACNO	CPPC_NEIGO
	DB	-	~	Н	7	-	-	-	-	Н	Н	~	-	7	H	~		-	٦	~	-	-		-
	Length	285	883	806	806	918	919	919	949	469	563	331	972	978	980	235	577	627	635	989	1321	428	448	205
æ	Query Match	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	59.3	59.3	58.1	58.1	58.1	58.1	57.0	57.0	57.0	57.0	57.0	57.0	55.8	55.8	54.7
	Score	52	52	25	52	25	52	25	52	51	51	20	20	20	20	49	49	49	49	49	49	48	48	47
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1.67e+01 1.6
GLUTATHIONE S-TRANSFER INVASIN PRECURSOR (OUT NADP-SPECIFIC GLUTAMAT NADP-SPECIFIC GLUTAMAT MINOR CAPSID PROTEIN L PHENYLALANYL-TRNA SYNT GESSOR ROTEIN C TYPE IIS RESTRACTION E 5-AMINOLEVULINIC ACID ACONITATE HYDRATASE, M PHYCOBLILSOME LINKER P MACROPHAGE COLONY STIM MACROPHAGE SECRIBER STIMELASE (GLUTAMATE RECEPTOR, 10
GTK1_RAT YADA_YERPS DHE4_AGABI VL2_HPV16 SYFB_YEAST CITA_KLEPN HEMA_IAME6 TTAI_FLAOK HEM1_HUWAN ACON_SCHPO ACO
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ALIGNMENTS

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                                                                                                            THE PRESENCE OF GLUTAMINE RESIDUE (NON-EDITED) DETERMINES CHANNELS WITH LOW CALCTUM PERMEAS AN ARGININE RESIDUE (EDITED) DETERMINES A HIGHER CALCIUM PERMEABLILITY ESPECIALLY IF THE PRECEDING SITES ARE FULLY EDITED (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBCLIULAR ASSEMBLE INTO A KAINATE-GATED HOWOMERIC CHANNEL THAT DOES CHANNELS, THAT CAN BE GATED BY AMPA (BY SIMILARITY).

TISSUE SPECIFICITY: MOST ABUNDANT IN THE CEREBELLUM AND THE
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92356790.

MORITA T., SAKIMURA K., KUSHIYA E., YAMAZAKI M., MEGURO H.,
ARAKI K., ABE T., MORI K.J., MISHINA M.;
"Cloning and functional expression of a cDNA encoding the mouse beta
2 subunit of the kainate-selective glutamate receptor channel.";
BRAIN RES. MOL. BRAIN RES. 14:143-146(1992).
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **ROEHLER W., BURNASHEV N., SAKMANN B., SEEBURG P.H.;
**Determinants of Ca2+ permeability in both TM1 and TM2 of high
affinity kannate receptor channels: diversity by RNA editing.";
**PUBLICH SATINATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT
**MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYMAPTIC
**ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE
NAMED ACCORDING TO THEIR SELECTIVE AGONISTS. MAY BE INVOLVED IN
THE TRANSMISSION OF LIGHT INFORMATION FROM THE RETINA TO THE
                                                                                                                                                                                                                                                                                                                  GREGOR P., O'HARA B.F., YANG X., UHL G.R.;
Expression and novel subunit isoforms of glutamate receptor genes
GluB5 and GluB6 ".
NEUROREPORT 4:1343-1346(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HERB A., HIGUCHI M., SPRENGEL R., SEEBURG P.H.; "O/R site editing in kainate receptor GluR5 and GluR6 pre-mRNAs requires distant intronic sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: TWO FORMS GLUR6 BETA2 AND GLUR6-2 ARE PRODUCED BY ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: EXPRESSED DURING BRAIN DEVELOPMENT EXPRESSION DROPS IN THE ADULT.
 Length 285;
                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROC. NATL. ACAD. SCI. U.S.A. 93:1875-1880(1996).
 Score 52; DB 1; L
Pred. No. 1.22e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 560-585 FROM N.A., AND RNA EDITING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 584-695 FROM N.A., AND RNA EDITING.
                          4; Mismatches
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
MEDLINE; 94083547.
60.5%;
60.0%;
                          6; Conservative
                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE)
 Ouery Match
Best Local Similarity
                                                 133 GGLIDSKGYG 142
                                                               1:1:111:1:
70 GALVDSKSYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96312506.
                                                                                                                                                                                                                                                                                                                                                                                 SE:UENCE FROM N.A. MEDLINE; 92356790.
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MEDLINE; 93213505.
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                          Matches
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                                                                                                                                                                                                                                                                                                                                                                      GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
61-NOTABARTE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUTA, ONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUTA, OMINO ACID RECEPTOR 4) (EAA4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAQLEKRSFCSAMVEELRMSLKCQRRLKHKPQAPVIVKTEE
                                                                                                                                                                                                                                        PIR; S35792; S35792.

PIR; A43954; A43954.

MGD; MGI:95815; GRIKZ.

PFAM, PFCOMOGO, 11g_Chan; 1.

TRANSMEMBRANE; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;

TRANSMEMBRANE; ALTERNATIVE SPLICING; RNA EDITING.

SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSFCSAMVEELRMSL -> ESSIWLVPPYHPDTV
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TISSUE-FETAL BRAIN;
MEDLINE; 95236039.
HOO K.H., NUTT S.L., FLETCHER E.J., ELLIOTT C.E., KORCZAK B.,
DEVERILL R.M., RAMPERSAD V., FANTASKE R.P., KAMBOJ R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRIKZ OR GLURG.
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN GLUR6-2 FORM).
MISSING (IN GLUR6-2 FORM).
I -> V (IN RNA EDITED VERSION).
Y -> C (IN RNA EDITED VERSION).
O -> R (IN RNA EDITED VERSION).
S -> G (IN REF. 1).
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Pred. No. 1.22e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100273 MW; 32E5917A CRC32;
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60.0%;
                                                                                                                                                                                                      D10054; D1001409; -.
                                                                                                                                                                                     EMBL; X66117; G312494; -.
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889
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Best Local Similarity
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Q13002;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U16126; G790532; -.
MIN; 138244; -.
PERM; PFOU060; 11g_chan; 1.
RECEPTOR: POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
                                                                PASCHEN W., BLACKSTONE C.D., HUGANIR R.L., ROSS C.A.;
"Human GluR6 kainate receptor (GRIK2): molecular cloning, expression,
polymorphism, and chromosomal assignment.";
GENOMICS 20:435-440(1994)
                                                                                                                                   PASCHEN W., HEDREEN J.C., ROSS C.A.; RNA editing of the glutamate receptor subunits GluR2 and GluR6 in human brain tissue.":
J. NEUROCHEM. 63:1596-1602(1994).
"Functional expression and pharmacological characterization of the human EAA4 (GluR6) glutamate receptor: a kainate selective channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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POTENTIAL.
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POTENTIAL.
POTENTIAL.
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                           RECEPT. CHANNELS 2:327-337(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEMBRANE; RNA EDITING.
SIGNAL 1 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
908
561
621
67
67
73
                                                 SEQUENCE FROM N.A.
                                                                                                                   RNA EDITING.
MEDLINE; 95016699.
                                                        94307730
                                                                                                                                                                                                TISSUE-BRAIN;
                                                                                                                                                                                      EDITING
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CARBOHYD
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MEDIANS OF JOURNALY AND ANNOUNCE OF TESSUE-BRAIN;

MEDIANS 9213505.

MEDIANS 9213505.

MEDIANS 9213505.

MEDIANS 9213505.

MEDIANS 96 (22+ permeability in both TM1 and TM2 of high affinity kainate receptor channels: diversity by RNA editing.";

MEDIANON 10:491-500(1993).

MANY STNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC ACTIONS OF GLIG ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE NAMED ACCORDING TO THEIR SELECTIVE AGONISTS. MAY BE INVOLVED IN THE TRANSMISSION OF LIGHT INFORMATION FROM THE RETINA TO THE HYPOTHAAMUS. THIS RECEPTOR BINDS KAINATE > QUISQUALARE.

CHARACTERIST THE RESERVE OF GLUTAMINE RESIDUE (NON-EDITED) DETERMINES CHANNELS CHANNELS (EDITED) DETERMINES A HIGHER CALCIUM PERMEABILITY ESPECIALLY IF DESCRIBED THE STRUCTURES (90% OF THE DECEMBER EDITED. THIS RECEPPOR IS NEARLY DESCRIBED. THE DESCRIBED IN ALL GRAY MATTER STRUCTURES (90% OF THE DECEMBER EDITED.)
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (REL. 32, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBUNIT: ASSEMBLE INTO A KAINATE-GATED HOMOMERIC CHANNEL THAT DOES
NOT BIND AMPA. GRIKZ ASSOCIATED TO GRIKS FORMS FUNCTIONAL
CHANNELS, THAT CAN BE GATED BY AMPA.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IS FOUND IN THE OLFACTORY
LOBE, PIRIFORM CORTEX, DENTATE GYRUS, HIPPOCAMPUS, GRANULAR CELL
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGEBJERG J., BETTLER B., HERWANS-BORGMEYER I., HEINEMANN S.F.; "Cloning of a cDNa for a glutamate receptor subunit activated by
                                             VERSION).
VERSION).
VERSION).
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAT).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "High-affinity kainate and domoate receptors in rat brain."; FEBS LETT. 307:139-143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOMELI H., WISDEN W., KOEHLER M., KEINAENEN K., SOMMER B., SEEBURG P.H.;
                                                                                                                                         Length 908;
                                                                                                                                                                       Indels
                                            I -> V (IN RNA EDITED VI
Y -> C (IN RNA EDITED VI
Q -> R (IN RNA EDITED VI
G -> S (IN REF. 2)
HW; D0058718 CRC32;
                                                                                                                                                      1.22e+00;
                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                   908 AA.
                                                                                                                                                                        4; Mismatches
             POTENTIAL.
POTENTIAL.
                                                                                                                                         Score 52;
Pred. No. 1
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                                                                                                          102583
                                                                                                                                                        60.08;
                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kainate but not AMPA.";
NATURE 351:745-748(1991).
                                                                                                                                                                                                                                                                                                   STANDARD;
423
430
546
567
571
621
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789
789
908 AA;
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                                                                                                                                                        Local Similarity
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70 GALVDSKSYA 79
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GRIK2 OR GLUR6.
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VARIANT
VARIANT
CONFLICT
SEQUENCE
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              CARBOHYD
CARBOHYD
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PCT-US99-13024-2-11.rsp

RECEPT. CHANNELS 3:41-49(1995).

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01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
6LUTAMATE RECEPTOR, IONOTROPIC KAINATE I PRECURSOR (GLUTAMATE RECEPTOR 5) (EXCITATORY AMINO ACID RECEPTOR 3) (EAGA3).
                                                                                                                                                                                                                                   GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                         EMBL; 211548; G56280; -.
PFAM; 211715; G56280; -.
PFAM; PF00060; lig_chan; l.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL; TRANSMEMBRANE; RNA EDITING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KORCZAK B., NUTT S.L., FLETCHER E.J., HOO K.H., ELLIOTT C.E., RAMPERSAD V., MCWHINNIE E.A., KAMBOJ R.K.; "CDNA cloning and functional properties of human glutamate receptor EAA3 (GluR5) in homomeric and heteromeric configuration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GREGOR P., O'HARA B.F., YANG X., UHL G.R.; "Expression and novel subunit isoforms of glutamate receptor genes
LAYER OF THE CEREBELLUM, AND IN CADDATE-PUTAMEN. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                              567 I -> C (IN RNA EDITED VERSION).

571 Y -> C (IN RNA EDITED VERSION).

521 Q -> R (IN RNA EDITED VERSION).

102470 MW; CA86C64C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Pred. No. 1.22e+00;
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TISSUE-FETAL BRAIN;
MEDLINE; 96172461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.5%;
Similarity 60.0%;
6; Conservative
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70 GALVDSKSYA 79
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MEDLINE; 94083547.
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GLK1_HUMAN
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LINEURREPORT 5:2625-2629(1994).

CHONGINEL L-GUITAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT MANY SYNASES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE NAMED ACCORDING TO THERR SELECTIVE ACONISTS. MAY BE INVOLVED IN THE TRANSMISSION OF LIGHT INFORMATION FROM THE RETINA TO THE HYPOTHALAMUS: THIS RECEPTOR BINDS DOMOATE > KAIRATE > L-GLUTAMATE > COUSCULLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CHOSOGLALITE > CNOX = DNOX > AMPA > DIHYDROKAINATE > NMDA.

CHOSOGLALICAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CHOSOGLATED YEASON (Q) ASSEMBLES INTO A FUNCTIONAL KAINATE-GATED HOMOMERIC CHANNEL, WHEREAS THE EDITED VERSION (R) IS UNABLE TO PRODUCE CHANNEL ACTIVITY WHEN EXPRESSED ALONE. BOTH EDITED AND UNEDITED VERSIONS CAN FORM FUNCTIONAL CHANNELS WITH GRIK4 AND GRIK5 (BY SIMILARITY).

CHOSOGRAPH OF THE UNCOTAGE CAN STANDANT IN THE CEREBELLUM AND THE SUPRACHIASAMTIC NUCLEIL (SCN) OF THE HYPOTHALAMUS.

CHOSOGRAPH OF THE COURT OF THE LIGAND-GATED IONIC CHANNELS FAMILY.

CHOSOGRAPH OF THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NR MIN: 138245; -.

NR PERMY PROMOGOS: 119_chan; 1.

NR PERMY PROMOGOS: 119_chan; 1.

NR PERMY PROMOGOS: 119_chan; 1.

NR TANNSMEMBRANE; PHOSPHORYLATION; RNA EDITING; ALTERNATIVE SPLICING.

PT SIGNAL.

SIGNAL.

1 30 POTENTIAL.

FT CIAIN 31 918 GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 1.

FT TRANSMEM 577 597 POTENTIAL.

FT TRANSMEM 616 636 POTENTIAL.

FT TRANSMEM 616 636 POTENTIAL.

FT TRANSMEM 835 POTENTIAL.

FT CARBOHYD 74 74 POTENTIAL.

FT CARBOHYD 75 75 POTENTIAL.

FT CARBOHYD 75 POTENTIAL.

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PHOSPHORYLATION (BY PKC) (POTENTIAL).
Q -> R (IN RNA EDITED VERSION).
MISSING (IN ISOPORM 2).
AFCFFYGLOCKQTHPTNSTSGTTLSTDLECGKLIREERGIR
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KSSFTSILTCHQRRTQRKETVA (IN ISOFORM 2).
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                                                                                                                                                    "RNA editing of human kainate receptor subunits.";
NEUROREPORT 5:2625-2629(1994).
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4A5251FB CRC32;
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103980 MW;
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                                                                        TISSUE-BRAIN;
MEDLINE; 95210645.
NUTT S.L., KAMBOJ R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 ;
918 AA;
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70 GALVDSKSYA 79
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                                      LT 6
GLK3_RAT
PAZ64: 035420;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOPATION UPDATE)
GLUTAMAIE_RECEPTOR, IONOTROPIC KAINATE 3 PRECURSOR (GLUTAMATE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92153417.

BETTLER B., EGEBJERG J., SHARWA G., PECHT G., HERMANS-BORGMEYER I., MOLL C., STEVENS C.F., HEINEMANN S.F.;

Cloning of a putative glutamate receptor: a low affinity kainate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                          RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA: VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "High-affinity kainate and domoate receptors in rat brain."; FEBS LETT. 307:139-143(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY: TISSUE-BRAIN;
MEDDLINE: 98050892.
SCHIFFER H., SWANSON G.T., HEINEMANN S.F.;
Rat GluR7 and a carboxy-terminal splice variant, GluR7b, ar.
functional kainate receptor subunits with a low sensitivity
                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN;
MEDLINE; 92354697.
LOMELI H., WISDEN W., KOEHLER M., KEINAENEN K., SOMMER B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 32-919 FROM N.A. (GLUR7A ISOFORM).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (GLUR7A ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (GLUR7B ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glutamate.";
NEURON 19:1141-1146(1997).
                                                                                                                                                                                                                            GRIK3 OR GLUR7
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SPRENGEL R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEEBURG P.H.
                                                                                                                                                                                                      (GLUR-7)
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                                        RESULT
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AF027331; G2598978; -. M83552; G204392; -.

EMBL; EMBL;

EMBL; 211716; G471274; -.

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PERMY, PEODOGO; 119_chan; 1.

KW RECEPTOR: POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN:
KW TRANSMEMBRANE; ALTERNATIVE SPLICING; SIGNAL.

FT CHAIN 32 919 GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 3.

FT CHAIN 32 563 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 637 67 POTENTIAL.

FT TRANSMEM 637 657 POTENTIAL.

FT CARBOHYD 76 76 POTENTIAL.

FT CARBOHYD 76 76 POTENTIAL.

FT CARBOHYD 77 POTENTIAL.

FT CARBOHYD 78 278 POTENTIAL.

FT CARBOHYD 415 POTENTIAL.

FT CARBOHYD 426 426 POTENTIAL.

FT CARBOHYD 415 POTENTIAL.
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G13003; O16136; O13004;
01-NOV-1997 (REL. 35, CASTED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
11-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 3 PRECURSOR (GLUTAMATE RECEPTOR 7) (GLUR-7) (EACL 7) (EACL 7) (EACL 7) (EACL 7)
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-1- FUNCTION: L-GLUTAMATE ACTS AS AN EXCITATORY NEUROTRANSMITTER AT MANY SYNAPSES IN THE CENTRAL NERVOUS SYSTEM. THE POSTSYNAPTIC ACTIONS OF GLU ARE MEDIATED BY A VARIETY OF RECEPTORS THAT ARE NAMED ACCORDING TO THEIR SELECTIVE AGONISTS. THIS RECEPTOR BINDS DOMOATE > KAINATE >> L-GLUTAMATE = QUISQUALATE >> AMPA = NNDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PURANAM R.S., EUBANKS J.H., HEINEMANN S.F., MCNAMARA J.O., Chromosomal localization of gene for human glutamate receptor
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PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 919;
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T -> I (IN REF. 4).

A -> P (IN REF. 4).

S -> P (IN REF. 4).

S -> P (IN REF. 4).

P -> A (IN REF. 4).

O MW; 9B6BE2E4 CRC32;
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Pred. No. 1.22e+00;
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RECEPT. CHANNELS 2:315-326(1994).
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60.0%;
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355
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290
241
341
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919 AA;
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TISSUE-FETAL BRAIN;
MEDLINE; 95236038.
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Best Local Similarity
Matches 6; Conser
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70 GALVDSKSYA 79
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MEDLINE; 94174381
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CONFLICT
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SEQUENCE
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MOD_RES
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 1 PRECURSOR (GLUTAMATE RECEPTOR
                                                                                                                                                                                      GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 3.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                PFAM; PF00060; lig_chan; l.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
TRANSMEMBRANE; RNA EDITING.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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GRIKS TO FORM HETEROMERIC RECEPTORS (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glutamate receptor channel with high affinity for domoate and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOMMER B., BURNASHEV N., VERDOORN T.A., KEINANEN K., SAKMANN B., SEEBURG P.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                            110 A -> S.
152 Q -> K (IN RNA EDITED VERSION).
103 R -> L (IN REF. 2).
104031 MW; 00CB78C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                           Length 919;
                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 1; L. Pred. No. 1.22e+00;
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01-NOV-1995 (REL. 32, LAST SEQ0
15-JUL-1998 (REL. 36, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                         60.5%;
60.0%;
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                                                                                                            EMBL; U16127; G790534; -. EMBL; U16128; G790536; -. EMBL; S69349; G545834; -. MIM; 138243; -.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RATTUS NORVEGICUS (RAT).
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415
426
433
548
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415
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426
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919 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 70 GALVDSKSYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
MEDLINE; 92224905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91026041
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GRIK1 OR GE
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLK1_RAT
P22756;
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                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                             VARIANT
VARIANT
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                                                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: EXPRESSED IN SUBSETS OF NEURONS THROUGHOUT THE DEVELOPING AND ADULT CENTRAL AND PERIPHERAL NERVOUS SYSTEMS. IN THE MEDIAL ANTIODALOID NUCLEI, MEDIAL HABENULAE, PYRIFORM AND CINGULATE CORTICES, AND PURKINNE CELL LAYER, ALSO HIGHLY EXPRESSED IN EMBRYONIC AND ADULT DORSAL ROOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPO0066; lig_chan; l.
PPO0066; lig_chan; l.
FOR: POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
MEMBRANE; PHOSPHORYLATION; ALTERNATIVE SPLICING; RNA EDITING.
POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.
DENERIS E.S., MOLL C., BORGMEYER U., HOLLMANN M., HEINEMANN S.; "Cloning of a novel glutamate receptor subunit, GluR5: expression in the nervous system during development."; NEURON 5:583-595(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST FOUR VARIANTS; GLURS-2, GLURS-2A, GLURS-2B/GLURS-1 AND GLURS-2C (SHOWN HERE); THAT ARISE BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY PKC) (POTENTIAL). PHOSPHORYLATION (BY PKC) (POTENTIAL). Q -> R (IN RNA EDITED VERSION).
                                                                                                                                                                       LOMELI H., WISDEN W., KOEHLER M., KEINAENEN K., SOMMER B., SEEBURG P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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POTENTIAL.
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EMBL, M83561; G204390; -...
EMBL, Z11712; G56274; -...
EMBL, Z11713; G56276; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JH0312; JH0312
PIR; S19808; S19808
PIR; S19807; S19807
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                    MEDLINE; 92354697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR; POSTS
TRANSMEMBRANE;
                                                                                                                                  TISSUE-BRAIN;
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                                                                                                                                         Gaps
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PPRAM: PF00158; Signa54; 1.
PHOTOSYNTHESIS; CHLOROPHYLL BIOSYNTHESIS; CAROTENOID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
                                                                                                                                                                                                                                                                                                               RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHODOBACTER GROUP;
RHODOBACTER.
                                                                                                                                        ;
0
MISSING (IN GLUR5-2).
MISSING (IN GLUR5-2B/GLUR5-1 AND GLUR5-2).
KG -> HY (IN GLUR5-2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                               Score 52; DB 1; Length 949;
Pred. No. 1.22e+00;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 1; Length 469;
Pred. No. 2.10e+00;
8; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       BURKE D.H., ALBERTI M., ARMSTRONG G.A., HEARST J.E.;
SUBMITTED (NOV-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- PATHWAY: CAROTENOID AND CHLOROPHYLL BIOSYNTHESIS.
                                           MISSING (IN GLURS-2A).
82 K -> L (IN REF. 2).
155 CA -> WR (IN REF. 2).
77 A -> G (IN REF. 2).
107840 MW; 7441125F CRC32;
                                                                                                                                                                                                                                                     01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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llarity 42.9%;
Conservative
                                                                                                               60.5%;
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                                                                                                                                                                                                                                STANDARD;
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                                             949
282
355
477
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12,
35,
                                                                                                                             Local Similarity
                                                                                                                                                              771 GGLIDSKGYG 780
                                                                                         949 AA;
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70 GALVDSKSYA 79
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MEDLINE; 89366654.
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872
282
354
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                                                                                                                                                                                                                                                                                          CRIJ PROTEIN.
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CRIJ_RHOCA
P26167;
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9
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P11793;
                                 VARSPLIC
VARSPLIC
CONFLICT
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SEQUENCE
VARSPLIC
VARSPLIC
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A LUBKOWSKI J., WLODAWER A., HOUSSET D., WEBER I.T., AMMON H.L.,
LUBKOWSKI J., WLODAWER A., HOUSSET D., WEBER I.T., AMMON H.L.,
LUBKOWSKI J., WLODAWER A., HOUSSET D., WEBER I.T., AMMON H.L.,

"Refined crystal structure of Acinetobacter glutaminasificans
glutaminase-asparaginase.";
LACTACKSTALLOGR. DS 08.0826-832(1994).

"ALSO CATALYSES: L-ASPARAGINE + H(2)O = L-GLUTAMATE + NH(3).

"L-CATALYTIC ACTIVITY: L-GLUTAMINE + H(2)O = L-GLUTAMATE + NH(3).

"L-SUBOUTT: HOWOTETRAMER.

"PROSTE; PSO0144; ASN.GLN ASE.1; 1.

PROSTE; PSO0144; ASN.GLN ASE.1; 1.

PROSTE; PSO017; ASN.GLN ASE.2; 1.

PROSTE; PSO017; ASPARAGINASE.; 1.

PROSTE; PSO017; ASPARAGINASE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANAKA S., ROBINSON E.A., APPELLA E., MILLER M., AMMON H.L.,
ROBERTS J., WEBER I.T., WLODAWER A.;
"Structures of amidohydrolases. Amino acid sequence of a glutaminase-
asparaginase from Acinetobacter glutaminasificans and preliminary
crystallographic data for an asparaginase from Erwinia
chrysanthemi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 78080774.
HOLCENBERG J.S., ERICSSON L., ROBERTS J.;
HAND acid sequence of the diazooxonorleucine binding site of
Acinetobacter and Pseudononas 7A glutaminase-asparaginase enzymes.";
BIOCHEMISTRY 17:411-417(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR'1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLUTAMINASE-SPRAGINASE (EC 3.5.1.38).
ACINEYOBACTER GLUTAMINASIFICANS.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
MORAXELLACEAE; ACINETOBACTER.
                                                                                           Q.
                         genes of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
BERA T.K., GHOSH S.K., DAS J.;
"Cloning and characterization of mutL and mutS genes of Vibrichlerae: nucleotide sequence of the mutL gene.";
WUCLEIC ACIDS RES. 17:6241-6251(1989).
-I- FUNCTION: MUTL IS INVOLVED IN THE METHYL DIRECTED REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                  -1- SIMILARITY: NONE WITH MUTL FROM OTHER BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 1; L6
Pred. No. 2.10e+00;
1; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                        563 AA; 64858 MW; 9F37C887 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rysanthemi.";
BIOL. CHEM. 263:8583-8591(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 59.3%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                        EMBL; X15438; G48369; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                              MISMATCHES IN DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 DPRTGVLVERK 303
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DNA REPAIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 DPSTGALVDSK 76
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P10172;
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WHEELER E.F., ROUSSEL M.F., HAMPE A., WALKER M.H., FRIED V.A.,
WHEELER E.F., ROUSSEL M.F., SHERR C.J.;
The amino-terminal domain of the v-fms oncogene product includes a
functional signal peptide that directs synthesis of a transforming
glycoprotein in the absence of feline leukemia virus gag sequences.";
J. VIROL. 59:224-233(1986).
I. FUNCTION: THIS PROTEIN IS THE RECEPTOR FOR CSF-1, IT IS A PROTEIN
TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
COUSSENS L., VAN BEVEREN C., SMITH D., CHEN E., MITCHELL R.L.,
ISACKE C.M., VERMA I.M., ULLRICH A.;
ISACKE C.M., VERMA I.M., ULLRICH A.;
IMM at carboxyl terminus of viral homologue of receptor proto-oncogene
fims at carboxyl terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of two genomic regions containing the KIT and the FMS receptor tyrosine kinase genes.";
                                                                                                   Gaps
                                                                                                                                                                                                   01-APR-1988 (REL. 07, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-JUN-1997 (REL. 35, LAST ANNOTATION UPDATE)
MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R)
(EC 2.7.1.112) (FMS PROTO-ONCOGENE) (C-FMS) (CD115).
                                                                                                                                                                                                                                                                                                                         HAMPE A., SHAMOON B.M., GOBET M., SHERR C.J., GALIBERT F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANDRE C., HAMPE A., LACHAUME P., MARTIN E., WANG X.P., MANUS V.,
HU W.X., GALIBERT F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the human c-fms gene in
                                      INVOLVED IN SUBSTRATE BINDING (BY SIMILARITY).

OD2AAF82 CRC32;
                                                                                                   ö
                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                              Score 50; DB 1; Length 331;
Pred. No. 3.57e+00;
4; Mismatches 0; Indels
                                                                                                                                                                                  972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-16 FROM N.A.
MEDLINE; 89261741.
VISVADER J., VERMA I.M.;
"Differential transcription of exon 1 of placental trophoblasts and monocytes.";
MOL. CELL. BIOL. 9:1336-1341(1989).
                                                           331 AA; 35485 MW;
                                                                             58.1%;
Similarity 55.6%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                         ONCOGENE RES. 4:9-17(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-16 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENOMICS 39:216-226(1997).
                                                                                                                                                                                  STANDARD;
 12
92
93
165
122
                                                                                        Local Similarity
                                                                                                                     182 GTLVEGKPY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97179223.
ANDRE C., HAMPE A.,
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                          70 GALVDSKSY 78
                                                                                                                                                                                                                                                                                                                  MEDLINE; 89239490.
HAMPE A., SHAMOON
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  12
92
93
165
122
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P07333;
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                             R PIR; X03663; G29900; -.

R PIR; S08123; TYHUMD.

MIM; 16470; --

MIM; 16470; --

MIM; 16470; --

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS001109; PROTEIN_KINASE_DOM; 1.

R PFAM; PF00047; 1g; 3.

R PFAM; PF00069; Pkinase; 2.

R HSSP; P11362; 1FGI.

R HSSP; P11362; 1FGI.

R HSSP; P1362; 1FGI.
R HSSP; P1362; 1FGI.
R HSSP; P1362; 1FGI.

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PHOSPHORYLATION (AUTO-) (IN VITRO) (BY SIMILARITY).
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PHOSPHORYLATION (AUTO-) (IN VITRO) (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACROPHAGE COLONY STIMULATING FACTOR
PROTEIN KINASES.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE EXTRACELLULAR DOMAIN CONTAINS FIVE IG-FOLD DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-) (IN VIVO)
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CYTOPLASMIC (POTENTIAL).
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IG-LIKE DOMAIN 2.
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IG-LIKE DOMAIN 4.
IG-LIKE DOMAIN 5.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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82705690 CRC32;
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                                                                                                                                                                                              FELINE SARCOMA VIRUS (STRAIN MCDONOUGH).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; MAMMALIAN TYPE C RETROVIRUSES.
                                                                                                                                     HAMPE A., GOBET M., SHERR C.J., GALIBERT F., "Nucleotide sequence of the feline retroviral oncogene v-fms shows unexpected homology with oncogenes encoding tyrosine-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE.
EXTRACELLUIAR DOMAIN CONTAINS FIVE IG-FOLD DOMAINS.
                                                             FMS TYROSINE KINASE TRANSFORMING PROTEIN (EC 2.7.1.112).
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ATP (BY SIMILARITY).
      KFMS_FSVWD STANDARD; PRT; 978 AA. P0545; 086597; 21-JUL-1986 (REL. 01, CREATED) 15-JUL-1999 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                            PROC. NATL. ACAD. SCI. U.S.A. 81:85-89(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; K01643; G323891; -.
EMBL; S59588; G237024; -.
PIR; A00654; TVWVMD.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TR; 1.
PROSITE; PS0011; PROTEIN_KINASE_TR; 1.
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978
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           PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION.
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01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-JAN-1990 (REL. 13, LAST ANNOFAZION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOFAZION UPDATE)
MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R)
(EC 27,1.112) (FMS PROTO-ONCOGENE) (C-FMS).
CSFIR OR FMS.
FELIS SILVESTRIS CATUS (CAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRAȚA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; FELIDAE; FELIS.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A31636; TVCTMD.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TR; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PFAM; PF00047; 19; 3.

PFAM; PF00069; PAINASE; 2.

HSSP; P11362; 1FG1.

PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; RECEPTOR; TRANSMEMBRANE; TRANSFERASE; GLYCOPROTEIN; PHOSPHORYLATION; ATP-BINDING; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASES.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE EXTRACELLULAR DOMAIN CONTAINS FIVE IG-FOLD DOMAINS.
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                                                                                                                                                                         L -> P (IN REF. 1).
QRTPPVAR -> RGPPL (IN REF. 1).
MW; 2F11BGFB CRC32;
                                                                                                                                                                                                                            Length 978;
                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                              Score 50; DB 1; Le
Pred. No. 3.57e+00;
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53.8%;
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978 AA;
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Best Local Similarity
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
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                         MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR.
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SEQUENCE FROM N.A.
STRAIN-S2B8C / AB972;
STRAIN-S2B8C / AB972;
STRAIN-S2B8C / AB972;
CHURCHER C.M., CONNOR R., COPSET T., DEAR S., DEVLIN K., FRASER A., GENTLES S., HAMLYN N., HORSWELL T.S., HUNT S., JAGELS K., JONES M., LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., WALSH S.V., WHITEHEAD S.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YILISZW.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
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P40455;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL 27.2 KD PROTEIN IN IMP2-DNA43 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 1; Length 980; Pred. No. 3.57e+00; 2; Mismatches 4; Indels
                                                                                                         EXTRACELLULAR (POTENTIAL).
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IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
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IG-LIKE DOMAIN 5.
IG-LIKE DOMAIN 5.
AFP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Similarity 53.8%;
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                                                                           Score 49; DB 1; Length 235; Pred. No. 6.03e+00;
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                                                                                                      6; Mismatches
                                                                                                                                                                                            Search completed: Wed Sep 1 16:29:07 1999 Job time: 10 secs.
                                                                          57.0%;
Similarity 46.2%;
6; Conservative
EMBL; 247047; G763194; -. EMBL; Z38059; G557771; -. PIR; S48382; S48382. HYPOTHETICAL PROTEIN.
                                                                                                                            207 DPSASLVIDSRSF 219
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:17:15 1999; MasPar time 6.29 Seconds 314.294 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-93) from PCTUS9913024.pep (6 of 12) 634 1 MEKFWAEFGQGYVQTPFLSE..........DSKSYAFSTSNDITSAAFVS 93 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 3:part13 14:part14 15:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 20:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 39:part39

Mean 27.254; Variance 116.070; scale 0.235 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	1 060-10	3 019+00	6 200+00	200400	1 510+01	1 510+01	1 800+01	100001	1 80e+01	1 809+01	1 800+01	1.80e+01	2 148+01	2 550+01	3 040+01	3.046+01
		Description	Phace T4 Oper constant	Hepatitis E virus bol	Neutral protease enco	Sequence of pentral p	Bacillus subtilis 145	Amino acid sequence o	Hybrid (1.3-1.4)-pre-	Protein encoded by OR	Hepatitis E virus atr	HEV strain protein en	Hepatitis E virus (HE	Protein encoded by OR	Amino acid sequence o	Protein encoded by OR	A. thallana ethylene	OETR ethylene respons
		ID	R97371	W76368	P94617	P51009	P95000	W75773	R06621	W71209	R91813	R51264	W81519	W80196	W75774	R14618	W73122	R74632
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		Match Length DB	17.3 65.	1693	520	521	242	623	239	1693	1693	1693	1693	1693	633	1693	613	613
æ	Query	Match	47.3	15:1	14.5	14.5	13.7	13.7	13.6	13.6	13.6	13.6	13.6	13.6	13.4	13.2	13.1	13.1
		Score	300	96	92	92	87	87	98	98	86	86	98	98	82	84	83	83
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	20000000000000000000000000000000000000	00000000000000000000000000000000000000			2011 2012 2014 2016 2017 2017 2017 2017 2017 2017 2017 2017	, 000 / 41111001110 / 100 / 40		RAGGE STATE	z x x x x x x x x x x x x x x x x x x x	MICROSPORT HCV CKS-N HCV CKS-N HCV CKS-N HCV CKS-N Sequence HCV Polyp HCV Polyp HCV Polyp HCV Polyp HCV Polyp Composite Compos	ospore- NSS ence CKS NSS CKS NSS CKS NSS ence en ein seq ence en titis C 1 polyp osite H osite H cosite H cosite H cosite H cosite H cosite H cosite H cosite H cosite H cosite H	MCCOSPORE-Specific MCC MSS encoded by HCV CKS-NSSE recommerce Composed by HCV CKS-NSSE recommerce encoded in Protein sequence encoded in HCV amino acid sequence encoded by Hepatide encoded by Peptide encoded by Hepatide C virus Composite HCV I polyprotein. Composite HCV HC-J Composite HCV HC-J Composite HCV HC-J Composite HCV MC-J Composite C virus Composite C virus Composite C virus C virus C virus C MPATILIS C virus		HCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		
ADE PERMENTA BOLT RESULT RESUL	45 80 LT 1 R97371 stan R97371: 07-JAN-1997 Phage T4 OR Phage T4: t Elilter; mol-	80 12.6 11 standard 11; 14 ORFX (f 14; tall 17 tall	tandar 997 (ORFX 7; tail	4044	tere t	oll 28 otein; 6 entry), product. e protei	້ ໝໍ 1/⊷ຕິ	M40038 HCV po ALIGNMENTS 5 AA. "gp34"	s s	cv po	olypro	rotei no-st	n. ructur	ů	. 096-	101
	## ABCCETIOPhage T4. ## ## ## ## ## ## ## ## ## ## ## ## ##	100pne 1947-1996 1-1996 1-1996 1-1996 1-1996 1-1996 1-1996 1-1996	1942 1942 1942 1942 1943 1943	= 14. U1302: US-323 BERG E 12/22. 53.	27. B 7.	60. from	T.	phage t	tail	fibre	Q Q	+ •	+ + **		<u>د</u> م	4
##800000000	self assemble in corresponding DC claim 7: Fig 7: A protein (R973 reading frame X T29053) of phag frames for tail frail fibre prot quantities in m stable nanostru	assemble into na seponding DNA no 7. Fig 9. 18 Pp. tein (R97371) of ing frame x of th ing frame x of th 33) of phage TV. es for tail fibre fibre proteins (fibre proteins (itles in microbile nanostructures	ole interpretation of the property of the property of the protest of the protect	le into na ng DNA ng 7; 83pp; 897371) of me X of th phage T4. tail fibre tail fibre fin microbil structures	A 83pp; E 83pp; E 1) of u of the of the fibre p the crobial tures.	eng ta ta This	nemble into nano-structure on and and pure that 7: 83pp; English. In (R97371) of unspecified frame X of the tail fibre of phage T4. This gene is for tail fibre proteins (so tail fibre proteins (so tail fibre proteins (so tail fibre proteins) and season anostructures.	1 - 010175	function function protein gion als e also R ified) c	iseful as in general so in general so in general so in general so in so	s the relinch 370 and be library	the produce of and R973 of produced on produced in grounder open conducted one produced in grounder blocks	s et lict see lisee lise se i	f c also also also also also also also also	ppen ppen ppen ppen ppen ppen ppen ppen	

1 mekfmaeiwtricpnailsesnsvrykisiagscplstagpsyvkfddnpvgsqtf ||||||||: | mEKFWAEFGGGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTF RESULT 2 ID W76368 standard; Protein; 1693 AA.

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Gaps 99 56

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Length 65;

Score 300; DB 19; Length 65 Pred. No. 1.86e-18; 3; Mismatches 7; Indels

Query Match
Best.Local Similarity 82.1%;
Matches 46; Conservative

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Disclosure; p; English.
Claimed replicon comprises a promoter and regulatory regions, capable of expressing alkaline and neutral protease genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë
                                                                                                                                                                                                                                                      Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation Claim 10; Page 17-24; 29pp; Japanese.
This sequence represents a Hepatitis E viral hollow particle protein. This polypeptides can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 frtsfydgavleangperynlsfdasqstmaagpfsptyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96; DB 35; Length 1693;
Pred. No. 3.01e+00;
21; Mismatches 25; Indels 3; Gaps
           03-DEC-1998 (first entry)
Hepatitis E virus hollow particle protein #1.
Hollow particle protein; virus; antibody; detection; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1990 (first entry)
Neutral protease encoded by npr gene.
Protease: expression systems; substilin; neutral protease;
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches 18; Indels
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                                                                                                                  /note= "Partial sequence"
                                                                                                                                                 08-SEP-1998.
28-FEB-1997; 062445.
28-FEB-1997; JP-062445.
(DENK-) DENKA SEIKEN KK.
(KAXU-) KOKURITSU YOBO EISEI KENKYUSHO.
WPI: 98-535037/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-1989.
29-MAR-1985; 717800.
29-MAR-1985; US-717800.
(GENE.) Genex Corp.
Magarajan V, Rhodes CS, Banner CDB; WPI: 89-053639/07.
N-PSDB; N91114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
221.520
/note="Mature"
27.520
/note="PRO-"
                                                                                     Location/Qualifiers
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Best Local Similarity 26.9%;
Matches 18; Conservative
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Best Local Similarity 27.8%;
Matches 15; Conservative
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                                                                        Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 fapgvsp 638
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                                                                                                                                   J10234383-A
                                                           infection
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The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing betaglucan from barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus to direct expression of poly:peptide Disclosure; Fig 4: 37pp; English.
The inventors claim a vector comprising a replicable plasmid containing the promoter and regulatory region of a gene selected from apr[BamP] and npr[BamP], for transformation of Bacillus to direct expression of polypeptide.
Sequence 521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1997 (first entry)
Bacillus subtilis lichenase.
Beer production; fermentation; barley; beta-glucan; hydrolysis;
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239 issesgkyvlrdlskptgtgiitydlqnreynlp-gtlvssttngfttssgraa 291
                              Replicable plasmidic expression vector - for transformation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
                                                                                                                                                                                                                        01-DEC-1991 (first entry)
Sequence of neutral protease encoded by the npr[BamP] gene.
Bacillus expression vector; secretion vector.
Bacillus amyloliquefaciens.
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Pred. No. 6.20e+00;
19; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                        /label= signal
28..21
/label= Pro sequence
222..521
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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P95000 standard; Protein; 242 AA.
P95000;
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P51009;
01-DEC-1991 (first entry)
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Local Similarity 27.8%;
les 15; Conservative
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08-SEP-1987; JP-224615.
(ASAK ) ASAHI BREWERIES KK.
WPI; 89-119863/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1984; 304662.
06-JUL-1983; US-511198.
08-JUN-1984; US-618902.
29-WAR-1985; US-717800.
(GENE-) GENEX CORP.
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Gaps

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New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes blscloure; page 26; 84pp; English.

This hybrid protein is encoded by the beta-glucanase-H1 gene.

Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the amylolique-faciens beta-glucanase and the carboxyl-terminal half of the B.macerans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glycosidic linkages in (1,3-1,4)-beta-glucans. C. Reducing sugars are obtd. at high temps. and thus this enzyme can be used in the mfr. of food prods., esp. beer and animal feed (eg for feeding poultry). See also Q05833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein production
Disclosure; Columns 55-64, 45pp; English.
W71209-11 represent the proteins encoded by the open reading frames (ORFs) of the DNA sequence of the Burmese isolate of an enterically transmitted nonA/AnnaB viral haptitis agent (ET-NAME). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV), detecting ET-NAME in Infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1998 (first entry) Protein encoded by ORF 1 of the Burmese isolate of ET-NANB. Enterically transmitted nonA/nonB hepatitis virus; identification; HEV; ET-NANB; detection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - useful for e.g. virus detection and viral
                                                                                                                                                                                                                                                                                                                                                                74 laltspsynkfdcgenrsvqtygyglyevrm-kpakntgivssfftytgptegtp 127
                                                                                                                                                                                                                                                                                                                                                                                    Hofemeister J, Thomsen KK, Olsen O, Vonwettstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86; DB 34; Length 1693;
Pred. No. 1.80e+01;
22; Mismatches 25; ThAble
                                                                                                                                                                                                                                                                                            Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam
                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                            Score 86; DB 1; L
Pred. No. 1.80e+01;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "not specified"
Misc_difference 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "not specified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W71209 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                          13.6%;
ilarity 25.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279823.
US-681078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-505888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1994; US-279823
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Borriss R, Hofemei
WPI; 90-275129/36.
N-PSDB; Q05832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yarbough PO;
WPI; 98-446186/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1989; U
13-OCT-1989; U
05-APR-1990; U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1988;
11-APR-1989;
                                                                                                                                                                                                                                                                                                                            14;
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Matches
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                                                  ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea (Laim 14: Pages 28-30; 50pp; English.

This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                 Amino acid sequence of lepidoteran-active HD573 toxin.
HD573 toxin; PCR; primer; amplification; Bacillus thuringlensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Heliocverpa zea; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 fisekygnggdslrfelsnttarytlrgngnsynlylrvssigsstirvtingrvytanv 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 YVQTPFLSESNSVRYKIS-IAGSCPLSTAGPSYVKF-QDNPVGSQTFSAGLHLRVFDPST 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
                                                  Gaps
                                                                                77 laltspsynkfdcgenrsvqtygyglyevrm-kpakntgivssfftytgptdgtp 130
                                                                                                      |: ::||| ||: : ||: || : || :|| || 36 LSTAGPSYVKFQ-DNPVGSQTFSAGLH-LRVFDPSTGALVDSKSYAFSTSNDTIS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...129
|Tabel=amino terminal of beta-amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybrid (1.3-1.4)-pre-beta-glucanase.
Hybrid pre-beta-glucanase; glucans; beer; animal feed; poultry.
Bacillus amyloliquefaciens, Bacillus macerans.
                                                  'n,
                Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87; DB 35; Length 623;
Pred. No. 1.51e+01;
26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133..236
/label=carboxyl-terminal of B.macerans
                                                  18;
            Score 87; DB 19; I
Pred. No. 1.51e+01;
19; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                     17-SEP-1998.
13-MAR-1997, US-040512.
13-MAR-1997, US-040512.
(MYCO ) WYCOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
WPI; 98-506734/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                   W75773 standard; Protein; 623 AA.
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(DEAK ) AKAD WISSENSCHAFT DDR.
          13.7%; S
larity 27.3%; P
Conservative 1
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Best Local Similarity 18.2%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1990; DK0044.
16-FEB-1989; DD-325800.
04-AUG-1989; DK-003848.
                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis. WO9840490-A1.
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 ntttnn 567
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                Query Match
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                                Best Loc
Matches
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572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 frtsfvdgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86; DB 19; Length 1693;
Pred. No. 1.80e+01;
22; Mismatches 25; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection Disclosure, Pages 9-13; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the protein prod. of ORF-1 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The
            protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. Daculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-077-1994 (first entry)
HEV strain protein encoded by ORF-1.
Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; antibody; detection; diagnosis; primates; stool suspension.
                                                                                                                                                                                                                                                     /note= "corresponding codon CAG"
misc_difference 1455..1693
/note= "10 bp nucleic acid sequence TGGTNTTYGA
has to be inserted between nucleotides
4390..4391 of T27394 before these amino
acid residues can be decoded"
                                                                                                                       R91813 standard; Protein; 1693 AA.
R91813;
26-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 ORF-1.
Hepatitis E virus, HEV: SAR-55 strain; enteric transmission; structural region; antigen; detection; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                    03-0CT-1994; US-316765.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Purcell RH, Tsarev SA;
WPI: 96-209320/21.
N-PSDB; T27394.
                                                                                                                                                                                                                            Location/Qualifiers
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Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                      immunisation; infection. Hepatitis E virus.
                                                                                                                                                                                                                                        misc_difference 1238
                                                                                                                                                                                                                                                                                                                                                          03-OCT-1995; U13102
                                                632 fapgvsp 638
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                                                                        65 FDPSTGA 71
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New hepatitis is virus DNA from Pakistani strain SAR-55 - used for, hepatitis E virus DNA from dagnosis of, and vaccination against hepatitis E virus infection
Disclosure; Pages 11-15; 204pp; English.

This represents a hepatitis E virus (HEV) open reading frame (ORF)-1 protein encoded by a DNA sequence designated SAR-55. SAR-55 also encodes HEV ORF-2 and ORF-3 proteins. A host organism transformed or transfected with a recombinant expression vector containing the SAR-55 uncleic acid with a recombinant expression vector containing the SAR-55 nucleic acid recombinant HEV proteins can be used to produce the HEV proteins, especially ORF-2 protein. The recombinant HEV proteins can be used as diagnostic agents and as vaccines for use against HEV infection. The detection of antibodies specific for use against HEV infection. The detection of antibodies specific for use against HEV ladagnosis of infection and diseases caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                                     for use in detection, diagnosis, vaccines and therapy of hepatitis E virus infection bisclosure; Page 57-62; 114pp; English.
The sequences given in R51264-66 are encoded by the hepatitis E virus frames (ORFS). These proteins can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV. The proteins can be used for detection and diagnosis of HEV infection. The HEV sak-55 cDNA was isolated from primates innoculated with stool suspensions obtained from hepatitis E patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 frtsfvdgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
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Hepatitis E virus (HEV) ORF-1 protein.
Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            Purified hepatitis E strain SAR-55 virus - used to develop prods.
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κ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-1997; US-840316.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Purcell RH, Robinson RA, Tsarev SA;
WPI: 98-568733/48.
N-PSDB; V71604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       passive immunisation; open reading frame; ORF
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Misc_difference 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "encoded by GGC"
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                                                                                                                                  18-SEP-1992; US-947263.
(USSH ) US SEC DEPT HEALTH.
Emerson SU, Purcell RH, Tsarev SA;
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W81519 standard; Protein; 1693 AA.
Hepatitis E virus strain SAR-55.
W09406913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 25.4%;
Matches 17; Conservative
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                                                             31-MAR-1994.
17-SEP-1993; U08849.
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09-APR-1998; U07418.
                                                                                                                                                                                                                            WPI; 94-118462/14.
N-PSDB; Q45197.
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PCT-US99-13024-2-06.rag

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02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD525 toxin.
HD525 toxin; PCR; primer; amplification; Bacillus thuringiensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R14618 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEPT HEALTH & HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.2%;
llarity 26.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1991; U02368.
05-APR-1990; US-505888.
(GENE-) GENELABS INC.
(USSH ) US DEPT HEALTH &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See Q14410 for ET1.1).
Sequence 1693 AA;
                                                                                                                                         Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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WPI; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R14618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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    methods are
during the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production the virus proteins - useful for diagnosis or vaccine production the virus claim 2: Columns 57-66; 47pp; English.

Claim 22: Columns 57-66; 47pp; English.

Wall96-98 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORFI sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 frtsfydgayletngperhnlsfdasqstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                572 frtsfydgayletngperhnlsfdasgstmaagpfsltyaasaagleyryyaagldhray 631
                                                                                                                                                                                                                                                                       HEV, and for monitoring the progression of such disease. Such method also useful for monitoring the efficacy of therapeutic agents during course of treatment of HEV infection and disease in a mammal. The antibodies can be used for detection or for passive immunisation of
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1998 (first entry)
Protein encoded by ORFI of ET-NANB (HEV) Burma strain DNA sequence.
Enterically transmitted non A non B hepatitis virus; ET-NANB;
Hepatitis E virus; HEV; Burma HEV isolate; vaccine;
                                                                                                                                                                                                         ä
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                                                                                                                                                           Length 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86; DB 36; Length 169
Pred. No. 1.80e+01;
22; Mismatches 25; Indels
                                                                                                                                                                             Pred. No. 1.80e+01;
22; Mismatches 25; Indels
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20-0CT-1998.
07-JUN-1998; 475807.
25-JUL-1994; US-279823.
17-JUN-1988; US-278997.
11-APR-1989; US-376742.
13-OCT-1989; US-420921.
05-JUL-1990; US-505888.
07-JUL-1990; US-505888.
07-JUL-1990; US-505888.
07-JUL-1990; US-505888.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam
                                                                                                                                                         DB 37;
                                                                                                                                                         Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W80196 standard; Protein; 1693 AA.
W80196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
ID W75774 standard; Protein; 633 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non A non B Hepatitis virus US5824649-A.
                                                                                                                                                       h
Similarity 25.4%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%;
Similarity 25.4%;
17; Conservative
                                                                                                                1693 AA;
                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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WPI; 98-582599/49.
                                                                                                                                                                                                                                                                                                                                  632 fapgvsp 638
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                                                                                                                                                                                                                                                                                                                                                                           65 FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDPSTGA 71
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                                                                                                                  Sequence
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                                                                                                                                                           Query Match
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                                                                                           татта 1 s.
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11-SEP-11998 105081.

13-MAR-1997; US-040512.

R 13-MAR-1997; US-040512.

A (MYCO) MYCOGEN CORP.

Muller-Cohn J, Narva KE, Schnepf HE;

Muller-Cohn J, Narva KE, Schnepf HE;

Muller-Cohn J, Narva KE, Schnepf HE;

New insecticidal Bacillus thuringlensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis.

PT Glaim 14; Pages 32-34; Sopp. English.

Tellothis virescens and Helicoverpa zea

Tellothis virescens and Helicoverpa zea

Tellothis virescens and Helicoverpa zea

This is the amino acid sequence of a novel Bacillus thuringlensis toxin used in the method of the invention, to control lepidopteran pests.

The new toxins are useful as pesticides, especially for the control of ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The colynuclectide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of for novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 fisekfgngsdslrfegsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by ORF 1 of Burmese ET-NANB viral strain.
enterically transmitted non-A, non-B hepatitis virus; hepatitis C;
HCV; E.coli strain BB4; ATCC deposit number 67717; Burma.
Enterically transmitted non-A, non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New viral proteins from non A-non-B hepatitis agent - used to treat and prevent enterically-transmitted non-A non-B hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 35; Length 633
Pred. No. 2.14e+01;
20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84; DB 3; L4
Pred. No. 2.55e+01;
20; Mismatches 24;
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Example 5; Fig 12; 149pp; English.

Example 5; Fig 22; 149pp; English.

This sequence is encoded by the Arabidopsis thaliana ethylene response (ETR) gene, designated OITR. The ETR gene is used in the antisense expression construct of the invention, which also contains a promoter. Expression of the construct in a plant cell results in a decreased response to ethylene by the cell. The constructs are useful for the production of plants which have a decrease in physiological responses to the presence of ethylene. Ethylene is a plant hormone which is involved in various positive plant controls e.g. growth, development and fruit ripening, and is also induced by environmental stresses wounding, pathogenic infection and flooding. Controllable, inducible expression of ethylene antisense constructs in transformed plant cells allows and vegetables.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A thaliana ethylene response protein QITR.

We Ethylene response gene: ETR: plant hormone; plant growth modulation; plant development control: fruit ripening.

Arabidopsis thaliana.

BY SE824868-A.

CO-OCT-1998.

CO-OCT-1998.

CO-JUN-1995; US-484101.

CO-JUN-1995; US-484101.

CO-JUN-1995; US-484101.

CO-JUN-1995; US-484101.

CALY O-JUN-1995; US-8655.

RO-JUN-1994: US-2634865.

RO-JUN-1994: US-263486.

CALY O-ALIFORNIA INST OF TECHNOLOGY.

RESPONSE TAB, Chang C, Meyerowitz EM;

RMPI: 98-582650/49.

N-PSDB: V59038, V59039.

Thissense constructs containing ethylene response nucleic acids response of call of transforming plant cells, to produce plants, which have decreased response in the presence of ethylene, for control of growth and development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 inlplinelfnsag-amhiphscplakigppvgrysppevvsvrvpl-lhlsnfggsdws 266
572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 3.04e+01;
17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                       JT 15
W73122 standard; Protein; 613 AA.
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Best Local Similarity 31.4%;
Matches 22; Conservative
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Search completed: Wed Sep 1 16:17:50 1999 Job time: 35 secs.

267 dl-sgkgyai 275 | :|:||: 71 ALVDSKSYAF 80

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                                                                                                                                                                                                          RI ORF.
DUGESIELLA SP.
EUKARYOTA; METAZOA; ARTHROPODA; CHELLCERATA; ARACHNIDA; ARANEAE;
MYGALOMORPHAE; THERAPHOSIDAE; DUGESIELLA.
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        Score 44; DB 2; Length 461;
Pred. No. 2.09e+01;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 64.7%; Score 44; DB 5; Length 488; Best Local Similarity 58.3%; Pred. No. 2.09e+01; Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P87306 PRELIMINARY; PRT; 545 AA.
P87306; Ol-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
HYPOTHETICAL 62.5 KD PROTEIN C31F10.04C IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 64.7%; Score 44; DB 3; Length 545; Best Local Similarity 54.5%; Pred. No. 2.09e+01; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
BURKE W.D., MALIK H.S., EICKBUSH T.H.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF015813; G2736044;
ENA-DIRECTED DNA POLYMERASE.
                                                                                                                                                      01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
REVERSE TRANSCRIPTASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-972:
WOOD V., RAJANDREAM M.A., BARRELL B.G., POHL T.;
WOOD TO, RAJANDREAM M.A., BARRELL B.G., POHL T.;
EMBL, 297204; E325252;
HYPOTHETICAL PROTEIN.
SEQUENCE 545 AA; 62479 MW; 2F16D503 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPBC31F10.04C.
SCH1ZOSACCHAROMYCES POWBE (FISSION YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA: ARCHIASCOMYCETES;
SCH1ZOSACCHAROMYCETALES: SCH1ZOSACCHAROMYCETACEAE;
SCH1ZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                         NON TER 1 1 2 SEQUENCE 488 AA; 55092 MW; FA67B24C CRC32;
                                                                                                                                           488 AA.
                                                                                                                                       PRT;
Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                   PRELIMINARY;
                                                   394 TTSADAVSSDFVG 406
                                                                 :|| |: |: ||:
81 STSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                   251 SKTSDGTGAAFV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 SNEDISTNFVT 374
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SEQUENCE_FROM N.A.
                                                                                                                    LT 14
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044317;
                                                                                                                    RESULT
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01-NOV-1996 (TREMBLELEL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLELEL. 03, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLELEL. 03, LAST ANNOTATION UPDATE)
POTASSIUM CHANNEL PROTEIN (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM CURRENT CLASS.
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JOHNSTON L., JOHNSTON J., LIGHTNING J., LLOYDER N., LATREILLE P., LIGHTNING J., LLOYDE C., MCMURRAR A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWINEEN S., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VANGHAN K., WATERSTON R., WALSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., P. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGING TO THE SHIV GENE SUBFAMILY, A HOMOLOGUE OF THE SHAKER GENE SHAL OF DROSOPHILA MELANOGASTER.
EMBL: M74898; G205041; -.
PFRAM: PF00520; 10n_trans; 1.
IONIC CHANNEL; TRANSMEMBRANE; 10N TRANSPORT; VOLTAGE-GATED CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB J, Pred. No. 2.09e+01; Street. No. 2.09e+01; Indels
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SIMILARITY).
SIMILARITY).
SIMILARITY).
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SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U40951; G1072232; -.
SEQUENCE 53 AA; 5833 MW; C4DA122E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MILLER N.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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$4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.7%;
Similarity 58.3%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                        NATURE 368:32-38(1994).
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78
78
110
136
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81 STSNDTTSAAFV 92
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MULTIGENE FAMILY
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TRANSMEM
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TRANSMEM
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Q00090
Q00090;
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BUKARYOTA; VIRIDIPLAMATAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE; 94237486.
BIBB M.J., SHERMAN D.H., OMURA S., HOPWOOD D.A.;
"Cloning, sequencing and deduced functions of a cluster of Streptomyces genes probably encoding biosynthesis of the polyketide antibiotic frenolicin.";
GENE 142:31-39(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREPTOMYCES ROSEOFULVUS.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
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BEVAN M., VANDENBOL M., JALLET C., PORTETELLE D., HOHEISEL
MEWES H.W., MAYER K., SCHUELLER C.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 371;
                                                                                                                                      Score 44; DB 11; Length 236 Pred. No. 2.09e+01; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
  SEGMENT S5 (BY SIMILARITY). SEGMENT S6 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
EU ARABIDOPSIS SEQUENCING PROJECT;
EUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL022223; E1283943;
HYPOTHETICAL PROTEIN.
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RECUENCE FROM N.A.
REEVES C.D., SOLIDAX C.L.;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF058302; G3170587; -.
SKOUENCE 461 AA: 49966 MW; 26EC2672 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 10;
Pred. No. 2.09e+01;
                                                                                      26261 MW; C4A458FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 AA; 40833 MW; 5BOF5AA1 CRC32;
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01-AUG-1998 (TREMBLREL. 07, LAST SEQ
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL 40.8 KD PROTEIN.
                                                                                                                                      64.7%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.7%;
38.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                   108 TNNEDVSGAFVT 119
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81 STSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                          82 TSNDTTSAAFVS 93
152 1
213 2
236 2
236 AA;
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Best Local Similarity
                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conser
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SEQUENCE
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065584
065584;
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068923
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026818;
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Q23582;
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MEDLINE; 94150718.
MEDLINE; 94150718.
MISCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MISCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THERRY MIEG J., THOMAS K., VAUDIN M., VAGGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., MILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 bb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAENORHABDITIS ELEGANS.
EUKARYOTA; META2OA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.17 8
012372
012372
01-372;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CHROMOSOME XII READING FRAME ORF YLL061W.
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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Pred. No. 1.24e+01;
1; Mismatches 3; Indels
                                                                                                                                                                                                 Score 46; DB 5; Length 268; Pred. No. 7.24e+00; 4; Mismatches 2; Indels
                                                     SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z70207; E1345607; -.
SEQUENCE 337 AA; 38483 MW; ABD004BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                            337 AA
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
09,
                                                                                                                                                                                                 Match 67.6%;
Local Similarity 53.8%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
F15A2.4 PROTEIN.
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                                                                                                                                                                                                                                                                                                            15 TINNNTIPNKFVS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 SKHNSTISATFV 328
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                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      Query Match
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SEQUENCE FROM N.A.
MEDLINE: 94150718.
WILSON R., ANDERSON K., BAYNES C., BERKS M.,
MISSON R., BUNSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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MEDILINE; 8169719.
MEDILINE; 8169719.
"REPARTY S.C., TSCHUDI C., KONIGSBERG W.H., RICHARDS F.F.;
"Reverse transcription of trypanosome variable antigen mRNAs infilated by a specific oligonucleotide primer.";
PRROC. NATL. ACAD. SCI. U.S.A. 80:1536-1540(1983).
EMBL; V01391; G10560;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 3; Length 583;
Pred. No. 1.24e+01;
5; Mismatches 1; Indels
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                                                                                                                                                                                                    SEQUENCE ....
STRUKALN-S288C.;
WINLIN-S288C.;
WINLIN-S288C.;
WINLIN-S286C.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 273166; E2457C3; --
EMBL; 247973; G642233; --
PFAM; PF00324; aa_permeases; 1.
PFAM; PF00324; aa_permeases; 1.
SROUENCE 583 AA; 64217 MW; BDES153C CRC32;
SEQUENCE FROM N.A.
WEDLER H., WEDLER E., SCHARFE M., WAMBUTT R.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                 SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO ADENOSINE A3 RECEPTOR. NCBI GI: 1072232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.09e+01;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 AA; 4068 MW; 551442D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
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01-NOV-1998 (TREMBLREL. 08, LA
SURFACE ANTIGEN (FRAGMENT).
TRYPANGSOMA BRUCEI BRUCET
                                                                                                                                                                                                                                                                                                                                                                                                                     66.2%;
50.0%;
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larity 63.6%;
Conservative
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81 STSNDTTSAAFV 92
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Best Local Similarity
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82 TSNDTTSAAFV 92
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DOMAIN
SEQUENCE
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Q94484
Q94484;
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                     009532;
01-NOV-1
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P87112
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Matches
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MEDLINE; 94150718.
HILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLER L., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAIREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WAPERSTON J.,
HIERRY MIEG J., THOMAS K., VAUDIN M., VAUGRAN K., WAPERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
P. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                            CAENORHABDITIS ELEGANS.
EUKARYOTA; META2OA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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                                                                                                                                                                                             Score 54; DB 4; Length 579;
Pred. No. 7.52e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 5; Length 241;
Pred. No. 4.20e+00;
1; Mismatches 1; Indels
SEQUENCE FROM N.A.

POWERS P.A., GREGG R.G., HOGAN K.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 1086953; G3155256; JOINED.
EMBL, 1086954; G2155256; JOINED.
EMBL, 1086955; G3155256; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WATERSTON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U3997; G1055122; -.
SEQUENCE 241 AA; 27445 MW; F0977197 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
CHISSOE S., WILSON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                (TREMBLREL. 01, LAST SEQUENCE UPDATE) (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                             774; Ca_channel_B; 1.
579 AA; 63705 MW; 651614EF CRC32;
                                                                                                                                                                                                                                                                                                                241 AA
                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                        U86956; G2155256; JOINED.
U86959; G2155256; JOINED.
U86960; G2155256; JOINED.
                                                                    U86961; G2155256; -. U86952; G2155256; JOINED.
                                                                                                                          U86957; G2155256; JOINED. U86958; G2155256; JOINED.
                                                                                                                                                                                                                                                                                                                                                                       SIMILAR TO GLUTAMATE RECEPTORS
                                                                                                                                                                                               79.4%;
larity 75.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.1%;
llarity 80.0%;
Conservative
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                                                                                                                                                  PF00018; SH3; 1.
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81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                            STSSDTTSNSFV 55
                                                                                                                                                                                                           Local Similarity
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SNDTTSAAFV 92
                                                                                                                                                               PF00774
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01-NOV-1998
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                Query Match
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Q20870
Q20870;
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                                                                    EMBL;
EMBL;
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PFAM;
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                                                                                                                                                               PFAM;
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RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-972;
BADCOCK K., CHUCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
BADCOCK K., CHUCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBARK/DDBJ DATA BANKS.
--- SUBMITTED (MAY-1997) TO EMBL/GENBARK/DDBJ DATA BANKS.
--- SUBCELLULAR IOCATION: NUCLEAR (POTENTIAL).
--- SIMILARITY: TO YEAST NOT1.
--- SIMILARITY: TO YEAST NOT1.
--- SIMILARITY: TO YEAST NOT1.
--- STATISTICAL PROTEIN; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION.
SEQUENCE 2100 AA: 237132 MM; 9A710DB4 CRC32;
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Pred. No. 4.20e+00;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 5; Length 982;
Pred. No. 4.20e+00;
1; Mismatches 1; Indels
                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 110.9 KD PROTEIN F07F6.6 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
CHISSOE S.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
ORF DG1007 (FRACHENT).
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    827 830 POLY-ARG.
982 AA; 110892 MW; B4285770 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P87112;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UF
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION
PUTATIVE FRANSCRIPTIONAL REGULATOR C20G8.06.
982 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2100 AA
                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: TO GLUTAMATE RECEPTOR
EMBL; U23486; G746452; -
WORMPEP; P707F6 6; CE01898.
PFAM; PF00060; lig_chan; l.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.1%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.1%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                 F07F6.6.
CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1601 SATNDETKAAFV 1612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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83 SNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GNDTISAAFV
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ID 099
AC 099
DT 011
DT 011
DE OF
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:31:44 1999; MasPar time 5.61 Seconds 126.558 Million cell updates/sec Run on:

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 Description: Perfect Score: Sequence: Title:

Tabular output not generated.

1 STSNDTTSAAFVS 13

PAM 150 Gap 11 Scoring table:

Post-processing:

179066 seqs, 54579741 residues

Searched:

Minimum Match 0% Listing first 45 summaries

sptremb19 Database:

1:Sp_archea 2:Sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 5:sp_hage 10:sp_lant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 21.936; Variance 22.856; scale 0.960 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	7.52e-02	7.52e-02	4.20e+00	4.20e+00	4.20e+00	7.24e+00	1.24e+01	1.24e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01	2.09e+01
		Description	CALCIUM CHANNEL BETA 1	L-TYPE CALCIUM CHANNEL	SIMILAR TO GLUTAMATE R	HYPOTHETICAL 110.9 KD	PUTATIVE TRANSCRIPTION	ORF DG1007 (FRAGMENT).	F15A2.4 PROTEIN.	CHROMOSOME XII READING	SURFACE ANTIGEN (FRAGM	SIMILAR TO ADENOSINE A	POTASSIUM CHANNEL PROT	HYPOTHETICAL 40.8 KD P	GLYCERALDEHYDE-3-PHOSP	REVERSE TRANSCRIPTASE	HYPOTHETICAL 62.5 KD P	SHAL 1 POTASSIUM CHANN	VOLTAGE-GATED K+ CHANN		KV4.3 POTASSIUM CHANNE	KV4.3 POTASSIUM CHANNE
SUMMARIES		TD.	088517	015331	020870	009532	P87112	094484	019474	912372	026818	023582	060000	065584	068923	044317	P87306	026040	063286	016992	P70622	060576
		BB	11	4	Ŋ	S	٣	'n	S	က	S	'n	1	10	7	2	m	ហ	11	ഗ	11	4
		Match Length DB	101	579	241	982	2100	268	337	583	37	53	236	371	461	488	545	575	611	623	636	989
	% Query	Match	79.4	79.4	69.1	69.1	69.1	9. 79	66.2	66.2	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7
		Score	54	54	47	47	47	46	45	45	44	44	44	44	44	44	44	44	44	44	44	44
	Result	No.	1	7	m	4	'n	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20

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2 09e+01 2 09e+01 2 09e+01 2 09e+01 2 09e+01 2 09e+01 3 51e+01 3 51e+01	RODENTIA; al cDNA Gaps 0;
SHAL-RELATED POTASSIUM KV4.3 FLAGELLIN (FRAGMENT). SIMILAR TO GTP-BINDING AGGLUTININ-LIKE ADHESI LAMININ ALPHA 2 CHAIN. CNDOD FOR BY C. ELEGAN HYPOTHETICAL 52.3 KD PHEROPHORIN III (FRAGMENT) PHEROPHORIN III (FRAGMENT) SIMILARITY TO A HOMEOB DPE. SODIUM-DEPENDENT TRANS SHALI. IMMEDIATE FOR BY C. ELEGAN DYSSIUM CRADOXIL-TER CODED FOR BY C. ELEGAN DYSSIUM CHANNEL PROTE BY C. ELEGAN IMMEDIATE FARLY PROTEIT UBIQUITIN CARBOXIL-TER CODED FOR BY C. ELEGAN DJ33ZK4.1 (HYPOTHETICAL HYPOTHETICAL 141.7 KD PROTEIN-TYROSINE PHOSP SSDNA BINDING PROTEIN.	TREY; PRT; 101 AA. UEL. 08, CREATED) UEL. 08, LAST SEQUENCE UPDATE) CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RO UE; MURINAE; MUS. IN H.P.T., WAHL M.A.; RATEd calcium channel beta 1 subunit, partial TO EMBL/GENBANK/DDBJ DATA BANKS. 1008; 11240 MW; 838619F3 CRC32; 11240 MW; 838619F3 CRC32; 79.44; Score 54; DB 11; Length 101; 75.04; Pred. No. 7.52e-02; ative 2; Mismatches 1; Indels 0; G
062897 006577 008385 008385 018286 013388 093022 095680 09579 09579 09579 097767 016749 016749 016749 016749 016749 017767 016749 017767 016749 017767 017767 017767 017767	% CREATED) 08, CREATED) 08, LAST SEQUENCE 08, LAST SEQUENCE 08, LAST SEQUENCE SUBUNIT (FRAGMENT) SEDENTA; VERTEBRATA; MURINAE; MUS. 1.P.T., WAHL M.A.; d calcium channel calcium channel EMBL/GENBANK/DDBJ 8; 40 MW; 838619F3 C 48; SCOTE 54; DB 0%; Pred. NO. 7.5 ve 2; Mismatch
64.7 636 11 64.7 655 14 64.7 655 14 64.7 665 21 64.7 1322 5 64.7 1322 5 63.2 110 3 63.2 2 20 63.2 2 488 10 63.2 552 2 63.2 553 2 63.2 543 5 63.2 649 11 63.2 649 14 63.2 1229 5 63.2 1229 6 63.2 2 550 11 63.2 1229 6 63.2 1229 11 63.2 1229 11 63.2 1229 11 63.2 1229 11 63.2 1229 11 63.2 1229 11	(TREMBLE (TREMBLE (TREMBLE (TREMBLE (TREMBLE NNEL BETA ; MURIDA ; MURIDA TISSUE- J. ASMUC oltage- ge; G32C 101 1
10000000000000000000000000000000000000	RESULT 1 1D 088517 AC 008517 DT 01-NOV-1998 (TREMBLRE DT 01-NOV-1998) CC CLICKORNATH; MCRIDAR NN A. SEQUENCE FROM N.A. STORMATH, MRIDAR NN A. STORMATH, TISSUE-RA HILDENBRAND J. ARMON RT SEQUENCE FROM N.A. SEQUENCE 1; SEQUENCE 101 AA: 15 CONSTREAM NN TER NON TER 101 1(SO SEQUENCE 101 AA: 17 BEST LOCAL SIMILATILY 7

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Search completed: Wed Sep 1 16:31:25 1999 Job time: 11 secs.
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STSNDTTSAAF 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE: 90269039.
CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R., HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A., PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovitus strain AD169."; CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).
                                                                                                                                                                        Gaps
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                                                                                                                                             Score 45; DB 1; Length 345; Pred. No. 5.97e+00; 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 416; Pred. No. 5.97e+00; 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          HUMAN CYTOMEGALOVIRUS (STRAÍN AD169).
VIRUSES: DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
BETAHERPESVIRINAE; CYTOMEGALOVIRUS.
                                           PROSITE; PS01266; ADENYLOSUCCIN_SYN_1; 1.
PROSITE; PS01218; ADENYLOSUCCIN_SYN_2; FALSE_NEG.
PFAM; PF00709; Adenylsucc_synt; 1.
HSSP; P12283; 1ADI.
                                                                                           OSYNTHESIS; LIGASE; GTP-BINDING.
18 24 GTP (POTENTIAL).
345 AA; 37820 MW; E15BE2C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 AA; 47416 MW; 8289EB89 CRC32;
                                                                                                                                                                                                                                                                                                     01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN IRL12 (TRL12).
                                                                                                                                                                                                                                                                      416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3066 AA
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           (REL. 15, CREATED)
                                                                                             PURINE BIOSYNTHESIS; LIGASE;
                                                                                                                                             Match 66.2%;
Local Similarity 50.0%;
tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.2%;
Similarity 50.0%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X17403; E298631; -. PIR; S09761; S09761. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                     EMBL; U67505; G1591267;
                                                                                                                                                                                             200 TSKDTTASSFAA 211
                                                                                                                                                                                                                     82 TSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 TSPNTASTTFVT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 TSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  IR12_HCMVA
P16810;
01-AUG-1990 (
                                    IIGR; MJ0561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 15
POLG_BCMVN
Q65399;
                                                                                                          NP_BIND
SEQUENCE
                                                                                                                                             Query Match
Best Local 5
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                                                                                                                                                                                                                                                                                                                                              GILBERTSON R.L.;
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA) (EC 3.4.22.-) (49 KD PROTEINASE) (49 KD-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP).

BEAN COMMON MOSAIC VIRUS (STRAIN NL-3 / MICHIGAN) (BCMV).
                                                                                                                                                                                                                                                                                                                                     EMBL; U19287; G1373002; --
PFAM; PF00271; helicase_C; 1.
PFAM; PF00560; RRA_dep_RNA_pol; 1.
PFAM; PF00767; Poty_coat; 1.
PFAM; PF00851; Peptidase_C6; 1.
PFAM; PF00863; Peptidase_C6; 1.
PFAM; PF00863; Peptidase_C6; 1.
AVDROASE; TRANSFERASE; THIOL PROTEASE; RNA-DIRECTED RNA POLYMERASE; COAT PROTEIN: POLYPEROTEIN; COVALENT PROTEIN-RNA LINKAGE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAY BE INVOLVED IN REPLICATION.
FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
PTM: UPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
INDIVIDUAL PROTEINS.
                                                                                                                                                              NON MOSAIC VIRUS (STRAIN NL-3 / MICHIGAN) (BCMV).
SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 3066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 KD PROTEIN 2.
GENOME-LINKED PROTEIN.
NUCLEAR INCLUSION PROTEIN A.
NUCLEAR INCLUSION PROTEIN B.
COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELPER COMPONENT PROTEINASE. PROTEIN P3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1258 1265 ATP (POTENTIAL).
3066 AA; 350387 MW; 67B875D6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-TERMINAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.97e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.2%;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                         VIRUSES; S:
POTYVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
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SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PURA_METJA
057981:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DANIELSON P.B., FOGLEMAN J.C.;
"Isolation and sequence analysis of cytochrome P450 12B1: the first
mitochondrial insect P450 with homology to 1 alpha,25 dlhydroxy-D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-hydroxylase.";
1NSECT BIOCHEM. MD. BIOL. 27:595-604(1997).
1- FUNCTION: PROBABLY INVOLVED IN STEROID HORMONES BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (PROBABLE).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                         DROSOPHILA ACANTHOPTERA (FRUIT FLY).
EUKARYOTA: METAZOA; ARTHROPODA: TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 119.3 KD PROTEIN IN PIP1-GLN3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (BY SIMILARITY).
CYTOCHRONE P630 12B1.
HEME (POTENTIAL).
53F97355 CRC32;
                                         Length 1036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 1; Length 532;
Pred. No. 3.44e+00;
2; Mismatches 0; Indels
                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U78485; G2674278; -.
FLYBASE: FBGN0022933; Daca\Cyp12b1.
PROSITE: PS00086: CYTOCHROME_P450; 1.
OXIDOREDUCTASE: MONOOXYGENASE: ELECTRON TRANSPORT; HEME;
MITOCHONDRION; TRANSIT PEPTIDE.
1036 AA; 109310 MW; CCDE5BE8 CRC32;
                                    Score 48; DB 1; L6
Pred. No. 1.11e+00;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                   15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CYTOCHROME P450 12B1 PRECURSOR (EC 1.14...).
                                                                                                                                                                                                                                                532 AA.
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llarity 53.8%;
Conservative
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77.8%;
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81 STSNDTTSAAFVS 93
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                                    Query Match
Best Local Similarity
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Best Local Similarity
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85 DTTSAAFVS 93
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CPP1_DROAC
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P40021;
SEQUENCE
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-1-FUNCTION: PLAYS AN IMPOS.
-1-CATACTIC ACTIVITY: GTP + IMP + L-ASPARTATE - GDP +
ORTHOPHOSPHATE + ADENVICOSUCCINATE.
-1-PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
-1-SIMILARITY: WITH OTHER ADENVICOSUCCINATE SYNTHETASES.
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STRAIN-S288C / AB972;

DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R., AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M., CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE.SMITH S., HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D., MOSEDALE D., NAKHARA K., NAMATH A., NORGERD R., OEFURR P., OH C., PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V., TAYLOR P., WEI Y., YELFON M., BOTSTEIN D., DAVIS R.W.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADENILOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE).
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ARCHAEA: EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Pred. No. 3.44e+00;
5; Mismatches 1.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
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Similarity 50.0%;
6; Conservative
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SCIENCE 273:1058-1073(1996)
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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HSSP; P00736; 1APQ.
G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE; RECEPTOR; GLYCOPROTEIN;
                                                                                                                                                                                                               CELL SURFACE GLYCOPROTEIN EMRI EXTRACELLULAR (POTENTIAL).
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EGF-LIKE 2. CALCIUM-BINDING (F
EGF-LIKE 4. CALCIUM-BINDING (F
EGF-LIKE 5. CALCIUM-BINDING (F
EGF-LIKE 6. CALCIUM-BINDING (F
EGF-LIKE 7. CALCIUM-BIN
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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                                                                              MIM; 600493; --
PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS0010; ASX_HYDROXI; 6.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 5.
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SIGNAL 1 17; PC
CHAIN 18 886 CD
DOMAIN 18 599 ED
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                                                                    EMBL; X81479; G784994; -.
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MEDLINE; 91186820.
FU Y.-H., MARZUUF G.A.;
FU Y.-H., MARZUUF G.A.;

"Site-directed mutagenesis of the 'zinc finger' DNA-binding domain of the nitrogen-regulatory protein NIT2 of Neurospora.";
MOL. MICROBIOL. 4:1847-185(1990).
-!- FUNCTION: MAJOR NITROGEN REGULATORY PROTEIN. DURING CONDITIONS OF NITROGEN LIMITATION IT TURNS ON THE EXPRESSION OF GENES FOR ENZYMES WHICH ARE REQUIRED FOR THE USE OF A VARIETY OF SECONDARY NITROGEN SOURCES, INCLUDING NITRATES, PURINES, AMINO ACIDS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-74-0R23-1A;
MEDLINE; 90158568.
FU Y.-H., MARZLUF G.A.;
Init-2, the major nitrogen regulatory gene of Neurospora crassa, encodes a protein with a putative zinc finger DNA-binding domain.";
MOL. CELL. BIOL. 10:1056-1065(1990).
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: NUCLEAR.
-1- INDUCTION: BY LACK OF A PRIMARY NITROGEN SOURCE.
-1- SIMILARITY: HIGH TO OTHER FUNGAL NITROGEN REGULATORY PROTEINS.
-1- SIMILARITY: TO GATA TRANSCRIPTION FACTORS IN THE ZINC-FINGER REGION.
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TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; ZINC-FINGER;
NUCLEAR PROTEIN; NITRATE ASSIMILATION; REPEAT.
TOWATH 49 110 3 X APPROXIMATE REPEATS.
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Score 48; DB 1; Length 886;
Pred. No. 1.11e+00;
2; Mismatches 3; Indels
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NA->DV: ABOLISH DNA-BINDING.
GL->DV: ABOLISH DNA-BINDING.
KR->NS: ABOLISH DNA-BINDING.
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CTNC->STNG: ABOLISH
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NITROGEN CATABOLIC ENZYME REGULATORY PROTEIN.
                                                                                                                                                                                                                                                             PRT; 1036 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A34755; A34755.
PROSITE; PSO0344; GATA_ZN_FINGER; 1.
PFAM; PF00320; GATA; 1.
HSSP; PI7429; 5GAT.
Query Match 70.6%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                             STANDARD;
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81 STSNDTTSAAFVS 93
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P19212;
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PCT-US99-13024-2-12.rsp

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                                                                                                            SALMONELLA TYPHIMURIUM.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 14028;
MEDLINE; 9538281.
BAUEMLER A.J., HEFFRON F.;
Identification and sequence analysis of lpfaBCDE, a putative fimbrial operon of Salmonella typhimurium.";
J. BACTERIOL. 177:2087-2097(1995).
-- SIMILARITY: BELONGS TO THE FIMH / LPFD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1; L
Pred. No. 1.11e+00;
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LPFD PROTEIN.
20D529B5 CRC32;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
12-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
LPFD PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U18559; G829374; -. STYGENE; SG10560; LPFD. PFAM; PF00419; Fimbrial; 1. FIMBRIA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN 25 SEQUENCE 355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 TSKNTTGATFV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 TSNDITSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                              SALMONELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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MNQASGLDLLKISYGKGARRKNRFKGSDGSTSSDTTSNSFV
                                                                                                                                                                                                                                                                                                                                                                          MEDINE, 27192022.
HULLIN R., SINGER-LAHAT D., FREICHEL M., BIEL M., DASCAL N.,
HOFMANN F., FLOCKERZI V.;
"Calcium channel beta subunit heterogeneity: functional expression of
cloned cDNA from heart, aorta and brain.";
EMBO J. 11:885-890(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X64298; G1500; -.
EMBL; X64299; G1498; -.
EMBL; X64299; G1502; -.
EMBL; X64299; G1502; -.
PROSITE: P550002; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00774; Ca_channel_B; 1.
DIONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; SH3 DOMAIN; MULTIGENE FAMILY;
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THIS PROTEIN IS A SUBUNIT OF THE DIHYDROPYRIDINE (DHP)
SENSITIVE CALCIUM CHANNEL.
-!- SUBUNIT: THE L-IYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA.
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, AORTA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- ALTERNATIVE PRODUCTS: THREE FORMS OF THE BETA-2 SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE: CAB2A, CAB2B (SHOWN HERE) AND CAB2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-2 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQ -> MLDRHLAAPHTQGLVLE (IN CABZA).
MISSING (IN CAB2C).
MPFFKK -> KQKQKS (IN CAB2C).
DF97DA5D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                          ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 1; Length 632;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HERE) AND CREAC.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER CALCTUM CHANNEL BETA SUBUNITS.
                                                                  632 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70943 MW;
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                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
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81 STSNDTTSAAFV 92
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632 AA;
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                              CACNB2 OR CACNLB2
                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEART
                                                             CCB2_RABIT
P54288;
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VARSPLIC
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VARSPLIC
SEQUENCE
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Gaps

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Length 355; 0; Indels

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WARDLINE; 95124926.

BAUD V., CHISSOE S.L., VIEGAS-PEQUIGNOT E., DIRIONG S., N'GUYEN V.C.,
AROE B.A., LIPINSKI M.;
AROE B.A., LIPINSKI M.;
TEMRI, an unusual member in the family of hormone receptors with
Seven transmembrane segments.";
GENOMICS 26:334-344(1955).

- FUNCTION: PROBBLY INVOLVED IN CELLULAR RESPONSE TO A HORMONE OR
AN INTERACTION WITH A PROTEIN LIGAND.
- FUNCTION: PROBBLY INVOLVED IN LIGAND.
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- ISSUE SPECIFICITY: WIDE EXPRESSION: INCREASED LEVELS IN
PERIPHERAL BLOOD MONOUNCLEAR CELLS.
- PRIN: N- AND O-GLYCOSYLATED; (POSSIBLE).
- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
EWR1_HUMAN STANDARD: PRT; 886 AA.
014246;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CELL SURFACE GLYCOPROTEIN EMRI PRECURSOR (EMRI HORMONE RECEPTOR).
                                                                                                                                                             HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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355 AA

PRT;

STANDARD;

LT 8 LPFD_SALTY P43663;

RESULT ID LP AC P4

Matches

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CONFLICT
CONFLICT
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SEQUENCE
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                                                                                              Matches
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                                                                                                                                                                                                                      POWERS P.A., LIU S., HOGAN K., GREGG R.G.;
"Skeletal muscle and brain isoforms of a beta-subunit of human
voltage-dependent calcium channels are encoded by a single gene.";
J. BIOL. CHEM. 267:22967-22972(1992).
                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CHANNEL BETA-1-B2 SUBUNIT
(BETA-1 ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TS -> SG (IN REF. 2).
G -> R (IN REF. 2).
G -> R (IN REF. 2).
KL -> TV (IN REF. 2).
T -> S (IN REF. 2).
T -> S (IN REF. 2).
T -> S (IN REF. 2).
SNTR -> LQHT (IN REF. 2).
I -> L (IN REF. 2).
I -> L (IN REF. 2).
A -> R (IN REF. 2).
A -> R (IN REF. 2).
B -> D (IN REF. 2).
C -> D (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M92303; G179806; -. EMBL; L06110; G187015; -. PIR; C44461; C44461. MIM; 114207; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50002; SH3; 1.
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                                                                                          SEQUENCE FROM N.A.
TISSUE-HIPPOCAMPUS;
MEDLINE; 93054616.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                           CACNB1 OR CACNLB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEART
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PROSITE; PSSO002; SH3; 1.
PRAM; PF00018; SH3; 1.
PFAM; PF00074; Ca_channel_B; 1.
IONIC CHANNEL; LON TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRAGNELL M., SAKAMOTO J., JAY S.D., CAMPBELL K.P.; "Cloning and tissue-specific expression of the brain calcium channel
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
115-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CHANNEL BETA-1-B2 SUBUNIT (BETA-1 ISOFORM A).
CACNB1 OR CANLLB1.
RATTUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                  Score 54; DB 1; Length 596; Pred. No. 3.03e-02; . 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
L -> M (IN REF. 2).
WP -> CA (IN REF. 2).
R -> Q (IN REF. 2).
OCC447D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 1; Le
Pred. No. 3.03e-02;
2; Mismatches 1;
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23B08C47 CRC32;
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557 557 L
571 572 WP
591 591 R
596 AA; 65638 MW;
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425 425 P
597 AA; 65679 MW;
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llarity 75.0%;
Conservative
                                                                                                    Query Match
Best Local Similarity 75.0%;
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
189
425
                                                                                                                                                                                   44 STSSDITSNSFV 55
                                                                                                                                                                                                                         81 STSNDTTSAAFV 92
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Best Local Similarity
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MEDLINE; 92038046
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6
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CCBA_RAT
P54283;
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SENSITION CALCIUM CHANNEL OF THE DIHYDROPYRIDINE (DHP)
SENSITIVE CALCIUM CHANNEL (BY SIMILARITY).
--- SUBUNIT THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS
ALPHA-1, ALPHA-2, BETA AND GAMA.
--- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.
--- ALTERNATIVE PRODUCTS: THREE FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING OF THE GENE.
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
--- SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a Lambert-Eaton myasthenic syndrome antigen."; ANN. NEUROL. 33:113-120(1993).
                               01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DIMYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-2 SUBUNIT (LAMBERT-EATON MYASTHENIC SYNDROME ANTIGEN B) (MYSB).
CACNB2 OR CACNLA2 OR MYSB.
                                                                                                                                                          EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                               MEDLINE; 93263585.
ROSENFELD M.R., WONG E., DALMAU J., MANLEY G., POSNER J.B.,
SHER E., FURNEAUX H.M.;
567 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567 AA; 62087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 79.4%;
Local Similarity 75.0%;
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S60415; G300417; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50002; SH3; 1.
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
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81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A48895; A48895.
MIM; 600003; -.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-FETAL BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STSSDTTSNSFV
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                                                                                                                                           HOMO SAPIENS
   CCB2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
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   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCTION: THIS PROFIED IS A SUBUNIT OF THE DIHYDROPYRIDINE (DHP)
SENSITIVE CALCIUM CHANNEL.
-:- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
-:- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROFIEN ASSOCIATED WITH
THE CYTOPLASMIC ASPECT OF THE SARCOLEMMA.
-:- ALTERNATIVE PRODUCTS: THEE, TISSUE-SPECIFIC, FORMS OF THE BETA-1
SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00774; Ca_channel_B; 1.
IONI CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN: PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89368946.

RUTH P., ROEHRKASTEN A., BIEL M., BOSSE E., REGULLA S., MEYER H.E., FLOCKERZI V., HOFFMANN F.;

"Primary structure of the beta subunit of the DHP-sensitive calcium channel from skeletal muscle.";

SCIENCE 245:1115-1118(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                        01-FEB-1991 (REL. 17, CREATED)
1-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANORATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-IM SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                              ORYCTOLAGUS CUNICULUS (RABBIT).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 524;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> R (IN G598370).
8AAC8B67 CRC32;
                                                                                                                        524 AA
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                 LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
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ilarity 75.0%;
Conservative
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57825
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                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
189
                                                                                                                                                                                                                                                                                                                                                         TISSUE-SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470
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                  55
                                     |||:|||| :||
STSNDTTSAAFV 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
189
470
499
304
324 AA;
                                                                                                                                                                                                                                (BETA-1 ISOFORM C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                    STSSDTTSNSFV
                                                                                                                                                                                                                                               CACNB1 OR CACNLB1
                                                                                                      RESULT 3
ID CCBC_RABIT
AC P19517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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FOUR SUBUNITS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIDIDATGLDAEENIÍPANHRSPKPSANSYTSPHSKEKRMP
FFKK -> AKQKQKS (IN ALTERNATE FORM 2).
4559C166 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDIDATGLDAEENDIPANHRSPKPSANSVISPHSKEKRMP
FFKK -> GAKSADEQDQWKTAGLFWRFT (IN
                                                                                                                                                                                                                                                                                                         PFAM; PF00018; 243; 1.
PFAM; PF00718; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOITAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 1; Length 567;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATE FORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 29, CREATED)
(REL. 29, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCBA_HUMAN
QC2641;
01-JUN-1994 (
01-JUN-1994 (
15-JUL-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95555
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Matches

8

81

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RESULT

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                                                                                                                                                                                                                                     A MEDLINE; 9332845.

RA ILES D.E., SEGERS B., SENGERS R.C.A., MONSIEURS K., HEYTENS L.,

RA HALLSALL P.J., HOPKINS D.M., ELLIS F.R., HALL-CURRAN J.L.,

RA HALLSALL P.J., HOPKINS D.M., ELLIS F.R., HALL-CURRAN J.L.,

STEWART A.D., WIERINGA B.;

"Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT "Genetic mapping of the beta 1- and gamma-subunits of the human

RT CONTRACTION: THE SRELETAL MUSCLE DHP-SENSITIVE CA(2+)

CC CONTRACTION COUPLING. THE SKELETAL MUSCLE L-TYPE CALCIUM CHANNEL IS COMPOSED OF

FIVE SUBUNIT: ALPHA-1, ALPHA-2, BETA, GAMMA AND DELTA.

CC SUBUNIT ARE PRODUCES THREE, TISSUE-SPECIFIC, FORMS OF THE GENE.

CC -1 TISSUE SPECIFICITY: SKELETAL MUSCLE.

CC -1 ALTERNATIVE PRODUCTS: THREE, TISSUE-SPECIFIC, FORMS OF THE GENE.

CC -1 SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.

CC -1 SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                  COLLIN I., WANG J., NARGEOT J., SCHWARTZ A.; "Molecular cloning of three isoforms of the L-type voltage-dependent calcium channel beta subunit from normal human heart."; CIRC. RES. 72:1337-1344(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 1; Length 523;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QG -> R (IN REF. 2).
MISSING (IN REF. 4).
AA -> RR (IN REF. 1 AND 3).
32CBEE9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM: PF00018; SH3; 1
PFAM: PF00774; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING;
                                                                                                                                     SEQUENCE FROM N.A.
POWERS P.A., GREGG R.G., HOGAN K.:
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L06112, G187019; --
EMBL, U86960; G2155255; --
EMBL, U86950; G2155255; JOINED.
EMBL, U86954; G2155255; JOINED.
EMBL, U86954; G2155255; JOINED.
EMBL, U86955; G2155255; JOINED.
EMBL, U86959; G2155255; JOINED.
EMBL, U86959; G2155255; JOINED.
EMBL, U86959; G2155255; JOINED.
EMBL, U86959; G2155255; JOINED.
EMBL, 221725; G38563; --
EMBL, 221726; G38565; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩.
                                                                                                                                                                                                                            SEQUENCE OF 146-209 FROM N.A.
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larity 75.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z21726; G38565; -.
MIM; 114207; -
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57863
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189
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      MEDLINE; 93265672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MULTIGENE FAMILY.
DOMAIN 100
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470
28
183
479
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6
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CARBOHYD
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
-:- ALTERNATIVE PRODUCTS: THREE, TISSUE-SPECIFIC, FORMS OF THE BETA-1 SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE.
-:- SIMILARITY: CONTAINS 1 SH3 DOWAIN.
-:- SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM: PF0018; SH3; 1.

PFAM: PF0018; SH3; 1.

IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;

GLYCOPROTEIN: PHOSPORYLATION ALTERNATIVE SPLICING; SH3 DOMAIN;

MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUB-SKELETAL MUSCLE;
MEDLINE; 93054616.
POWERS P.A., LIU S., HOGAN K., GREGG R.G.);
Skeletal muscle and brain isoforms of a beta-subunit of human voltage-dependent calcium channels are encoded by a single gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCBC_HUMAN STANDARD; PRT; 523 AA.
CCBC_HUMAN STANDARD;
01-JUN-1994 (REL. 29, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITYE L-TYPE, CALCIUM CHANNEL BETA-IM SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
E -> G (IN REF. 2).
G -> R (IN REF. 3).
AA -> RR (IN REF. 3).
AA -> RR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 1; Length 478;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOL. CHEM. 267:22967-22972(1992).
                                                                                                                                                                                                                                                                                   EMBL, M92302; G179804; -.
EMBL, M75560; G179744; -.
EMBL, L06111; G187017; -.
EMBL, U86960; G2155254; -.
EMBL, U86952, G2155254; JOINED.
EMBL, U86954; G2155254; JOINED.
EMBL, U86955; G2155254; JOINED.
EMBL, U86955; G2155254; JOINED.
EMBL, U86955; G2155254; JOINED.
EMBL, U86955; G2155254; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U86958; G2155254; JOINED
EMBL, U86959; G2155254; JOINED
PIR; B44461. B44461.
MIM; 114207:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53006 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BETA-1 ISOFORM C) (BETA-1A)
CACNB1 OR CACNLB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 79.4%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
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STSNDTTSAAFV 92
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478 AA;
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CALCIUM CHANNEL; SH3 DOMAIN;

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Wed Sep 1 16:31:14 1999; MasPar time 2.98 Seconds 123.152 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

not generated. Tabular output

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 Description: Perfect Score: Sequence:

1 STSNDTTSAAFVS 13

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Post-processing:

summaries Listing first 45

swiss-prot37 Database:

1:swissprot

Mean 22.697; Variance 22.190; scale 1.023 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Pred. No.	3.03e-02	1.11e+00	1.11e+00	1.11e+00	3.44e+00	3.44e+00	5.97e+00	5.97e+00	5.97e+00	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.75e+01	1.75e+01	1.75e+01						
Description	DIHYDROPYRIDINE-SENSIT	LPFD PROTEIN PRECURSOR	CELL SURFACE GLYCOPROT	NITROGEN CATABOLIC ENZ	CYTOCHROME P450 12B1 P	HYPOTHETICAL 119.3 KD	ADENYLOSUCCINATE SYNTH	HYPOTHETICAL PROTEIN I	GENOME POLYPROTEIN [CO	VOLTAGE-GATED POTASSIU	PRE-MRNA SPLICING FACT	HYPERSENSITIVITY RESPO	LAMININ ALPHA-2 CHAIN	LAMININ ALPHA-2 CHAIN	DNA-DIRECTED RNA POLYM	METHYLENETETRAHYDROFOL	HYPOTHETICAL 38.2 KD P						
SUMMARIES ID	CCBB_HUMAN	CCBC_HUMAN	CCBC_RABIT	CCB2_HUMAN	CCBA_HUMAN	CCBA_RAT	CCB2_RABIT	LPFD_SALTY	EMR1_HUMAN	NIT2_NEUCR	CPP1_DROAC	YEM3_YEAST	PURA_METJA	IR12_HCMVA	POLG_BCMVN	CIKL_DROME	PR28_YEAST	HRA1_XANCV	LMA2_MOUSE	LMA2_HUMAN	RPC9_YEAST	FOLD_MYCPN	YEB7_YEAST
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Length	478	523	524	267	296	597	632	355	988	1036	532	1076	345	416	3066	490	588	607	3106	3110	142	269	337
% Query Match	79.4	79.4	79.4	79.4	79.4	79.4	79.4	70.6	70.6	70.6	9.19	9. 79	66.2	66.2	66.2	64.7	64.7	64.7	64.7	64.7	63.2	63.2	63.2
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ALIGNMENTS

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MEDLINE; 93265672.
COLLIN I., WANG J., NARGEOT J., SCHWARTZ A.;
Molecular cloning of three isoforms of the L-type voltage-dependent calcium channel beta subnit from normal human heart.";
CIRC. RES. 72:1337-1344(1993).
                      002640;
01-JUN-1994 (REL. 29, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-1-B1 SUBUNIT
(BETA-1 ISOPORM B) (BETA-2) (BETA-1C).
HOMO SAPIENS (HUMAN).
                                                                                                                                                       SECTENCE FROM N.A.
TISSUE-HIPPOCAMPUS;
MEDLINE; 93054616.
POWERS P.A., LIU S., HOGAN K., GREGG R.G.;
"Skeletal muscle and brain isoforms of a beta-subunit of human voltage-dependent calcium channels are encoded by a single gene.";
J. BIOL. CHEM. 267:22967-22972(1992).
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MEDILINE; 92110010.
WHILLIAMS M.E., FELDAN D.H., MCCUE A.F., BRENNER R.,
VELICELEBI G., ELLIS S.B., HARPOLD M.M.;
"Structure and functional expression of alpha 1, alpha 2, and
Subunits of a novel human neuronal calcium channel subtype.";
NEURON 8:71-84(1992).
                                                                                                         HOMO SAPIENS (HUMAN).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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               PRT;
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Search completed: Wed Sep 1 16:32:49 1999 Job time : 14 secs.

97 TSTNQTTSNSFV 108 :::|:||| :|| 81 STSNDTTSAAFV 92

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Baud, V.; Chissoe, S.L.; Viegas-Pequignot, E.; Diriong, S.;
N'Guyen, V.C.; Roe, B.A.; Lipinski, M.
Gonomics (1995) 26:334-344
EMRI, an unusual member in the family of hormone receptors
with seven transmembrane segments.
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*superfamily nitrogen regulatory protein nit-2; GATA-type
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#Journal Mol. Cell. Biol. (1990) 10:1056-1065
#title nit-2, the major nitrogen regulatory gene of Neurospora crassa, encodes a protein with a putative zinc finger DNA-binding domain.
#cross-references MuID:90158568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrogen regulatory protein nit-2 - Neurospora crassa
#formal_name Neurospora crassa
13-Jul-1990 #sequence_revision 26-Jul-1996 #text_change
16-Feb-1997
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#formal_name Saccharomyces cerevisiae
28-May-1993 #sequence_revision 24-Feb-1995 #text_change
21-Nov-1997
                                                                                                                                                                                                                            ##cross-references GDB:378349; OMIM:600493
##map_position 19p13.3-19p13.3
##map_position framsmembrane protein
SUMMARX
#length 886 #molecular-weight 97679 #checksum 2055
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#region zinc finger GATA motif
#length 1036 #molecular-weight 109295 #checksum 2
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##cross-references GB:X81479; NID:g784994
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##residues 1-1036 ##label FUY
##cross-references GB:M33956
                                                                                                                 preliminary
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserv
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Hullin, R.; Singer-Lahat, D.; Freichel, M.; Biel, M.; Dascal, N.; Hofmann, F.; Flockerzi, V.
EMBO J. (1992) 11:885-890
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J. Bacteriol. (1995) 177:2087-2097
Identification and sequence analysis of lpfABCDE, a putative
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calcium channel protein beta chain CaB2b - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
rabbit
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03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
09-Sep-1997
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##residues 1-632 ##label HUL
##cross-references EMBL:X64298; NID:91499; PID:91500
*# | #length 632 #molecular-weight 70943 #checksum 1583
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2; Mismatches 1; Indels
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Pred. No. 3.61e+00;
4; Mismatches 0; Indels
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Matches 9; Conservative
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##molecule_type mRNA
##residues 1-597 ##label RES
across-references MUID:93054616
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J. Biol. Chem. (1992) 267:22967-22972
Skeletal muscle and brain isoforms of a beta-subunit of human
voltage-dependent calcium channels are encoded by a single
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                                                                 DHP-sensitive
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Ann. Neurol. (1993) 33:113-120
Cloning and characterization of a Lambert-Eaton myasthenic
            Ruth, P.; Roehrkasten, A.; Biel, M.; Bosse, E.; Regulla, Meyer, H.E.; Flockerzi, V.; Hofmann, F. Science (1989) 245:1115-1118
Primary structure of the beta subunit of the DHP-sensitiv calcium channel from skeletal muscle.
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##experimental_source fetal brain
##note sequence extracted from NCBI backbone (NCBIN:132135,
NCBIP:132136)
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#length 524 #molecular-weight 57868 #checksum 8438
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##cross-references GB:M25817
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#journal FEBS Lett. (1991) 291:253-258
#title Cloning and tissue-specific expression of the brain calcium channel beta subunit.
#cross-references MUID:92038046
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#formal_name Rattus norvegicus #common_name Norway rat
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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L-type voltage-gated calcium channel B subunit - human
#formal_name Homo sapiens #common_name man
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##ROLecule_type mRNA
##molecule_type mRNA
##residues 1-597 ##label PRA
##cross-references GB:X61394; NID:955893; PID:955894
##cross-references GB:X61394; MD:955893; PID:955894
##length 597 #molecular-weight 65679 #checksum 8572
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Collin, T.; Wang, J.; Nargeot, J.; Schwartz, A.
Circ. Res. (1993) 72:1337-1344
Molecular cloning of three isoforms of the L-type
voltage-dependent calcium channel B subunit from
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*binding_site phosphate (Thr) (covalent) (by protein kinase C) *status predicted\
*binding_site carbohydrate (Asn) (covalent) *status predicted\
*binding_site phosphate (Thr) (covalent) *status predicted\
*binding_site phosphate (Thr) (covalent) (by cAMP-dependent kinase) *status predicted\
*length 478 *molecular-weight 52934 *checksum 6465
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Circ. Res. (1993) 72:1337-1344
Molecular cloning of three isoforms of the L-type
voltage-dependent calcium channel B subunit from normal
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L-type voltage-gated calcium channel B subunit - human
#formal_name Homo sapiens #common_name man
12-hug-1996 #sequence_revision 12-hug-1996 #text_change
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Pred. No. 1.44e-01;
2; Mismatches 1; Indels
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##residues 1-478 ##label WIL
##cross-references GB:M76560; NID:g179743; PID:g179744
##experimental_source hippocampus
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*accession 165766
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Powers, P.A.; Liu, S.; Hogan, K.; Gregg, R.G.
J. Ball. Chem. (1992) 267:22972
Skeletal muscle and brain isoforms of a beta-subunit of human voltage-dependent calcium channels are encoded by a single
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Circ. Res. (1993) 72:1337-1344
Molecular cloning of three isoforms of the L-type
Voltage-dependent calcium channel B subunit from normal
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calclum channel protein beta chain,
dinydropyridine-sensitive, skeletal muscle · rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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#formal_name Homo sapiens #common_name man
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
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B44461 #type complete voltage-dependent calcium channel beta subunit betalB1
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##residues 1-522 ##label RES
##cross-references GBL.06112; NID:9187018; PID:9187019
XY #length 522 #molecular-weight 57834 #check
                                                     #formal_name Homo sapiens #common_name man
10-Jun-1993 #sequence_revision 18-Nov-1994
20-Mar-1998
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Pred. No. 1.44e-01;
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Best Local Similarity 75.0%;
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ACCESSIONS

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:32:35 1999; MasPar time 4.57 Seconds 113.947 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 1 STSNDTISAAFVS 13 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 22.122; Variance 24.813; scale 0.892 Statistics:

Pred. No. is the number of results predicted by chance to have a score, greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01		1.44e-01	1.44e-01	3.61e+00	3.61e+00	3.61e+00	9.97e+00	1.64e+01	1.64e+01	1.64e+01	2.67e+01	2.67e+01	2.67e+01	2.67e+01	2.67e+01
		Description	voltage-dependent cal	L-type voltage-gated	calcium channel beta-	voltage-dependent cal	L-type voltage-gated	calcium channel prote	myasthenic syndrome a	voltage-dependent cal	calcium channel prote	L-type voltage-gated	calcium channel prote	long polar fimbrial o	probable hormone rece	nitrogen regulatory p	hypothetical protein	adenylosuccinate synt	hypothetical protein	probable membrane pro	variant surface qlyco	potassium channel pro	potassium channel pro	probable helicase (EC	
SUMMARIES		ID	A44461	165766	JH0566	B44461	165767	A41347	A48895	C44461	S18304	I52859	S21048	D56271	A57172	A34755	S50536	A64370	S09761	820929	A21112	157681	A35312	A39624	ММНОМН
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æ	Query	Match	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	9.02	9.02	70.6	9. 79	66.2	66.2	66.2	64.7	64.7	64.7	64.7	64.7
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	ALIGNMENTS #type complete pendent calcium channel beta subunit betalM isoform men Homo sapiens #common_name man sequence_revision 18-Nov-1994 #text_change 1997 1919 A.; Liu, S.; Hogan, K.; Gregg, R.G. then. (1992) 267:22967-22972 then. (1992) 267:22079 then. (1992) 267:22079 then. (1992) 267:22079 to the EMBL Data Library, Pebruary 1993 to the EMBL Data Library, Pebruary 1993 to the EMBL Data and gamma subunits of the L-type dependent calcium channel on chromosome 17q and mas candidate genes for malignant hyperthermia blitity. 83 #flabel ILE BL:221725, NID:938562; PID:938563 BL:221725, NID:938562; PID:938563	DB 2; Length 475; 1.44e-01; natches 1; Indels 0;
SS3868 SS5003 BS5003 BS5003 S73463 SS0472 SS0597 SS	ALIGNMENTY ALIGNMENTY human mal_name Homo sapien mal_name Homo sapien Sep-1997 61; S31919 fis, P.A.; Liu, S.; H fish rober (1992) 26 fish rober (1992) 27 fish rober (1992) 26 fish rober (α.Σ
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3106 110 11436 11436 1269 1269 1269 1269 1269 1269 111024 111024	A4461 *type c voltage-dependent - human *formal name Homo 10-Jun-1993 *seque 10-Sep-1997 A44461; S31919 A44461; S31919 A44461; Chem. (19 Powers, P.A.; Liu, J. Biol. Chem. (19 Seletal muscle an voltage-dependen roes MUD: 93054616 A44461 L-type nucleic acid preliminary preliminary preliminary preliminary preliminary L-type nucleic acid 1-475 *falabel 11475 *falabel 11475 *falabel 1185, D. E.; Segers S31919 Rall-Curran, J.; submitted to the E Genetic mapping of voltage-dependen exclusion as can susceptibilitity. S31919 Preliminary L-type DNA L-type DNA	92 92
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40000000000000000000000000000000000000	RESULT ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal #title #secession ##setaus ##molecule ##molecule ##mote ##molecule	Query M Best Lov Matches Db 44

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useful for recombinant production of the channel for screening of useful for recombinant production of the channel for screening of its modulators, and diagnosis of Lambert Eaton Syndrome Claim 3: Columns 219-224: 166pp. English.

The present scquence represents a splice variant of the beta subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The Na encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribt, each having slightly different properties. In addition, the cranscribt of the alpha I subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Disclosure: Page 163-165; 288pp; English.

To isolate DNA encoding the Beta I subunit, a human hippocampus cDNA library was screened by hybridisation to a DNA fragment encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate encoding in the overlapping clones until the overlapping clones until the overlapping clone such and sequenced. Five alternatively spliced forms of the
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11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME; N-PSDB; Q87839.
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
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01-DEC-1995 (first entry)
Human calcium channel subunit beta 1-3,
Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                              (SIBI-) SIBIA NEUROSCIENCES·INC.
Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
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Local Similarity 75.0%;
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                                                                                      04-APR-1988; US-176899.
04-APR-1989; US-603751.
04-APR-1989; WO-U01408.
20-FEB-1990; US-482384.
30-NOV-1990; US-52206.
31-AAY-1995; US-45543.
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81 STSNDTTSAAFV 92
                                                      31-MAY-1995; 455543.
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WPI; 98-456192/39.
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WO9504822-A.
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             beta 1.1, expressed in skeletal muscle, beta 1.2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-4, expressed in aorta tissue and HEX 293 cells, and beta 1-5, expressed in HEX 293 cells. Full-length DNA clones encoding the beta 1-2 and beta 1-3 subunits have been constructed. The subunits beta 1-1, beta 1-2, beta 1-4 and beta 1-5 have been identified by nucleic acid amplification; analysis as alternatively spliced forms of the beta subunit. Sequences of the beta 1 splice variants are set forth in Q87838/R72611, Q87839/R72612 and QQ87831-Q87833 and
beta 1 subunit have been identified. These forms are designated
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
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N'ESTA VALORIE DE L'ALTON CHANNEL BLOB SUB: UNIT PROTEIN -
USEUL FOR ACCOMDINANT PRODUCTION OF THE CHANNEL FOR SCREENING OF
USEUL FOR TECOMDINANT PRODUCTION OF THE CHANNEL FOR STATEMENT 
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
Beta-1 subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
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Human calcium channel beta subunit.
Beta subunit; human; calcium channel; assay; detection;
characterisation; Lambert Eaton Syndrome; LES; diagnosis.
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Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
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Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
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Local Similarity 75.0%;
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04-APR-1989; US-603751.
04-APR-1989; WO-U01408.
20-FEB-1990; US-482384.
33-NOV-1990; US-745206.
31-AAZ-1995; US-455543.
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04-APR-1994; US-223305.

04-APR-1989; US-603751.

04-APR-1989; WO-U01408.

20-FEB-1990; US-482384.

30-NOV-1990; US-482206.

15-AUG-1991; US-745206.
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04-APR-1994; US-223305.
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                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams ME
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                                                                                                                                                              11-AUG-1998
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Disclosure; Columns 125-130; 166pp; English.

The present sequence represents the beta subunit of a human calcium channel: Calcium channels are membrane-spanning, multi-subunit channel. Calcium channels are membrane-spanning, multi-subunit channel. Calcium channels are membrane-spanning, multi-subunit in proteins that allow controlled entry of calcium into cells.

This leads to depolarisation events required for muscle contraction. The recombiant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, glving more than one form of the protein from the same transcribed, glving more than one form of the protein from the sectivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a squence 530 AA;
                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for agonists and antagonists of calcium channels of calcium 2; page 11-13; 13pp; German.

A first oligonucleotide probe (046075) complementary to nucleotides 361-400 of the VDCC beta-subunit from rabbit skeletal muscle was used to screen a human hippocampus cDNA library. A 1.9kb cDNA fragment was isolated for further screening to isolate human vDcC neta-subunit coding sequences. Clone HBB3 was sequenced and nucleotides 1-1288 were found to have 92% homology to the rabbit beta-subunit; from position 1289 there is no detectable homology. The anino acid sequence R39565 was deduced from the open reading frame. See also Q46076 and Q46077.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channels - useful in calcium-flux studies and screening systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human neuronal beta-unit cDNA of voltage dependent calcium
                                                                                                                                                                                                                                                                                                                      DB 33; Length 530;
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W63144 standard; Protein; 598 AA.
W63144 standard; Protein; 598 AA.
W3144.
M2-1998 (first entry)
Human calcium channel beta subunit splice variant beta3.
Beta subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 8; Length 571; Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1994 (first entry)
Human neuronal VDCC beta-subunit encoded by clone HBB3.
Voltage-dependent calcium channel; VDCC; beta-subunit; calcium flux; ss.
                                                                                                                                                                                                                                                                                                                      Score 54; DB 33; I
Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r. 13
R39565 standard; Protein; 571 AA.
R39565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 19.4%; Local Similarity 75.0%; hes 9; Conservative
                                                                                                                                                                                                                                                                                                                  79.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER AG.
Spreyer P, Unterbeck A;
WPI; 93-265734/34.
N-PSDB; Q46078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1993,
06-JUL-1992; 222126.
17-FEB-1992; DE-204716.
06-JUL-1992; DE-222126.
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DE4222126-A.
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Disclosure; Page 129-131; 150pp; English.

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                                                                                                                                                                                                                                                                                                                            obtaining agonists and antagonists

Disclosure: Page 160-163; 285pp; English.

To isolate DNA encoding the Betel subunit, a human hippocampus

To isolate DNA encoding the Betel subunit, a human hippocampus

To isolate DNA encoding the Betel subunit, a human hippocampus

CDNA library was screened by hybridisation to a DNA fragment

encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate

overlapping clones until the overlapping clones encompassing DNA

encoding the entire human calcium channel beta 2 subunit were

solated and sequenced. Five alternatively spliced forms of the

beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the

CNS, beta 1-3, also expressed in the CNS, beta 1-4, expressed in

corta tissue and HEX 293 cells, and beta 1-3, expressed in HEX 293

cells. Full-length DNA clones encoding the beta 1-2 and beta 1-3,

subunits have been constructed. The subunits beta 1-2,

beta 1-4 and beta 1-5 have been identified by nucleic acid

amplification analysis as alternatively splice variants are set

forth in Q87838/R72611, Q87833/R72612 and QQ87831-Q87833 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding specific human calcium channel sub-units - used for identifying calcium channel agonists and antagonists and diagnosing Lambert Eaton syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human calcium channel subunit; diagnosis; agonist; antagonist;
Lambert Eaton syndrome.
                                                                                                                                                                            11-AUG-1994; U09230.
11-AUG-1993; US-105236.
05-NOV-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gllespie A, Harpold MM, Mccue AF, Williams ME;
N-PSDB; Q87838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 14; Length 478; Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-1993 (first entry)
Sequence of splice variant beta 1-2 of beta human calcium
channel subunit.
                                                                                                                                                                                                                                                                                                 DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for
                                                                          Human calcium channel suvunit beta 1.
Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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15-AUG-1991: US-745206.
10-APR-1992: US-868354.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Brenner R, Ellis SB, Feldman DH, Harpold MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                            R72611 standard; Protein; 478 AA.
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75.08;
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81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q37819
                                                                                                                               Homo sapiens
WO9504822-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
WO9304083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams ME;
                                            R72611;
01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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            RESULT
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To developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists.

To isolate DNA encoding the Beta I subunit, a human hippocampus companies are abbit skeletal muscle calcium channel beta subunit.

To isolate DNA encoding the Beta I subunit, a human hippocampus concoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate concoding the entire human calcium channel beta 2 subunit were concoding the entire human calcium channel beta 2 subunit were solated and sequenced. Five alternatively spliced forms of the isolated and sequenced. Five alternatively spliced forms of the beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the beta 1-5, expressed in HEK 293 cells, and beta 1-6, expressed in HEK 293 cells, and beta 1-7, expressed in HEK 293 cells. Full-length DNA clones encoding the beta 1-2 and beta 1-2, expressed in the cells. Full-length DNA clones encoding the beta 1-1, beta 1-2, expressed in militation analysis as alternatively spliced forms of the beta subunit. Sequences of the beta 1 splice variants are set forth in QNY88/RY2611, QNY831-QNY831-QNY833 and
Five alternatively spliced forms of the human calcium channel beta I subunit have been identified and DNA encoding a number of forms have been isolated. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta and HEK 293 cells, and beta 1-5, expressed in HEK 293 cells.
                                                                                                                                                                                                                        Gaps
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11-AdG-1994 UG-230.
11-AdG-1993; US-105556.
05-NOV-1993; US-149097.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
WPI; 95-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 14; Length 479; Pred. No. 1.78e+01;
                                                                                                                                                                             Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1995 (first entry)
Human calclum channel subunit beta 1-1.
Calclum channel subunit; antagonist; agonist; diagnosis;
Lambert Baton Syndrome.
                                                                                                                                                                        Score 54; DB 6; LA
Pred. No. 1.78e+01;
                                                                                                                                                                                                                        2; Mismatches
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12-OCT-1998 (first entry)
Human calcium channel beta-1 subunit.
                                                                                                                                                                                                                                                                                                                                                                      T 10
R72604 standard; Protein; 479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W63156 standard; Protein; 523 AA
                                                                                                                                                                        / Match 19.4%;
Local Similarity 75.0%;
nes 9; Conservative
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Similarity 75.0%;
9; Conservative
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Best Local Similarity
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WO9504822-A.
                                                                                                                                  Sequence
                                                                                                                                                                           Query Match
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be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha I subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified myasthenic antigenic polypeptide and its corresp. antibody - useful for diagnosing and treating proliferation of neoplastic cells in patient with Lambert-Eaton myasthenic syndrome Claim 5; Page 26-77; 48pp; English.

The sequence is that of myasthenic antigenic polypeptide (MAP) encoded by the cDNA clone p mysB. MAP can be used to detect antibodies associated with parameoplastic sensory neuronopathy such as Lambert-Eaton myasthenic syndrome (LEMS). These antibodies are used to determine if a patient with neurological symptoms has a tumour expressing MAP, to inhibit proliferation of neoplastic cells in LEMS.
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                               Myasthenic antigenic polypeptide.
MAP; antibody detection; LEMS; Lambert-Eaton myasthenic syndrome;
paraneoplastic sensory neuronopathy; p mys B; mysB; ss.
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                                                                                                             Length 219;
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                                                                                                                                             1; Indels
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Human neuronal VDCC beta-subunit encoded by clone HBB1.
Voltage-dependent calcium channel; VDCC; beta-subunit;
                                                                                                           Score 54; DB 33; 1
Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 8; Le
Pred. No. 1.78e+01;
2; Mismatches 1;
                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-1993; U00227.
10-JAN-1992; US-820312.
(SLOK ) SLOAN KETTERING INST CANCER.
                                                                                                                                                                                                                                                    T. 5
R39697 standard; Protein; 240 AA.
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R39563 standard; Protein; 478 AA.
                                                                                                          79.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.4%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
Spreyer P, Unterbeck A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1992; 222126.
17-FEB-1992; DE-204716.
06-JUL-1992; DE-222126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furneaux HM, Posner JB;
WPI; 93-243126/30.
N-PSDB; Q46673.
                                                                                                                                                                         44 stssdttsnsfv 55
                                                                                                                                                                                           |||:|||| :||
81 STSNDTTSAAFV 92
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                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spreyer P, Unterbe
WPI; 93-265734/34.
N-PSDB; Q46076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 STSNDTTSAAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium flux; ss
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9314098-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
DE4222126-A.
                                                                                                                                                                                                                                                                                                  19-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R39563;
09-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1993
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                         Matches
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Without vaccing human calcium channel alpha 1B sub:unit protein - useful for recombinant production of the channel for screening of useful for recombinant production of the channel for screening of its modifiators, and diagnosis of Lambert Eaton Syndrome Claim 3: Columns 217-220; 166pp; English.

The present sequence is encoded by a splice variant of the beta subunit of a human calcium channel. Calcium channels are membrane-spanning, an uniti-subunit proteins that allow controlled entry of calcium ions into calls. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same creativity of the alpha 1 subunit with IgG molecules from the serum of a midividual with Lambert Eaton Syndrome (LES) can be used as a minimal contraction.
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               Claim 2; Page 5-7; 13pp; German.
A first oligonucleootide probe (Q46075) complementary to nucleotides A first oligonucleootide probe (Q46075) complementary to nucleotides 151-400 of the VDCC beta-subunit from rabbit skeleta! muscle was used to screen a human hippocampus cDNA library. A 1.9kb cDNA fragment was isolated for further screening to isolate human VDCC beta-subunit coding sequences. Clone HBBI was sequenced and found to have 92% homology to the rabbit beta-subunit. The amino acid sequence R39563 was deduced from the open reading frame.
See also Q46077-Q46078.
                                                                                                                                                                                                                                                                                                                              Gaps
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    useful in calcium-flux studies and screening systems

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-~hes 1; Indels
                                                                                                                                                                                                                                                                                    Length 478;
                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human calcium channel beta subunit splice variant beta?
Beta subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SIBI-) SIBIA NEUROSCIENCES INC.
Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
                                                                                                                                                                                                                                                                                Score 54; DB 8; Le
Pred. No. 1.78e+01;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W63143 standard; Protein; 478 AA. W63143;
                                                                                                                                                                                                                                                                             Query Match 79.4%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic for the disease.
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04-APR-1994; US-223305.

04-APR-1989; US-603751.

04-APR-1989; WO-U01408.

04-APR-1989; WO-U01408.

20-FEB-1990; US-482384.

30-NOV-1990; US-620050.

15-AUG-1991; US-745206.
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81 STSNDTTSAAFV 92
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                                                                                                                                                                                                                                      478 AA;
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STSNDTTSAAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1998
                                                                                                                                                                                                                                        Sequence
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Williams ME;

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(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF,
    05-NOV-1993; US-149097
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 98-456192/39.
                                                                   WPI; 95-090900/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 stssdttsnsfv
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81 STSNDTTSAAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V42707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists.

To isolate DNA encoding the Beta I subunit, a human hippocampus to isolate DNA encoding the Beta I subunit, a human hippocampus conversing a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate encoding the entire human calcium channel beta subunit.

A hybridising clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were isolated and sequenced. Five alternatively spliced forms of the beta 1 subunit have been identified. These forms are designated beta 1 subunit have been identified. These forms are designated conta tissue and HEK 293 cells, and beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-1, expressed in the corta tissue and HEK 293 cells, and beta 1-5, expressed in the corta tissue and hex 293 cells, and beta 1-5, expressed in the corta tissue and beta 1-5 have been identified by nucleic acid maplification analysis as alternatively spliced forms of the beta subunit. Sequences of the beta 1 splice variants are set forth in Q87838/R72611, Q87833-Q88881-Q8888-R72611, Q87833-Q88883-R72612 and QQ88831-Q88883-R72612.
                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1995.
11-AdG-1994.
11-AdG-1993: US-105536.
05-NOV-1993: US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME;
WPI: 95-090900/12.
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
                                           Length 216;
                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                  R72605;
01-DEC-1995 (first entry)
Human calcium channel subunit beta 1-4.
Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human calcium channel subunit beta 1-5.
Calcium channel subunit; antagonist; agonist; dlagnosis;
                                           Score 54; DB 33; 1
Pred. No. 1.78e+01;
                                                                                         2; Mismatches
                                                                                                                                                                                                                                                    RESULT 2
ID R72605 standard; Protein; 216 AA.
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R72606 standard; Protein; 219 AA.
                                           79.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.4%;
Best Local Similarity 75.0%;
Matches 9; Conservative
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01-DEC-1995 (first entry)
                                                                                       9; Conservative
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                                                                                                                                     44 stssdttsnsfv 55
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81 STSNDTTSAAFV 92
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11-AUG-1993; US-1055
                                                                 Best Local Similarity
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA;
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WO9504822-A.
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
WO9504822-A.
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Sequence
                                           Query Match
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                                                                                         Matches
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Useful for recombinant calcium channel alpha IB sub:unit protein -
useful for recombinant production of the channel for screening of
its modulators, and diagnosis of Lambert Eaton Syndrome
Disclosure; Columns 227-230; 166pp; Eaton Syndrome
Disclosure; Columns 227-230; 166pp; Eaton Syndrome
The present sequence represents the beta-5 subunit of a human calcium
channel. Calcium channels are membrane-spanning, multi-subunit proteins
that allow controlled entry of calcium ions into cells. This leads
to depolarisation events required for muscle contraction. The recombinant
subunit, when expressed with nucleic acids encoding the comprise calcium
channel, can be used in assays for the detection and characterisation of
compounds that modulate the channel: The DNA encoding the subunits can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                   Disclosure: Page 258-259; English.

Disclosure: Page 258-259; English.

To isolate DNA encoding the Beta I subunit, a human hippocampus.

Con Albrary was screened by hybridisation to a DNA fragment encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate overlapping clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were sconding the entire human calcium channel beta 2 subunit were solated and sequenced. Five alternatively spliced forms of the tasolated and sequenced in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-4, expressed in the CNS, beta 1-7, expressed in the CNS, beta 1-1, and have been constructed. The subunits beta 1-1 and beta 1-5 have been identified by nucleic acid amplification analysis as alternatively spliced forms of the beta 1-2, chan beta 1-2, chan beta 1-2, chan beta 1-2, chan beta 1-3, ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human calcium channel beta-5 subunit.
Beta-5 subunit; human; calcium channel; assay; detection;
characterisation; Lambert Eaton Syndrome; LES; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.Aug-1998.
31.HAX-1995; 455543.
404-APR-1994; US-223305.
404-APR-1999; US-176899.
404-APR-1999; US-603751.
404-APR-1999; US-603751.
404-APR-1999; US-603751.
405-REB-1990; US-620250.
415-AUG-1991; US-742306.
405-AUG-1995; US-455543.
406-AUG-1995; US-455543.
406-AUG-1995; US-455543.
406-AUG-1995; US-455543.
406-AUG-1995; US-455543.
406-AUG-1995; US-455543.
406-AUG-1995; US-455643.
406-AUG-1996; US-455643.
406-AUG-1996; US-455643.
406-AUG-1996; US-45643.
406-AUG-1996; US-45643.
406-AUG-1998; US-45643.
406-
                          nseq
                                                                                        developing prods. for studying calcium channels, e.g. obtaining agonists and antagonists
DNA encoding human calcium channel sub-unit(s) developing prods. for studying calcium channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W63158 standard; Protein; 219 AA.
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Similarity 75.0%;
9; Conservative
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Thu Sep

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Wed Sep 1 16:33:07 1999; MasPar time 4.43 Seconds 62.340 Million cell updates/sec MPsrch_pp Run on:

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 Description: Perfect Score:

Tabular output not generated.

1 STSNDTTSAAFVS 13 Sequence: 170751 seqs, 21266608 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

| part1 | 2:part2 | 3:part3 | 4:part4 | 5:part5 | 6:part6 | 7:part1 | 1:part1 | 2:part9 | 10:part10 | 11:part11 | 12:part12 | 13:part13 | 4:part14 | 15:part15 | 16:part16 | 16:part16 | 16:part16 | 16:part16 | 16:part16 | 16:part20 | 2:part22 | 2:part23 | 24:part24 | 25:part25 | 26:part26 | 27:part27 | 28:part28 | 29:part29 | 30:part30 | 31:part31 | 32:part34 | 35:part35 | 36:part36 | 37:part37 | 38:part38 | 39:part39 | 39:part30 | 39:

Mean 15.573; Variance 46.313; scale 0.336 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Pred. No.		T./ge+OT	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.780+01	1.78e+01							
			Description		naman carciam channel	Human calcium channel		calcium	Myasthenic antigenic	Human neuronal VDCC b	Human calcium channel	Human calcium channel	Sequence of splice va	Human calcium channel	Human calcium channel	Human calcium channel	Human neuronal VDCC b	Human calcium channel	Human calcium channel	Sequence of splice va
201111111111111111111111111111111111111			10	w62157	10100	R72605	R72606	W63158	R39697	R39563	W63143	R72611	R33551	R72604	W63156	W63147	R39565	W63144	R72612	R33552
			DB		ו	14	14	33	æ	œ	33	14	9	14	33	33	œ	33	14	9
			Match Length DB	216	7	216	219	219	240	478	478	478	478	479	523	530	571	598	598	598
	æ	Query	Match	707		79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4
			Score		5	54	54	54	54	54	54	54	54	24	54	54	54	54	54	54
		Result	S S		1	7	3	4	2	9	7	80	σ	10	11	12	13	14	15	16

1.78e+01 2.29e+02 2.29e+02 2.29e+02 2.29e+02 2.29e+02 2.29e+02 2.39e+02 3.74e+02 3.74e+02 3.74e+02 3.74e+02 4.76e+02	.76e+0
Human neuronal calciu Human Kv potassium ch Human Kv potassium ch Human Kv potassium ch Human Kv potassium ch Merosin major subunit Merosin major subunit Merosin major subunit Bovine poly-inmunogio Gamma-1 heavy chain a Z. Japonica phosphoen Human 26s proteasome AFP-1 (Ala 2460 val). AFP-1 (Ala 2460 val). AFP-1 (Ala 2460 val). CEA-specific antibody CEA-specific antibody CEA-specific antibody GEM-specific antibody GEM-specific antibody GEM-specific antibody GEM-specific antibody GEM-specific antibody GAM-1 heavy chain a Achromobacter lyticus Achromobacter lyticus Achromobacter lyticus Sequence of antibody Protease	locase encoded by . lividans protease rystal protein CryE
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660 636 636 636 31 1130 1130 130 130 130 130 130 130 13	1 A C
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ALIGNMENTS

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The Public National National Part of the channel of the channel for screening of useful for recombinant production of the channel for screening of the useful for recombinant production of the channel for screening of the meditators, and diagnosis of Lambert Eaton Syndrome Disclosure; Columna 225-228; 166pp; English.

The present sequence represents the beta-4 subunit of a human calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcribt, each having slightly different properties. In addition, the reactivity of the alpha I subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.
                                       W63157;
12-OCT-1998 (first entry)
Human calcium channel beta-4 subunit.
Beta-4 subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                              11.AdC-1998.

3 13.AdC-1995; 455543.

3 04.APR-1995; US-223305.

4 04.APR-1989; US-176899.

5 04.APR-1989; US-101408.

5 04.APR-1999; US-62236.

7 20.FEB-1990; US-482384.

7 30.NOV-1991; US-745206.

8 31.AMR-1995; US-45543.

4 (SIBI-) SIBIA NEUROSCIENCES INC.

8 MILLIAMS ME;

8 WILLIAMS ME;
T 1
W63157 standard; Protein; 216 AA.
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PCT-US99-13024-2-11.rspt

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                                                                                                                                                                                                                                                                                              LT 14
070461 PRELIMINARY; PRT; 492 AA.
070461
010461
01-AUG-1998 (TREMBLREL. 07, CAFATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
NONCARBOXYLATE TRANSPORTER MCT3.
RATTUS NORPEGICUS (RAT)
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GALLUG GALLUS (CHICKEN).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA; AVES;
NEOGNATHAE: GALLIFORMES: PHASIANIDAE: PHASIANINAE; GALLUG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 492;
Score 50; DB 2; Length 371;
Pred. No. 9.22e+00;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.1%; Score 50; DB 13; Length 542
Best Local Similarity 61.5%; Pred. No. 9.22e+00;
Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 11; Length 492
Pred. No. 9.22e+00;
3; Mismatches 1; Indels
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PHILD N.J., YOON H.;
SUBMITIED (APPT) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AFRO0240; 629198807; -.
SEQUENCE 542 AA; 58085 MW; 836DA7B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINA;
PHILP N.J., YOON H.;
PHILP N.J., APON H.;
EMBLYED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF05928; G3170609; -.
SEQUENCE 492 AA; 51590 MW; 20F051CI CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
MONOCARBOXYLATE TRANSPORTER 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 AA.
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Best Local Similarity 61.5%;
Matches 8; Conservative
Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                    164 DDGTGNLIQSSSY 176
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66 DPSTGALVDSKSY 78
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67 PSTGALVDS-KSY 78
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013151
013151,
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AC 07
DT 01
DD 0
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Search completed: Wed Sep 1 16:29:45 1999 Job time: 21 secs.

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SEQUENCE FROM N.A.

STRAIN-MC58 / NRCC 4728, 406Y / NRCC 4030, AND M982B / NRCC 4725;

STRAIN-MC58 / NRCC 4728, 406Y / NRCC 4030, AND M982B / NRCC 4725;

STRAIN-MC58 / NRCC 4728, 406Y / NRCC 4030, AND M982B / NRCC 4725;

WARACHUK M. W.;

J. BIOL. CHEM. 271:28271-28276(1996).

-! FUNCTION: TRANSFERS SIALIC ACID FROM THE SUBSTRATE CMP-SIALIC ACID DONOR TO THE TERMINAL BETA-D-GLUCOSAMINE ON THE LICTO-N NEOTESTRAOSE BRANCH OF THE LIPOOLIGOSACCHARIDE.

-! CATALYTIC ACTIVITY: CMP-N-ACETYL-BETA-D-GLUCOSAMINE - CMP +

BETA-D-GALACTOSYL-1,4-ACETYL-BETA-D-GLUCOSAMINE - CMP +

ALPHA-N-ACETYLNEURAMINYL-2,3-BETA-D-GALACTOSYL-1,4-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEISSERIA MENINGITIDIS.
BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA
 BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP.
RHIZOBIACEAE; AGROBACTERIUM.
                                                                                MEDLINE; 96425889.
THBURRIUS A., DE LUCA N., HUSSAIN H., JOHNSTON A.W.B.;
"Expression of exoy gene, required for exopolysaccharide synthesis in Agrobacterium, is activated by the regulatory ros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BETA-GALACTOSIDE ÀLPHA-2,3-SIÀLYLTRANSFERASE) (ALPHA 2,3-ST)
(LIPOOLIGOSACCHARIDE SIALYLTRANSFERASE) (LST).
                                                                                                                                                                                                                                                                Score 50; DB 2; Length 262;
Pred. No. 9.22e+00;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 371 AA.
P72097
P72097; P72099; P72100; P72101;
D72007; P72099; P72100;
O1-JUN-1998 (TREMBLREL. 06, CREATED)
O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALVILTRANSFERASE (EC 2.4,99.-)
(BETA-GALACTOSIDE ALPHA-2,3-SIALVILTRANSFERASE) (ALPHA
                                                                                                                                                                                                                                  262 AA; 28124 MW; DF7A4568 CRC32;
                                                                                                                                                gene.";
MICROBIOLOGY 142:2621-2629(1996)
EMBL; X95394; E220383; --
PFAM; PF00202; aminotran_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- PATHWAY: GLYCOSYLATION.
EMBL: 060660, G1546004; -.
EMBL: 060661, G1546009; -.
EMBL: 060662, G1546009; -.
TRANSFERASE; GLYCOSYLTRANSFEI
VARIANT
                                                                                                                                                                                                                                                                 Query Match 58.1%;
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                 110 STGVLVPPKGY 120
                                                                                                                                                                                                                                                                                                                                                       242
273
371 AA;
                                                 SEQUENCE FROM N.A. STRAIN-T1305 LAC9;
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                                                                                                                                                                                                                TRANSFERASE
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SEQUENCE
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015308
015308
015308
01-3809
01-380-1998 (TREMBLREL. 05, CREATED)
01-380-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-380-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
MONOCARBOXIATE TRANSPORTER MCT3 (FRGGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHOMPATA: VERTEBRATA: MAMMALIA; RODENTIA;
                                                                                                                                                                                                                                                    STRAIN-POB1;
BIBOLLET-RUCHE F., BRENGUES C., GALAT-LUONG A., GALAT G., POURRUT X., VIDAL N., VEAS F., DURAND J.P., CUNY G.;
J. VIROL. 71:307-313(1997).
EMBL; U37209; G1353456; -.
ENBL; PRO0317; GP41; 1.
ENVELOPE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 9.22e+00;
5; Mismatches 2; Indels
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Pred. No. 9.22e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C3H;
PHILP N.J., YOON H.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF019111; G2407664; -
ION_TER
SEQUENCE 156 AA; 16253 MW; DB394B9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 12 044188 PRELIMINARY; PRT; 262 AA. 044188 044189. 01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) W-AMINO-TRANSFERASE-LIKE PROTEIN.
                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENVELOPE GLYCOPROTEIN (FRACMENT).
                                                                                                                                                                                             SIMIAN IMMUNODEFICIENCY VIRUS (SIV-AGM).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                             142 AA; 16852 MW; C58A9A91 CRC32;
                                                                               142 AA.
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                                                                             PRT;
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Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%;
Similarity 46.7%;
7; Conservative
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AGROBACTERIUM RADIOBACTER.
                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 EPDSGGLSRDSRSYT 100
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49
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67 PSTGALVDS-KSY
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NON_TER
SEQUENCE
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Q87600
Q87600;
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Score 51; DB 14; Length 1340;
Pred. No. 5.58e+00;
4; Mismatches 3; Indels (
                                                                              CYTOPLASMIC INCLUSION PROTEIN
                                                                                                             NIA PROTEASE.
NUCLEAR INCLUSION PROTEIN B.
COAT PROTEIN.
MW; 12C01867 CRC32;
                                                                                        6K2 PROTEIN
VPG PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE.
REPLICASE.
ARCH. VIROL. 140:1473-1482(1995).
EMBL; D38543; D1008127; -.
PFAM; PF00080; RNA_dep_RNA_Dol; 1.
PFAM; PF000863; Peptidase_C4; 1.
PGAM; PF00863; Peptidase_C4; 1.
NOW_TER 1 1 1 CHAIN 17 69 6K2 PROJ CHAIN 70 261 VPG PROJ CHAIN 262 504 NIA PROJ CHAIN 262 504 NIA PROJ
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1527 2169
2170 2222
2223 2414
2415 2657
3179 3493
3179 3493 AA; 393818 M
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01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                              151873
                                                                                                                                                                  59.3%;
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larity 50.0%;
Conservative
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69
261
504
1025
1340
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70 26
262 50
505 102
1026 134
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Best Local Similarity
                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                  POTYVIRUS.
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SEQUENCE
                                                                                                                                              SEQUENCE
                                                                                                                                                                  Query Match
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039734
039734;
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                                                                                                                                                                                                                                                                                                                                                                                                                   "Similarity among the Drosophila (6-4)photolyase, a human photolyase homolog, and the DNA photolyase-blue-light photoreceptor family."; SCIENCE 272:109-112(1996).
                                NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.
                                       OHARA O.;
"Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA RES. 5:31-39(1998).
EMBL; AB011135; D1026419; -.
SEQUENCE 870 AA; 94665 MW; EB9CD3F4 CRC32;
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                           STRAIN-PHR: TISSUE-OVARY;
MEDLINE; 96178677.
IKENAGA M.; YAMAMOTO K., TOH H., INUI T., AYAKI H., NOMURA T.,
IKENAGA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence analysis of two nuclear inclusion body and coat protein genes of a sweet potato feathery mottle virus severe strain (SPFWV-S) genomic RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
SWEET POTATO FEATHERY MOTILE VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SEVERE;
MEDLINE; 95390803.
MORI M., SAKAI J., KIMURA T., USUGI T., HAYASHI T., HANADA K.,
NISHIGUCHI M.;
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                       DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA, DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.3%; Score 51; DB 5; Length 540; 35.7%; Pred. No. 5.58e+00; active 6; Mismatches 3; Indels
                                                                                                                              Score 52; DB 4; Length 870;
Pred. No. 3.35e+00;
5; Mismatches 3; Indels
                                                                                                                                                                                                                            540 AA; 62548 MW; 62F139EE CRC32;
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                                                                                                                              60.5%;
42.9%;
                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D83701; D1012739;
                                                                                                                                                                         798 EPAQDSLVQSESYT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 EPWKASLVDQRAYG 469
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66 DPSTGALVDSKSYA 79
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                                                                                                                                         Best Local Similarity
SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                    MEDLINE; 98290545
                                                                                                                                                                                                                                                                                               PHOTOLYASE.
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                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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For a complete nucleotide sequence and genome organization of sweet potato

For feathery mottle virus (S strain) genomic RNA: the large coding region

For the PI gene. "."

ARCH. VIROL. 142:1553-1562(1997).

BEBL; B86371; D1023570; -..

BRBL; B86371; D1023570; -..

BRBL; B86371; D1023570; -..

BRBM; PF00851; PRALCase_C; 1..

BRBM; PF00851; Peptidase_C; 1..

BRBM; PF00851; PP0851; PP
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                                                                                                                                                                                                                                                                                                                                                             SWEET POTATO FEATHERY MOTTLE VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S STRAIN;
MEDLINE; 98336489.
SARI J., MORI M., MORISHITA T., TANAKA M., HANADA K., USUGI T.,
NISHIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 5.58e+00;
4; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NISHIGUCHI M.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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MW; A02EFA05 CRC32;
PRT; 3493 AA
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046178 PRELIMINARY; PRT; 552 AA.
046178 CARBELREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RADIAL SPOKEHEAD.
STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).
EUKARYOTA, METAZOA; ECHINODERMATA; ECHINOZOA; ECHINOIDEA; ECHINOIDEA; ECHINOZOA; ECHINOZOA; SCHINOIDEA;
                                                                                                    HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                     TISSUE-BRAIN;
MEDLINE; 98290545.
NAGASE T., ISHIKAWA K., MIYAJIWA N., TANAKA A., KOTANI H., NOMURA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE; 98119758.
GGINGRAS D., GGGNON C.;
"Molecular cloning and characterization of a radial spoke head protein of sea urchin sperm axonemes: involvement of the protein in the regulariton of sperm motility.";
MOL. BIOL. CELL 9:513-522(1998).
EMBL; U73123; G2905895; --
SEQUENCE 552 AA; 62723 MM; 898CFCCC CRC32;
                                                                                                                                                                                                                                                             OHARA O.;
Prediction of the coding sequences of unidentified human genes. IX
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA RES. 5:31-39(1998).
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Pred. No. 3.35e+00;
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Pred. No. 3.35e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
  01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
KIAA0574 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                  EMBL; ABO11146; D1056430; -.
NON_TER 1
SEQUENCE 405 AA; 42409 MW; 09BA9932 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.5%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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07,
08,
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67 PSTGALVDSKSY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||||:||
71 ALVDSKSYA 79
                                                                               KIAA0574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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060309
060309;
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                                                                                                                                                    BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; CAMPYLOBACTER GROUP; CAMPYLOBACTER.
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                                                                                                                                                                                                                                        STRAIN=UAS80;
MEDLINE; 90384493.
TAYLOR D.E., HIRATSUKA K.;
"Use of non-radioactive DNA probes for detection of Campylobacter jejuni and Campylobacter coli in stool specimens.";
MOL. CELL. PROBES 4:261-271(1990).
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HENDERSON J., WOOD A.C., EMERY M.J., WREN B.W., KETLEY J.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X82628; E315368; -.
PERM: PF00089; LYPPS11; 1.
PFAM: PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 2; Length 368;
Pred. No. 4.07e-01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB 2; Length 472;
Pred. No. 4.07e-01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        HIRATSUKA K.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U27271, 6881375; -.
PRAM: PF00089; LYppsin; 1.
PFAM: PF00595; PDZ; 2.
HEAT SHOCK; PROTEASE.
                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN/SERINE PROTEASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 368 AA; 39491 MW; A5062589 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AA; 50940 MW; 6CBCA101 CRC32;
    368 AA
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    PRT;
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04,
08,
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Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 65.1%;
Local Similarity 72.7%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OLT 3 O46120 O46120 O46120; O10120; O10120; O10120; O10120; O10120197 (TREMBLREL. 0401-1094 (TREMBLREL. 0601-NOV-1998 (TRE
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                            CAMPYLOBACTER JEJUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SGGALVDSRGY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 SGGALVDSRGY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||||||::|
68 STGALVDSKSY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-UA580;
Q46094
Q46094;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
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ID 060320
AC 060320;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:29:24 1999; MasPar time 5.26 Seconds 145.242 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (66-79) from PCTUS9913024.pep (11 of 12) 86

1 DPSTGALVDSKSYA 14 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 24.488; Variance 26.991; scale 0.907 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Pred. No.	7.85e-02	4.07e-01	4.07e-01	3.35e+00	3.35e+00	3.35e+00	5.58e+00	5.58e+00	5.58e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	1.51e+01	1.51e+01
			Description	GLUCOSYLTRANSFERASE.	HEAT SHOCK PROTEIN/SER	SERINE PROTEASE.	KIAA0574 PROTEIN (FRAG		KIAA0563 PROTEIN.	PHOTOLYASE.	POLYPROTEIN (FRAGMENT)	POLYPROTEIN.	ENVELOPE GLYCOPROTEIN	MONOCARBOXYLATE TRANSP	W-AMINO-TRANSFERASE-LI	CMP-N-ACETYLNEURAMINAT	MONOCARBOXYLATE TRANSP	MONOCARBOXYLATE TRANSP	RETINAL EPITHELIAL MEM	SIMILARITY TO MYOSIN H	PATERNALLY EXPRESSED P	YCDH.	HEMAGGLUTININ (FRAGMEN
SUMMARIES			TD.	054178	046094	046120	060320	046178	060309	024281	088274	039734	087600	035308	044188	P72097	070461	013151	090632	004626	061138	034966	092324
			DB	~	~	7	4	S	4	S	14	14	14	11	7	~	11	13	13	10	77	~	14
			Match Length DB	1577	368	472	405	552	870	540	1340	3493	142	156	262	371	492	542	542	1133	1378	319	327
	æ	Query	Match	9.89	65.1	65.1	60.5	60.5	60.5	59.3	59.3	59.3	58.1	58.1	58.1	58.1	.58.1	58.1	58.1	58.1	58.1	57.0	57.0
			Score	59	56	56	52	52	52	51	51	51	20	20	20	20	20	20	20	20	20	49	49
		Result	. S	1	7	9	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20

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Gaps

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Score 59; DB 2; Length 1577; Pred. No. 7.85e-02; 2; Mismatches 2; Indels

Ouery Match
Best Local Similarity 69.2%;
Matches 9; Conservative 260 DAETGALVDSNEY 272

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                                 SEQUENCE FROM N.A.
MEDLINE; 94374705.
MEDLINE; 04374705.
MEDLINE; O.O., BRUTON C.J., CHATER K.F.;
SEQUENCE Of the essential early region of phi C31, a temperate phage of Streptomyces spp. with unusual features in its lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92276337.
SULAVIK M.C., TARDIF G., CLEWELL D.B.;
"Identification of a gene, rgg, which regulates expression of glucosyltransferase and influences the Spp phenotype of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                           194 AYMNADFIIDPDGNREPMPEFDGAAVLHVTDETWA-FKPVETGPDVFAQFLHLRQTFD 250
                                                                                                                                                                                                                                                                                                                                                                     STREPTOCOCCUS GORDONII.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
STREPTOCOCCUS.
                                                                                                                                                                                                                          NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CHALLIS;
MEDLINE; 96157084.
VICKERMAN M.M., SULAVIK M.C., CLEWELL D.B.;
"Molecular analysis of Streptococcus gordonii glucosyltransferase
phase variants.";
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Pred. No. 1.68e+00;
7; Mismatches 11; Indels
                                                                                                                                                           Score 83; DB 9; Length 281;
Pred. No. 1.68e+00;
17; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                    development...
GENE 147:29-40(1994).
EMBL; X76288; G579071; -.
SEQUENCE 281 AA; 31680 MW; 0E734629 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1693 AA.
                                                                                                                                                                                                                                                                                    PRT; 1577 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 QDDGTVKKNFAVELNGKILYFDAETGALVDSNEY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEV. BIOL. STAND. 85:309-314(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gordonîı Challis.";
J. BACTERIOL. 174:3577-3586(1992).
BEBL; Ul2643; G1054877; -
EMBL; M89776; G153795; -.
PFAM: PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                           01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.2%;
Matches 14; Conservative
                                                                                                                                                         Query Match
Best Local Similarity 24.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-96 FROM N.A. STRAIN-CHALLIS;
                                                                                                                                                                                                                                                                                             Q54178; Q54247;
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                    PRELIMINARY;
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VIRUSES; DSDNA VIRUSES,
LAMBDA PHAGE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSFERASE.
SEQUENCE 1
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039221
039221;
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054178
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572 FRISFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVGAGLDHRAI 631
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  SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
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                                                                                                                                                                                                                                          S.K.
                                                                                                                                  PANDA S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 15.1%; Score 83; DB 14; Length 1693; Local Similarity 23.9%; Pred. No. 1.68e+00; les 16; Conservative 23; Mismatches 25; Indels
                                                                                                                                                                                                            SEQUENCE FROM N.A.

ANSARI I.H., NANDA S.K., DURGAPAL H., JAMEEL S., PANDA
"Translational analysis of complete HEV genome.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF02891; G256543; -.

EMBL; AF076239; G3328379; -.
                                                                         SEQUENCE FROM N.A.
STRAIN-HYDERABD, INDIA;
STRAIN-HYDERABD, INDIA;
STRAIN-HYDERABL S. F. PANI
SUBMITIEN (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                               1693 AA; 185620 MW; E8D755D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Wed Sep 1 16:13:32 1999 Job time: 27 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632 FAPGVSP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 FDPSTGA 71
VIRUSES; SSI
                                                                                                                                                                                                                                                                                                                                                                          POLYPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                             572 FRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                              BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                          Length 1693;
                                                                                                                                            22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 84; DB 2; Length 622;
Pred. No. 1.21e+00;
26; Mismatches 26; Indels
                                                                    DONATI M.C., FAGAN E.A., HARRISON T.J.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X98292; E1175751; -.
07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                          1693 AA; 185190 MW; 287742F6 CRC32;
                                                                                                                          Score 86; DB 14;
Pred. No. 6.27e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                      622 AA; 69729 MW; 65E72171 CRC32;
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                                                                                                                                                                                                                                                        622
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SHANGHAI I (S-1);
STRAIN-SHANGHAI I (S-1);
WU D., CAO X.L., BAI Y.Y., ARONSON A.I.;
FEMS MICROBIOL. LETT. 81:31-36(1991).
EMBL; X57252; G40286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X57252; G40286; -. PFAM; PF00555; endotoxin; 1.
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05,
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01,
                                                                                                                           15.6%;
25.4%;
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Similarity 18.2%;
12; Conservative
                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLREL. 0:
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
CRYILC DELTA-ENDOTOXIN.
                                                                                                                                                                                                                                                       PRELIMINARY;
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01-AUG-1998 (TREMBLREL.
METHYL TRANSFERASE.
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01-JAN-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
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                                                                                                                                   Local Similarity
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                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                 632 FAPGVSP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C34B7.2 PROTEIN.
                                                                                                                                                                                                             | |: ::
65 FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 NTTTNN 566
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                                                              STRAIN-HEV037
                                                                                                TRANSFERASE
                         VIRUSES; SS
                                                                                                                                                                                                                                                                                                                                        BACILLUS.
                                                                                                           SEQUENCE
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                                                                                                                            Query Match
                                                                                                                                                                                                                                              LT 10
Q45743
Q45743;
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P90770
P90770;
                                                                                                                                                                                                                                                                                                                     PLASMID.
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., REAUSCOUGH R., ANDERSON K., COPERY J., COULSON A., BONFIELD J., BURTON J., CONNELL M., COPERY J., COULSON A., GRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., JONES M., KERSHAW J., KIRSTEN J., LATREILLE P., LIGHER M., JOHNSTON L., FIGHTHING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., STADEN R., SULSTON J., THERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON J., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

**2.2 M.** Defection of the property of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRASSICA OLERACEA (CAULIFLOWER).
EUKARYOTA; VIRIDIALAMTE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES: SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; BRASSICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 ERWEVEIVHGYVRQEYIFLPIG-RISLTIIGRRSTKYAGTRFLKRGANPTGNVANYVETE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EKFWAEFGOGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGS-QTFSAGL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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EMBL; U87239; G2738025; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 83; DB 10; Length 180;
Pred. No. 1.68e+00;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 IPHTCPLAKIGPPVGKFAPPEVVSVRVPL-LHLSNFQGSDWSDL-SGKGY 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 5; Length 921;
Pred. No. 1.21e+00;
22; Mismatches 32; Indels
                                  TO EMBL/GENBANK/DDBJ DATA BANKS.
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LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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EMBL; 283220; E1344511; -.
SEQUENCE 921 AA; 106698 MW; 21DE4C35 CRC32;
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUEN
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTY
PUTATIVE ETHYLENE RECEPTOR (FRAGMENT).
BOERS.
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Best Local Similarity 36.0%;
Matches 18; Conservative
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08,
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Best Local Similarity 24.7%;
Matches 19; Conservative
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038022,
01002-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
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BACTERIOPHAGE PHI-C31.
HARRIS B.;
SUBMITTED (DEC-1996)
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SEQUENCE FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
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632 FAPGVSP 638
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MEDLINE: 92251377.
UCHIDA T., SUZUKI K., HAYASHI N., IIDA F., HARA T., OO S.S.,
WANG C.K., SHIKATA T., ICHIKAWA M., RIKHHISA T., MIZUNO K., WIN K.M.;
"Hepatitis E virus: CDNA cloning and expression.";
MICROBIOL. IMMUNOL. 36:67-79(1992).
                                                                                                                                                                                        TAM A.W., SMITH M.M., GUERRA M.E., HUANG C.C., BRADLEY D.W., FRY K.E.
REYES G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 FRTSFVDGAVLETNGPERHNLSFDASOSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
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MEDLINE: 92271462.
FRY K.E., TAM A.W., SMITH M.M., KIM J.P., LUK K.C., YOUNG L.M.,
PIATAK M., FELDMAN R.A., YUN K.Y., PURDY M.A., ET AL.;
"Hepatitis E virus (HEV): strain variation in the nonstructural gene
region encoding consensus motifs for an RNA-dependent RNA polymerase
and an ATP/GTP binding sile.";
VIRUS GENES 6:173-185(1992).
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VIRUSES; SSRNA POȘITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of hepatitis E virus isolated directly from a single source during an outbreak in China.";
VIRUS RES. 28:233-247(1993).
EMBL: LO8816; G330009;
SEQUENCE 1693 AA; 185052 MW; 30A917E1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 92335008.
AYE T.T:, UCHIDA T., MA X.Z., IIDA F., SHIKATA T., ZHUANG H.,
WIN K.M.;
"Complete nucleotide sequence of a hepatitis E virus isolated from
the Xinjiang epidemic (1986-1988) of China.";
NUCLEIC ACIDS RES. 20:3512-3512(1992).
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SECUENCE FROM N.A.
MEDLINE; 92115700.
TSAREV S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEGTERS L.J.,
MALIX I.A., 10BAL M., PURCELL R.H.,
"Characterization of a prototype strain of hepatitis E virus.";
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).
                                                                                                                                                                                                                                       "Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.",
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Pred. No. 6.27e-01;
22; Mismatches 25; Indels
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                           full-length viral genome.";
VIROLOGY 185:120-131(1991).
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Best Local Similarity 25.4%;
Matches 17; Conservative
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081344;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
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HEPATALIIS E VIRUS COMPLETE GENOME.
HEPATITIS E VIRUS (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
CALICIVIRUS.
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HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
CALICLYIRUS.
                                                                                                                                                                                                                                                                           STRAIN-HEBEL;
MEDLINE; 93348763.

MEDLINE; 93348763.

BI S.L., PURDY M.A., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
BI S.L., PURDY M.A., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
BI S.L., PURDY M.A., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
SOURCE during an outbreak in China.";
VINGS RES. 28:233-247(1993).

VINGS RES. 28:233-247(1993).

SEQUENCE 1693 AA; 185271 MW; EF762F9E CRC32;
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Pred. No. 6.27e-01;
22; Mismatches 25; Indels
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Pred. No. 6.27e-01;
22; Mismatches 25; Indels
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EMBL/GENBANK/DDBJ DATA BANKS.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
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nes 17; Conservative
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Best Local Similarity 25.4%;
Matches 17; Conservative
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YIN S.R., PURCELL R.H.,
SUBMITTED (MAR-1996) TO
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PRELIMINARY;
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LETCHWORTH G.J., SCHWYZER M.;
"Nuclectide sequence analysis of a 30-kb region of the bovine herpesvirus I genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus.";
VIROLOGY 210:100-108(1995).
                                                                                                                                                                         Gaps
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LI Y., LU Z., SUN L., ROPP S., KUTISH G.F., ROCK D.L., VAN ETTEN J.L.;
"Analysis of 74 kb of DNA located at the right end of the 330-kb chlorella virus PBCV-1 genome.";
VIROLOGY 237:350-377(1997).
EMBL; U42580; G2447164; -.
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SCHWYZER M., PACES V., LETCHWORTH G.J., MISRA V., BUHK H.J.,
LOWERY D.E., SIMARD C., BELLO L.J., THIRY E., VLCEK C.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                    Score 96; DB 14; Length 114;
Pred. No. 2.00e-02;
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                                                                                                                                         18; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-JUDA;
SCHWYZER M.;
SCHWYZER M.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 248053; G971327; -.
EMBL; AJO04801; E1187337; -.
HYPOTHETICAL PROTEIN.
FROUENCE 299 AA; 32379 MW; A3897D4A CRC32;
                                                                                                                                                                                                                                                                                                                                                 VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                          065574;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 32.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 92; DB 14; Le
Pred. No. 8.15e-02;
9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 PRFVCEVREIPAGPPTFTSSSITHLRV-EPSTGALL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA
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                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL. 01,
(TREMBLREL. 01,
(TREMBLREL. 08,
                                                                                                                    Query Match
Best Local Similarity 27.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.7%;
Best Local Similarity 47.2%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                         BOVINE HERPESVIRUS TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-COOPER, AND JURA;
MEDLINE; 95313343.
                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Q65581
Q65581;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1999 (
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STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
DAVIS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAWMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 IAESYLQQSFLSEDTYIR-KSAIIGA-GLSGSSEA-LELLSEAIETQDLYEQL-L-ILNA 117
                                                                                                 SEQUENCE FROM N.A.
STRAIN-SCHOENBORKEN;
MEDLINE; 96135223.
SCHMITT J., KEIL G.M.;
Identification and characterization of the bovine herpesvirus 1 UL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGGGTVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                               gene and gene product which are not essential for virus replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAVIS R.W.; "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis."; SCIENCE 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89; DB 2; Length 566;
Pred. No. 2.28e-01;
25; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
BOVINE HERPESVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (MAX-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE001308; G3328771; -
HYPOTHETICAL PROTEIN.
SEQUENCE 566 AA; 63508 MW; ClalC491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 63.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLAMYDIA TRACHOMATIS.
BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
                                                                                                                                                                                                                                                                                                                                                                               16.7%; Score 92; DB 14; 1
larity 47.2%; Pred. No. 8.15e-02;
Conservative 9; Mismatches 6
                                                                                                                                                                                                                                                      in cell culture.";
J. VIROL. 70:1091-1099(1996).
EMBL; X91751; G1006650; -.
SEQUENCE 300 AA; 32450 MW; 86377347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 PRFVCEVREIPAGPPTFTSSSITHLRV-EPSTGALL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           566 AA
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Best Local Similarity 26.2%;
Matches 17; Conservative
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protein - protein database search, using Smith-Waterman algorithm Wed Sep 1 16:13:05 1999; MasPar time 9.45 Seconds 450.572 Million cell updates/sec MPsrch_pp Run on:

>PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 1 MEKFWAEFGGGYVQTPFLSE......GLHLRVFDPSTGALVDSKSY 78 Description: Perfect Score: Sequence:

Tabular output not generated.

PAM 150 Gap 11 Scoring table:

179066 segs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremp19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 5:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_vinus

Mean 37.051; Variance 67.149; scale 0.552 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

21 80 14.5 275 14 Q68469 POLYPROTEIN (FRAGMENT) 4.41e+00 22 80 14.5 275 14 Q68469 POLYPROTEIN (FRAGMENT) 4.41e+00 23 80 14.5 275 14 Q68469 POLYPROTEIN (FRAGMENT) 4.41e+00 24 80 14.5 357 5 001993 VCZ7ATL I PROTEIN. 25 80 14.5 2436 14 Q81756 POLYPROTEIN. 4.41e+00 26 80 14.5 2436 14 Q81756 POLYPROTEIN. 4.41e+00 27 79 14.3 370 3 Q04083 D9461.24P. 28 79 14.3 860 1 O59003 B60AA LONG HYPOTHETICA 6.06e+00 29 79 14.2 3011 14 O3609 POLYPROTEIN. 31 78 14.2 3011 14 O3669 POLYPROTEIN. 32 78 14.2 3011 14 O3669 POLYPROTEIN. 33 78 14.2 3011 14 O3660 POLYPROTEIN. 34 78 14.2 3011 14 O3660 POLYPROTEIN. 35 77 14.0 3011 14 O3651 LECITHINASE. 36 77 14.0 470 2 O85325 LECITHINASE. 37 77 14.0 470 2 O85325 PUTATIVE MONOSACCHARID 1.13e+01 41 77 14.0 1464 11 O65328 PEPB. 41 77 14.0 1464 11 O65328 PEPB. 42 77 14.0 1464 11 O65328 N-METHYL-D-ASPARTATE R 1.13e+01 44 77 14.0 2 O31388 ZX1067.2 PROTEIN 1.38e+01 41 77 14.0 1464 11 O63728 N-METHYL-D-ASPARTATE R 1.13e+01 41 77 14.0 1464 11 O63728 ZX1067.2 PROTEIN 1.36e+01 41 77 14.0 1464 11 O63728 ZX1067.2 PROTEIN 1.36e+01 41 77 14.0 1464 11 O63728 ZX1067.2 PROTEIN 1.36e+01 41 77 14.0 1464 11 O63728 ZX1067.2 PROTEIN 1.36e+01 41 77 14.0 1464 11 O63728 ZX1067.2 PROTEIN 1.36e+01	RESULT 1 OB1876 PRELIMINARY; PRT; 1693 AA. AC 081876 DE 081876 AC 081876 AC 081876 DE 081876 DE 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE) DE COMPLETE GENOME SEQUENCE. OC VIRIOSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE; CALICIVIRUS. RA 11 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA UCHIDA T.; AL SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS. SEQUENCE 1693 AA; 184840 MW; 8952DD38 CRC32; QUERY MATCH Best Local Similarity 26.9%; Pred. No. 4.78e-03; MATCHES 18; CONSELVATIVE 22; MISMATCHES 24; Indels 3; Gaps 3; AL SCOUENCE 1693 AA; INSMATCHES 24; Indels 3; Gaps 3; Best Local Similarity 26.9%; Pred. No. 4.78e-03; MATCHES 18; CONSELVATIVE 22; MISMATCHES 24; Indels 3; Gaps 1; H 1;	TESULT 2

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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB3
NAB3 OR YPL190C.
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P38138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                EYNKGYNFFSGLSDSEVARYQKEAITGHRPTWTVGVN-KNAKNGPTQSQTRSGSAGAQAR 82
                                                                                         EUKARYOTA; EUGLENO20A; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA
                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                             15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANORATION UPDATE)
15-DUL-1998 (REL. 36, LAST ANORATION UPDATE)
PRECEPTOR-TYPE ADENYLATE CYCLASE GRESAG 4.2 (EC. 4.6.1.1) (ATP
PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 LSTAERSQFDVTPLGGVPLRGVSEPVEVYQLNAVPGRSF-AELRLDRVLD 490
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Pred. No. 1.59e+00;
16; Mismatches 17; Indels
   Length 171;
                                  11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 Score 80; DB 1; I Pred. No. 1.59e+00;
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                                                                                                                                                                                                                                              572 AA
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(REL. 31, LAST SEQUENCE UPDATE)
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PFAM; PF00211; guanylate_cyc; 1.
HSSP; Q02846; 1AWL.
                                                                                                                                                                                                                                                                               (REL. 36, CREATED)
(REL. 36, LAST SEQ)
(REL. 36, LAST ANN
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Best Local Similarity 30.0%;
Matches 15; Conservative
Query Match
Best Local Similarity 37.5%;
Matches 24; Conservative
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                                                                                                                                                                                                                                              STANDARD;
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251
572
10
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77
152
152 AA;
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P38996;
01-FEB-1995 (
01-FEB-1995 (
                                                                                                                                        83 MRDP 86
                                                                                                                                                                         64 VFDP 67
                                                                                                                                                                                                                            LT 13
CY42_TRYBB
Q99396;
                                                                                                                                                                                                                                                                               15-JUL-1998
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CARBOHYD
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SEQUENCE
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DUBOIS E., EL BAKKOURY M., GLANSDORFF N., MESSENGUY F., PLERARD A., SCHERRIS B., VIERENDEELS F.;
SCHERRIS B., VIERENDEELS F.;
SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                  EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES; SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                           WILSON S.M., OBERDORF A.M., DATAR K.V., SWEDLOW J.R., PADDY M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-007-1994 (REL. 30, CREATED)
01-00T-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-00T-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE FAMILY 31 GLUCOSIDASE IN PCS60-ABD1 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
                                                                                                                                                                                                                                                    RIEGER M., MUELLER-AUER S., SCHAEFER M.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                              SWANSON M.S.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 QGY-VQTPF-LSESNSVRYKISIAGSCPLSTAGPSYVKFQDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 QGYGSQPPIPMNQSYG-RYQTSIPPPPPQQQIPQGYGRYQAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 1; L
Pred. No. 1.59e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FB180EDB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
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POLY-ASP.
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POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z73546; E246917; -...
PIR; S48529; S48529.
SGD; L0001228; NAB3.
PFAM; PF00076; rrm; 1.
RNA-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%;
larity 32.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U05314; G476220; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                723
765
769
802 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EC 3.2.1.-).
YBR229C OR YBR1526.
                                                                                                SEQUENCE FROM N.A.
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DOMAIN
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                                                         ö
                                                                                                                                                                                                                                                                                         LEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-THYMUS;
MEDLINE, 9605936.
MEDLINE, 9605936.
"The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5.";
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91130578.

HU Q., DAVIDSON D., SCHWARTZBERG P.L., MACCHIARINI F.,
LENARDO M.J., BLUESTONE J.A., MATIS L.A.;
Lidentification of RIk, a novel protein tyrosine kinase with
predominant expression in the T cell lineage.";
J. BYOL. CHEM. 270:1928-1934(1995).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- TISSUE SPECIFICITY: EXPRESSED IN EARLY THYMOCYTES, T CELLS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE BTK SUBPAMILY.
                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE_PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-LIVER;
HIGASHITSUJI H., NONOGUCHI K., ARII S., FURUTANI M., KANEKO Y.,
NAKAYAMA H., FUJITA J.;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-THYMUS;
SOMMERS C.L., HUANG K., GRINBERG A., CHARLICK D.A., KOZAK C.A.
                                                         ö
                                                                                                                                                                                                                                   TXK OR RLK.
MUS MUSCULOS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA: SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                              Score 82; DB 1; Length 527;
Pred. No. 7.96e-01;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
45 45 H -> R (IN REF. 2
527 AA; 61239 MW; 8DF019E3 CRC32;
                                                                                                                                                   527 AA
                                                                              242 LRYPVGLMGSCLPATAGFSYEKWEIDP 268
                                                                                            :|| :: ||| :||| | : :|
24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                 MAMM. GENOME 6:476-480(1995)
                               Query Match
14.9%;
Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U16145; G562125; -. EMBL; U19607; G643065; -.
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                         LYMPHOCYTE KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-THYMUS
                                                                                                                                        TXK_MOUSE
P42682;
SEQUENCE
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LS -> SF (IN REF. 3).

Y -> D (IN REF. 3).

Y -> D (IN REF. 3).

R -> T (IN REF. 3).

R -> T (IN REF. 3).

R -> T (IN REF. 3).
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-I. SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
MGD; MGI:102960; TXX.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH3; 1.
PROSITE; PS50001; SH3; 1.
PFAM; PF00017; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
TRANSTERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YCB2_PSEDE STANDARD; PRT; 171 AA. P29944; 01-APR-1993 (REL. 25, CREATED) 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHETICAL 19.0 KD PROTEIN IN COBS 5'REGION (ORF2). PSEUDOMONAS DENTRIFICANS.
                                                                                                                                                                                                                                                                                                            SH3.
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.13e+00; 7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 AA; 18973 MW; 5DDD21D5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81;
                                                                                                                                                                                                                                                                                        POLY-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 LRYPIGLLGSCLPATSGFSYEKWEIDP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M62869; G151167; ...
PIR; B38162; B38162.
PROSITE; PS00636; DNAJ_1; FALSE_NEG
PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61108 MW;
                                                                                                                                                                                                                                                                SH3 DOMAIN; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 44.4%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; PROTEOBACTERIA
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272
497
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HSSP; P08622; 1XBL.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
6
272
497
527 AA;
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271
277
299
390
420
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TISSUE-BLOOD
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PROSITE; E
PROSITE; E
PROSITE; E
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MOD_RES
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 YMMGFSLGASIMTNYLGEESDRTKIECAISVSNPFDLYNSAYF-INSTPMGSRFYSPAL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMALUW UNC IMBACOL.U4.
SACCHAROWYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI: ASCONYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEDMAN K., BROWN D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                   UL-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
HYPOTHETICAL 51.4 KD PROTEIN IN RAR1-SCJ1 INTERGENIC REGION.
YMR2510W OR YM8261.04.
                                                                                                                                                        Score 83; DB 1; Length bli.
Pred. No. 5.61e-01;
....arrhes 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82; DB 1; Length 449;
Pred. No. 7.96e-01;
18; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WALSH S.V.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE UPFO017 FAMILY.
                                                                                                        EMBL; 274697; E249958; -.
EMBL; 274024; E248895; -.
EMBL; 274024; E248895; -.
EMPL; 274024EIIII FORDIASE.
SEQUENCE 611 Aa; 67205 MM; 9DF140EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51437 MW; FE884F32 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TXK_HUMAN STANDARD; PRT; 527 AA. P42681; 014220; 01-NOV-1995 (REL. 32, CREATED) 1-EB-1996 (REL. 33, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                            449 AA.
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                    319 VRFQHLPVPFELYSDGIDLPVFE 341
                                                                                                                                                                                                                                           44 VKFQDNPVGSQTFSAGLHLRVFD 66
                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQU
01-NOV-1997 (REL. 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS01133; UPF0017; 1. PFAM; PF00561; abhydrolase; 1. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.9%;
ilarity 27.1%;
Conservative
                                                                                                                                                                    Query Match 15.1%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 249809; G854462; -.
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                          YM60_YEAST
Q03649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                            HAIRE R.N., OHTA Y., LEWIS J.E., FU S.M., KROISEL P.M., LITMAN G.W., "TXK a novel human tyrosine kinase expressed in T cells shares sequence identity with Tee family kinases and maps to 4p12."; HUM. MOL. GENET. 3:897-901(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIZER, 96197775.

OHTA Y., HAIRE R.N., AMEMIYA C.T., LITMAN R.T., TRAGER T., RIESS O., LITMAN G.W.;

"Human Txx: genomic organization, structure and contiguous physical linkage with the Tec gene.";

ONCOGENE 12:937-942(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF000019; PK1nase; 1.
HSSP; Q06187; 1AWW.
TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN. BELONGS TO THE BIK SUBFAMILY.
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PS00109; PROTEIN_KINASE_IYR;
PS50011; PROTEIN_KINASE_DOM;
PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, L27071, G684986; -...
EMBL, U34379; G1161364; -...
EMBL, U34369; G1161364; JOINED.
EMBL, U34369; G1161364; JOINED.
EMBL, U34370; G1161364; JOINED.
EMBL, U34371; G1161364; JOINED.
EMBL, U34372; G1161364; JOINED.
EMBL, U34373; G1161364; JOINED.
EMBL, U34374; G1161364; JOINED.
EMBL, U34374; G1161364; JOINED.
EMBL, U34375; G1161364; JOINED.
EMBL, U34375; G1161364; JOINED.
EMBL, U34375; G1161364; JOINED.
EMBL, U34375; G1161364; JOINED.
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                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-BLOOD;
MEDLINE; 95038742.
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE, 89330163.
HAMERS A.M., PEL H.J., WILLSHAW G.A., KUSTERS J.G.,
VAN DER ZELIST B.A.M., GAASTRA W.;
The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";
MICROB. PATHOG. 6:297-309(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-H37RV;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILANITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JORDI B.J.A.M., WILLSHAW G.A., VAN DER ZEIJST B.A.M., GAASTRA W.;
"The complete nucleotide sequence of region 1 of the CFA/I fimbrial
operon of human enterotoxigenic Escherichia coli.";
DNA SEQ. 2:257-263(1992).
-1- FUNCIION: MAX SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIACEAE;
                                                                      01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
CFA/I FIMBRIAL SUBUNIT C PRECURSOR (COLONISATION FACTOR ANTIGEN I
                                                                                                                                                                                                                                        PLASMID NTP513.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CFA/I FIMBRIAL SUBUNIT: 7AF76347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTIGEN; SIGNAL; FIMBRIA; OUTER MEMBRANE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 85; DB 1; Le
Pred. No. 2.75e-01;
14; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MTCY274.45C OR MTCY338.01C.
MYCORACTERIUM TUBERCULOSIS.
                                  869 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AFIQSQTINLSDSGKYKRLSISGNSALGITDTSY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 GYVQTPFLSESNSVRYK-ISIAGSCPLSTAGPSY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Conservative 1
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                               STANDARD:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-ENTEROTOXIGENIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M55661; G145510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 92329981.
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                                                                                                                                                                                                                  ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                      ESCHERICHIA.
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                      CFAC_ECOLI
P25733;
                                                                                                                                                                      SUBUNIT C).
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Q10830;
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Matches
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                                                                                                                                                                                                                                   572 FRISFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
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                                                                                                                                                                                                                                                                3; Gaps
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FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHIZOBIUM SP. (STRAIN NGR234).
PLASMID SYM PNGR234A.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATURE 387:394-401(1997).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: NONE OBVIOUS.
EMBL; M80581; G329998; -.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERRET X.; "Molecular basis of symbiosis between Rhizobium and legumes.";
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                                                                                                                                             Length 1693;
                                                                                                                                      Score 86; DB 1; Length 1693
Pred. No. 1.92e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 85; DB 1; Length 703; Pred. No. 2.75e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                      (POTENTIAL).
FBCA2483 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
08-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 76.2 KD PROTEIN Y4II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMID; TRANSMEMBRANE
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POTENTIAL.
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                                                                      32 ATP
185149 MW;
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                                                                                                                                        Query Match
Best Local Similarity 25.4%;
Matches 17; Conservative
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Best Local Similarity 27.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHIZOBIACEAE; RHIZOBIUM.
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1163
270
377
452
664
                                                                      982
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                                                                                            1693 AA;
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                                                                                                                                                                                                                                                                                                                                632 FAPGVSP 638
                                                                      975
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                                                ATP-BINDING.
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AC 01-NOV-1997

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SEQUENCE
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Length 869; 8; Indels

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CALICIVIRIDAE;

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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
16-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.7.7.48); HELICASE];
HERPAITIS E VIRUS (STRAIN PAKISTAN) (HEV).
VIRUSES; SERNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSAREY S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEGTERS L.J.,
MALIK I.A., IQBAL M., PURCELL R.H.;
CARARACHETIZATION of a profotype strain of hepatitis E virus.";
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992)
-!- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE ACENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.7.7.48); HELICASE).
HEPATITIS E VIRUS (STRAIN BURMA) (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.":
VIROLOGY 185:120-131(1991).
-1- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A40778; MNWWHE.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                        TAM A.W., SMITH M.M., GUERRA M.E., HUANG C.-C., BRADLEY D.W., FRY K.E., REYES G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
C560BE14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86; DB 1; L
Pred. No. 1.92e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
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1693 AA; 185191 MW;
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Local Similarity 25.4%;
les 17; Conservative
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 92024067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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FDPSTGA 71
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POLN_HEVPA
P33424;
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EUKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
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Pred. No. 9.43e-04;
22; Mismatches 24; Indels
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-!- SIMILARITY: BELONGS TO THE UPF0017 FAMILY.
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
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1693 AA; 185215 MW; FFCB786D CRC32;
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
011-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LOTE EMBRYOGENESIS ABUNDANT PROTEIN EMBB.
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Best Local Similarity 34.0%;
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                                                     Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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VITAMIN D-BINDING PROT
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(1-78) from PCTUS9913024.pep (5 of 12)
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The 5'-terminal sequence of the hepatitis C virus genome. PC1285
                                                                                                                                                                                                                                                                                                                                                                             ##status preliminary ##molecule_type genomic RNA ##residues 1-3011 ##label OKA ##cross-references EMBL:D10749; NID:g221586; PID:d1002057; PID:g221587
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#formal_name hepatitis C virus
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#journal Mamm. Genome (1995) 6:476-480
#title The murine form of TXK, a novel TEC kinase expressed title thymus maps to chromosome 5.
#cross-references WilD:96059336
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submitted to the EMBL Data Library, March 1992
840770
Best Local Similarity 44.4%; Pred. No. 2.96e+00;
Matches 12; Conservative 7; Mismatches 8; Indels
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7; Mismatches 8; Indels
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Hum. Mol. Genet. (1994) 3:897-901
TXK, a novel human tyrosine kinase expressed in T cells shares sequence identity with Tec family kinases and maps
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tyrosine Kinase - human
#formal_name Homo sapiens #common_name man
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#map_position 4p12-4p12
CLASSIFICATION #superfamily protein-tyrosine kinase tec; pleckstrin re
homology; protein kinase homology; SH2 homology; SH3
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                S55092 #type complete
hypothetical protein YMR210w - yeast (Saccharomyces
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#domain SH2 homology #label SH2\
#domain protein Kinase homology #label KIN
#length 527 #molecular weight 61239 #checksum
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submitted to the EMBL Data Library, June 1995
S55092
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                                                         hypotherical protein YM8261.04
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-sep-1995
04-sep-1998
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Pred. No. 2.15e+00;
18; Mismatches 22
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Pred. No. 2.15e+00;
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#cross-references MUID:95038742
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Best Local Similarity 27.1%;
Matches 16; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
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#authors Hu, Q.; Davidson, D.; Schwartzberg, P.L.; Macchiarini, F.;
#fauthors Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.
#journal J. Biol. Chem. (1995) 270:1928-1934
#title Identification of rlk, a novel protein tyrosine kinase with predominant expression in the T cell lineage.
#cross-references MUID:95130578
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Nature (1998) 392:353-358

The complete genome of the hyperthermophilic bacterium
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                 flagellar L-ring profein FlgH - Aquifex aeolicus
*formal_name Aquifex aeolicus
08-May-1998 *sequence_revision 08-May-1998 *text_change
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protein-tyrosine kinase (EC 2.7.1.112) rlk - mouse
resting lymphocyte kinase
#formal_name Mus sp. #common_name mouse
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
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#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase AFP-binding motif
#length 527 #molecular-weight 61108 #checksum 785
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Pred. No. 2.96e+00;
25; Mismatches 16; Indels
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#type complete
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##cross-references GB.AE000752; N
##experimental_source strain VF5
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#cross-references MUID:98196666
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Wu, D.; Cao, X.L.; Bai, Y.Y.; Aronson, A.I.
FEMS Microbiol. Lett. (1991) 81:31-36
Sequence of an operon containing a novel delta-endotoxin gene from Bacillus thuringlensis.
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Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
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hypothetical protein Rv2913c - Mycobacterium tuberculosis
(strain H37RV)
#formal_name Mycobacterium tuberculosis
#formal_1998  #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501 FISEKYGNGGDSLRFELSNPTARYTLRGNGNSYNLYLRVSSIGSSTIRVTINGRVYTANV 560
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                                                  #formal_name Bacillus thuringiensis
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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#formal_name phage phi-C31
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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delta-endotoxin
#length 622 #molecular-weight 69729 #checksum
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Pred. No. 1.56e+00;
17; Mismatches 24; Indels
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##cross-references EMBL:X76288; NID:9432610; PID:9579071
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Pred. No. 1.13e+00;
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##cross-references EMBL:X57252; NID:940283; PID:940286
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##residue
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                         delta-endotoxin
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Local Similarity 18.2%;
Nes 12; Conservative
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Best Local Similarity 24.1%;
Matches 14; Conservative
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S38913
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T.K., a novel human tyrosine kinase expressed in T cells shares sequence identity with Tec family kinases and maps
                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references GB:Z74024; GB:AL123456; NID:g3250700; PID:e1301028;
PID:g3250707
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III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D. Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S. Murphy, L.; Ollver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squeres, B.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature (1998) 393:537-544
Deciphering the bloiogy of Mycobacterium tuberculosis from the complete genome sequence.
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tyrosine kinase - human (fragment)
#formal_name Homo saplens #common_name man
29-May-1998 #sequence_revision 29-May-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haire, R.N.; Ohta, Y.; Lewis, J.E.; Fu, S.M.; Kroisel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rv2913c
#length 611 #molecular-weight 67204 #checksum 9971
                                                                                                                                                                                                                                                                                                                              preliminary; nucleic acid sequence not shown;
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Pred. No. 2.15e+00;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%; Score 83; DB 2; Len Similarity 43.5%; Pred. No. 1.56e+00; 10; Conservative 5; Mismatches 8;
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                                                                                                                                                                                                                                           the complete genome sequence. tcross-references MUID:98295987
                                                                                                                                                                                                                                                                                                                                                       translation not shown
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#accession I38375
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Matches 12; Conservative
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##molecule_type DNA
##residues 1-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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RESULT

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##cross-references GB:AE001308; GB:AE001273; NID:q3328766; PID:q3328771 ##experimental_source serotype D, strain UM-3/Cx
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Hepatitis E virus (HEV): strain variation in the nonstructural gene region encoding consensus motifs for an RNA-dependent RNA polymerase and an ATF/GTP binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley D.W.; Fry, K.E.; Reyes, G.R.
#journal virology (1991) 185:120-131
#title Hepatitis E virus (HEV): molecular cloning and sequencing the full-length viral genome.
#cross-references MuID:92024067
#accession A40778
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##residues 967-1693 ##label FRY
##residues 967-1693 ##label FRY
##cross-references GB:M32400; NID:g330021; PID:g330022
##note sequence extracted from NCBI backbone (NCBIN:104572,
NCBIP:104573)
IFICATION #superfamily hepatitis E virus nonstructural protein
RDS ATP; nonstructural protein; nucleotidyltransferase
#length 1693 #molecular-weight 185191 #checksum 6520
                                                                                                                                                                                                                                                                                                                            63 IAESYLQQSFLSEDTYIR-KSAIIGA-GLSGSSEA-LELLSEAIETQDLYEQL-L-ILNA 117
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RNA-directed RNA polymerase (EC 2.7.7.48)
#formal_name hepatitis E virus
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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22; Mismatches 25; Indels
                                                                                                                                                                                                                                        Score 89; DB 2; Length 566;
Pred. No. 2.14e-01;
25; Mismatches 18; Indels
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##residues 1-1693 ##label TAM
##cross-references GB:M73218; NID:g330024
RWCF A48547
                                                                                                                                                                                                 #length 566 #molecular-weight 63507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86;
                                    ##status
##molecule_type DNA
##residues 1-566 ##label ARN
#cross-references MUID:99000809
#accession G71525
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#accession A48547
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Best Local Similarity 26.2%;
Matches 17; Conservative
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Similarity 25.4%;
17; Conservative
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#title The complete nucleotide sequence of region 1 of the CFA/I
finbrial operon of human enterotoxigenic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jordi, B.J.; Willshaw, G.A.; van der Zeijst, B.A.; Gaastra
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Dev. Genet. (1990) 11:299-309
Characterization of IMP-E3, a gene active during imaginal
disc morphogenesis in Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C56617 #type complete
cfaC protein precursor - Escherichia coli plasmid NTP113
#formal_name Escherichia coli
05-7an-1996 #sequence_revision 05-Jan-1996 #text_change
20-Mar-1998
ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster) #formal_name Drosophila melanogaster 31-Dec-1993 *text_change 16-Feb-1997 *A61046
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DS membrane protein
IX #length 331 #molecular-weight 36583 #checksum 8221
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Pred. No. 8.12e-01;
14; Mismatches 8;
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Pred. No. 8.12e-01;
12; Mismatches 18
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##residues
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larity 32.4%;
Conservative
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Best Local Similarity 31.9%;
Local 15; Conservative
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##residues 1-33
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.25 Seconds 500.410 Million cell updates/sec Wed Sep 1 16:13:51 1999; Run on:

not generated fabular output Description: Perfect Score:

.....GLHLRVFDPSTGALVDSKSY 78 >PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 1 MEKFWAEFGOGYVQTPFLSE......GLHLRV Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 37.846; Variance 68.015; scale 0.556 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7.69e-02 2.14e-01 8.12e-01 1.13e-01 1.15e-00 1.15e-00 2.15e-00 2.15e-00 2.15e-00 2.15e-00 2.15e-00 2.15e-00 3.15e-00 4.05e-00 4.05e-00 4.05e-00 4.05e-00 5.55e-00 6.05e-00 6.05e-Tak - mouse polyprotein precursor hypothetical protein GRESAG protein - yeast glucan 1,4-alpha-gluc vitellogenin precurso genome polyprotein - hypothetical protein vitamin D-binding pro hypothetical protein probable OMP [leader genome polyprotein -ecdysone-induced memb cfaC protein precurso parasporal crystal pr hypothetical protein hypothetical protein tyrosine kinase - hum hypothetical protein tyrosine kinase - hum flagellar L-ring prot protein-tyrosine kina Description SUMMARIES S61248 G71525 A61046 C56617 C56617 C56617 C189375 S139375 S139375 S14200 S46123 ü DB Query Match Length 299 1696 869 869 869 282 282 611 611 171 171 171 171 171 1659 3011 3011 472 Score Result No No

5.556 5.556 5.556 6.556	change ', V.; Rock, ' the bovine gene is simplex in	4; Gaps 4; trachomatis t_change
vitamin D-binding pro 5 vitamin D-binding pro 5 parasporal crystal pr hypothetical protein 5 hypothetical protein 5 probable membrane pro 7 xaa Pro dipeptidase h 7 parasporal crystal pr parasporal crystal pr probable membrane pro 7 genome polyprotein - ribosomal protein - 1 cholesteryl ester tra 1 pepB protein - stery 1 N-methyl D-aspartate 1 rich protein - human 1	vine herpesvirus 1 ssvirus 1 ission 18-Sep-1997 #text_ Z.; Kutish, G.F.; Paces chwyzer, M. a Library, January 1995 sis of a 30-kb region of itch exhibits a colinear ill to UL4 genes of herpe g971311; PID:g971327 sster virus gene 53 prote	DB 2; Length 299; 7.69e-02; tches 6; Indels ALL 79 11: ALV 73 peptide] - Chlamydia Cx) Cx) Chomatis sion 13-Sep-1998 #tex i. Lammel, C.J.; Fan, I. W.P.; Olinger, L.; E.V.; Davis, R.W. gate intracellular pa
VYHUD S39787 F71000 S57080 E64757 C69960 A29913 T00758 C12053 C12	Type complete bovine herpe bovine herpe sequence_real sequence_real bovine herpe strike for the form of the form o	คี ยี ของเลีย ก็ม เรื่อง
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RESULT

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For region 1.71

GB2212511-A.

GB-NOV-1988; G27024.

R-NOV-1987; US-122714.

GHR) Chiron Corporation.

GHR) Chiron M. Choo QL, Kuo G;

WPI: 89-215054/30.

N-PSDB; N90319.

The pattitis C virus gene - used for prodn. of polynuclectide probes, polypeptide(s) and antibodies for diagnosis, prevention and treatment of infection.

The sequence is the peptide encoded by the hepatitis C virus care used to diagnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines.

The region shown overlaps with clone 25c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.5%; Score 80; DB 1; Length 170; Best Local Similarity 37.8%; Pred. No. 3.26e+01; Matches 17; Conservative 11; Mismatches 13; Indels
                                p90150;
1-NOV-1989 (first entry)
Sequence of hepatitis C virus cDNA insert in clone 14c
Hepatitis C virus; clone 14c; clone 25c; probe; vaccine.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 15
P90150 standard; protein; 170 AA.
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Search completed: Wed Sep 1 16:15:06 1999 Job time : 37 secs.

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New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea controlling lepidopteran pests, especially Ostrinia nubilalis, Fages 36-38; 50pp; Engdish.

This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Strinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
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Amino acid sequence of lepidoteran-active 8612 toxin.
8612 toxin; PCR; primer; amplification; Bacillus thuringlensis; probe;
lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 fisekfgnqgdslrfeqsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV genes and the corresponding proteins - used in the production of anti-HCV antibodies and the detection of HCV infection claim 11; Pages 18-32; 35pp; Japanese. (74770 encodes R66995 the HC-J1/protein, the cDNA can be used in the construction of an expression vector for the transformation of a host cell; and then be used in the production of proteins and peptides, useful in the preparation of monoclonal and polyclonal HCV-specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1995 (first entry)
Hepatitis C virus gene HC-01/protein.
Hepatitis C virus; HCV gene HC-J1/protein; specific antibodies.
Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches 23; Indels
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Pred. No. 2.27e+01;
                                                                                                                                  13-MAR-1997; US-040512.
(MYCO ) MYCOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
WPI; 98-506734/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 12
R66995 standard; Protein; 3011 AA.
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                                                   Helicoverpa zea; hybridisation.
Bacillus thuringiensis.
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22.08;
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10-DEC-1993; 345753.
10-DEC-1992; JP-360705.
                                                                                                         17-SEP-1998.
13-MAR-1998; U05081
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Best Local Similarity
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N-PSDB; Q74770.
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                                                                                        WO9840490-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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ID R4
AC R4
DT 27
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Purified hepatitis C virus

and associated nucleic acids and polypeptide(s)

claim 13: Figure 18: 139pp: English.

It is the sequence encoded in the hepatitis C virus (HCV) cDNA insert in clone 14c. Tag a - the region of overlap with the HCV antigen encoded in clone 25c. It is an epitope which could be used as immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insert in clone 14c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplification using nested primers resulted in 7 adjacent HCV DNA fragments which could be assembled into a full-length sequence. The DNA sequence was determined and translated into the genomic amino acid sequence. Comparison of the LG genomic amino acid sequence comparison of the LG genomic amino acid sequence with that from HCV-1 showed 134 amino acid differences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New plasmid pHCV-162 is a mammalian expression systems for HCVD proteins - useful for diagnosing HCV infection and as vaccines for preventing HCV infection and as vaccines Example 1; page 39-49; 100pp; English.

RNA was isolated from the plasma of a HCV seropositive human (designated "LG") and cDNA was prepared from it. The CDNA was PCR amplified using specific primers with sequences based on the prototype HCV-1 CDNA sequence (GENBANK M62321). Further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
..
HCV genomic amino acid sequence isolated from infected human I
Hepatitis C Virus; Non-A, non-B hepatitis Virus; HCV; NANBHV;
human growth hormone; HGH; secretion signal; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1990 (first entry)
Sequence encoded in the hepatitis C virus (HCV) cDNA inse
Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2116 vpspeffteldgvrlh-rfappckpllrdevsfrvglhdypvgsq 2159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
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                                                                                                                                                                                                                                                                                                                                            Desai SM, Devare SG, Frail DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.7%; Score 81; DB 8; L. Best Local Similarity 40.0%; Pred. No. 2.72e+01; Matches 18; Conservative 10; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 1; L
Pred. No. 3.26e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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14-NOV-1988; US-271450; US-122714.
(CHIR) Chiron Corp.
HOUGHLON M, Choo q-L, Kuo G;
WPI; 89-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P92033 standard; protein; 170 AA
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Best Local Similarity 37.8%;
Matches 17; Conservative
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/*tag= a
                                                                                                                                                                                                   05-AUG-1993,
29-JAN-1993; U00907,
31-JAN-1992; US-830024,
(ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                        Bode Si, Casey JM, I
Yamaguchi J, Zeck BJ;
WPI; 93-258673/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3011 AA;
                                                                                                                                 Hepatitis C Virus.
WO9315193-A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis E virus infection
Disclosure; Pages 11-15; 204pp; English
Disclosure; Pages 11-15; 204pp; English
Disclosure; Pages 11-15; 204pp; English
This represents a hepatitis E virus (HEV) open reading frame (ORF)-1
Protein encoded by a DNA sequence designated SAR-55. SAR-55 also encodes
HEV ORF-2 and ORF-3 proteins. A host organism transformed or transfected
with a recombinant expression vector containing the SAR-55 nucleic acid
can be used to produce the HEV proteins, especially ORF-2 protein. The
recombinant HEV proteins can be used as diagnostic agents and as vaccines
for use against HEV infection. The detection of antibodies specific for
HEV can be used for the diagnosts of infection and diseases caused by
HEV, and for monitoring the progression of such disease. Such methods are
also useful for monitoring the efficacy of therapeutic agents during the
course of treatment of HEV infection and disease in a mammal. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of lepidoteran-active HD525 toxin.
HD525 toxin: PCR: primer: amplification: Bacillus thuringlensis; probe lepidoptera; pest; pesticide; Ostrinia nubilalis; Hellothis virescens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 frtsfydgayletngperhnlsfdasgstmaagpfsltyaasaagleyryvaagldhray 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis E virus (HEV) ORF-1 protein.
Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
passive immunisation; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for detection or for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hepatitis E virus DNA from Pakistani strain SAR-55 - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%; Score 86; DB 37; Length 1693; 25.4%; Pred. No. 1.09e+01; vative 22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1998; U07418.
11.APR-1997; US-840316.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
EMERSON SU, PUTCELL RH, RObinSON RA, TSAREV SA;
WPI; 98-568733748.
                                                                                                                                                                                                                                                                                                                                       GTG"
                                                                                                                                                                                                                                                                                                                                                                                    *
000
                                                                                                                                                                                                                                             'note= "encoded by CAG"
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(MYCO ) MYCOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /note= "encoded by
1662
                                                                                                                                                                                                                                                                                          'note- "encoded by
                                                                                                                                                                                                                                                                                                                                                                                  "encoded by
                                          standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W75774 standard; Protein; 633 AA.
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Bacillus thuringiensis.
WO9840490-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W75774;
02-DEC-1998 (first entry)
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies can be used
                                                                                                                                                                                                                       Misc_dlfference 1238
                                                                                                                                                                                                                                                                     Misc_difference 1244
                                                                                                                                                                                                                                                                                                             Misc_difference 1352
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13-MAR-1998; U05081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                          Hepatitis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632 fapgvsp 638
                                                                                                                                                                                                                                                                                                                                                            Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 98-568733,
N-PSDB; V71604
                                                                                   02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                  T 8
W81519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammals
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controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea (Laim Hi, Pages 32.34; 50pp; English.

This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the me sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë,
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A positive clone ET1.1 was identified in a library prepared from bile of cynomolgus monkeys infected with the Burma strain of ET-NANB. Both strands of ET1.1 were sequenced. Identity of the sequence with sequences in etiologic agents has been confirmed by locating a similar sequence in a viral strain isolated in Burma. This protein is sencoded by the longest ORF (ORF 1) of the Burma strain. Sequence 1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 frtsfødgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    511 fisekfgngsdslrfegsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 YVQTPFLSESNSVRYKIS-IAGSCPLSTAGPSYVKF-QDNPVGSQTFSAGLHLRVFDPS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Protein encoded by ORF 1 of Burmese ET-NANB viral strain.
Protein encoded by ORF 1 of Burmese ET-NANB viral strain.
Enterically transmitted non-A, non-B hepatitis virus. hepatitis
Enterically transmitted non-A, non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New viral proteins from non A-non-B hepatitis agent - used to treat and prevent enterically-transmitted non-A non-B hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84; DB 3; Length 1693
Pred. No. 1.57e+01;
20; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches 23; Indels
useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN.
Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ,
                                                                                                                                                                                                                                                                                                                                                                                                             Score 85; DB 35;
Pred. No. 1.31e+01;
New insecticidal Bacillus thuringiensis toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
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W75775 standard; Protein; 633 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r 10
R14618 standard; Protein; 1693
R14618;
                                                                                                                                                                                                                                                                                                                                                                                                                15.4%;
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Local Similarity 26.6%;
les 17; Conservative
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02-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-1991.
05-APR-1991; U02368.
05-APR-1990; US-505888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Disclosure; Pages 9-13, 121pp; English.

The present sequence is the protein prod. of ORF-1 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enertically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. 196 or 19M) in blood, plasma, crebbrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunishing an animmal against HEV infection. The protein is identified as a band of greater than
                                                                                                                                                                                                                                                                                                                                          572 frtsfvdgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                                                                                        Hepatitis E virus proteins - useful for diagnosis or vaccine production the virus claim 22; Columns 57-66; 47pp; English.

Claim 22; Columns 57-66; 47pp; English.

Wa0196-98 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF; sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB.
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                           /note- "10 bp nucleic acid sequence TGGTNTTYGA has to be inserted between nucleotides 4390..4391 of 127394 before these amino acid residues can be decoded"
                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F91813,
26-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 ORF-1.
Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
Structural region; antigen; detection; antibody; vaccine;
                                                                                                                                                                                                                                                                                    Score 86; DB 36; Length 1693;
Pred. No. 1.09e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated and purified hepatitis E virus strain SAR-55 DNA
                                                                                                                                                                                                                                                                                                                22; Mismatches 25; Indels
                                       Tam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "corresponding codon CAG"
                                       Reyes GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-1995; U13102.
03-OCT-1994; US-316765.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Purcell RH, Tsarev SA;
WPI; 96-209320/21.
N-PSDB; T27394.
                         (GENE-) GENELABS TECHNOLOGIES INC.
Bradley DW, Fry KE, Krawczynski KZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
misc_difference 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R91813 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                     15.6%;
25.4%;
                                                                                                                                                                                                                                                                                                                17; Conservative
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05-JUL-1990; US-505888
              US-475807
                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                98-582599/49.
                                                                                                                                                                                                                                                                                                                                                                                              632 fapgvsp 638
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                                                                               N-PSDB; V66321
                                                    Yarbough PO;
                                                                                                                                                                                                                                                           Sequence
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572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
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                                                                                                                                                                                                                                                  protein production
Disclosure, Columns 55-64; 45pp; English.
W71209-11 represent the proteins encoded by the open reading frames W71209-11 represent the proteins encoded by the open reading frames transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as EFF), detecting ET-NANB in infected samples, e.g. by specific amplification of virus-derived DN sequences and for producing recombinant viral proteins for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-0c1-1998 (first entry)
Protein encoded by ORF 1 of the Burmese isolate of ET-NANB.
Enterically transmitted nonA/nonB hepatitis virus; identification;
HEV; ET-NANB; detection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis E virus DNA - useful for e.g. virus detection and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781.
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                                                                                                                           Length 1693;
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15.6%; Score 86; DB 34; Length 169
Best Local Similarity 25.4%; Pred. No. 1.09e+01;
Matches 17; Conservative 22; Mismatches 25; Indels
                                                                                                                                                                      25; Indels
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(GENE-) GENELABS TECHNOLOGIES INC.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam A,
                                                                                                                         Score 86; DB 19;
Pred. No. 1.09e+01;
                                                                                                                                                                        22; Mismatches
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Misc_difference 1552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           W71209 standard; Protein; 1693 AA.
                                                                                                                      Query Match
Best Local Similarity 25.4%;
Matches 17; Conservative
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US-367486.
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                                                                          1693 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis virus.
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19-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-0CT-1989;
05-APR-1990;
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                                                                            Seguence
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Length 623;

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This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD573 toxin.
HD573 toxin: PCR: primer: amplification; Bacillus thuringiensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation [Claim 10; Page 17-24; 29pp; Japanese. This sequence represents a Hepatitis E viral hollow particle protein. This sequence represents a Hepatitis E viral hollow particle protein. This polypeptides can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frtsfydgayleangperynlsfdasgstmaagpfsptyaasaaglevryvaagldhrav 631
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                                                Hepatitis E virus hollow particle protein #1.
Hollow particle protein; virus; antibody; detection; immunoassay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 17.4%; Score 96; DB 35; I Local Similarity 26.9%; Pred. No. 1.66e+00; les 18; Conservative 21; Mismatches 25;
                                                                                                                                                                                  1..1693
/note= "Partial`sequence"
                                                                                                                                                                                                                                                                                       28-FEB-1997; 062445.
28-FEB-1997; JP-062445.
(DENK-) DENKA SEIKEN KK.
(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
WPI: 98-535037/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1998. USD81.
13-MAR-1998 (USD81.
13-MAR-1997) US-040512.
(MYCO ) MYCOGEN CORP.
MULLET-COAN J , Narva KE, Schnepf HE;
N-PSDB; V52610.
                                                                                                                                                        Location/Qualifiers
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W75773 standard; Protein; 623 AA.
                      03-DEC-1998 (first entry)
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WO9840490-Al.
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                                                                                                                               Hepatitis virus.
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                                                                                                     infection
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                                                                                                                                                                                  Protein
W76368;
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A (USSH ) US SEC DEPT HEALTH.

Emerson SU, Purcell RH, Tsarev SA;

NPI: 94-118462/14.

R-PSDB: 045197.

Purified hepatitis E strain SAR-55 virus - used to develop prods.

To use in detection, diagnosis, vaccines and therapy of hepatitis E virus infection, diagnosis, vaccines and therapy of hepatitis E virus infection.

The sequences given in R51264-66 are encoded by the hepatitis E virus infection in R51264-66 are encoded by the hepatitis E virus infection in R51264-66 are encoded by the hepatitis E virus infective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. The HEV SAR-55 CDNA was isolated from primates innoculated with stool successive in the stool served in the stool served successive in the served su
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                                                                                                                                                                         Gaps
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Pred. No. 1.09e+01;
22; Mismatches 25; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by ORF1 of ET-NANB (HEV) Burma strain DNA sequence. Enterically transmitted non A non B hepatitis virus; ET-NANB; Hepatitis E virus; HEV; Burma HEV isolate; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORF;
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7
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HEV strain protein encoded by ORF-1.
Hepatitis E virus; HEV; strain SAR-55; open reading frame; Cantibody; detection; diagnosis; primates; stool suspension.
W09406913-A.
                                                                     26; Mismatches 26; Indels
      DB 35;
9.05e+00;
      Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                R51264 standard; Protein; 1693 AA.
R51264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             л 5
W80196 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.4%;
Marches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic probe.
Non A non B Hepatitis virus.
US5824649-A.
Query Match 15.8%;
Best Local Similarity 18.2%;
Matches 12; Conservative
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17-SEP-1993; UO8849.
18-SEP-1992; US-947263.
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US-279823.
US-208997.
US-336672.
US-367486.
US-420921.
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07-JUN-1995; 4
25-JUL-1994; U
117-JUN-1988; U
116-JUN-1989; U
13-OCT-1989; U
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266+01 25

80 14.5 499 38 W67010 80 14.5 509 20 W08378 80 14.5 516 6 R3378 80 14.5 516 6 R33575 80 14.5 516 6 R33575 80 14.5 516 7 R33441 80 14.5 516 7 R33441 80 14.5 758 7 R33535 80 14.5 7766 1 P92041	14.5 2261 1 P90164 14.5 2301 1 P92047 14.5 2435 5 R25135 14.5 2436 5 R28582 14.5 2436 1 P92050 14.5 2462 1 P90288 14.5 2772 2 R06123	80 14.5 2816 7 R34009 HCV-1 polyprotein. 80 14.5 2894 5 R24440 Composite HCV HC-J 80 14.5 2894 13 R70230 Composite hepatitis 80 14.5 2955 2 R08124 Hepatitis C virus	80 14.5 3011 16 R90931 80 14.5 3011 4 R21519 80 14.5 3011 26 W40480 80 14.5 3011 28 W40038 80 14.5 3011 6 R31621	79 14.3 458 23 79 14.3 458 11	RESULT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		PA (GOLD/) GOLDBERG E B. PI GOLDBATG EB; DR WPI: 96-221942/22. DR N-PSDB; T29053. PT New proteins derived from T4 phage tail fibre proteins - that c PT self assemble into nano-structure(s), useful as filters etc, all presents of the contractions
(MZ)	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd MPsrch_pp protein - protein database search, using Smith-Waterman algorithm	Run on: Wed Sep 1 16:14:29 1999; MasPar time 5.88 Seconds 281.992 Million cell updates/sec	Title: >PCT-US99-13024-2 Description: (1-78) from PCTUS9913024.pep (5 of 12) Perfect Score: 551 Sequence: 1 MEKFWAEFCQGYVQIPFLSEGLHLRVFDPSTGALVDSKSY 78	Scoring table: PAM 150 Gap 11 Searched: 170751 seds, 21266608 residues	essing:	Database: a-geneseq35 1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38	Statistics: Mean 26.730; Variance 108.537; scale 0.246 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Gaps New proteins derived from T4 phage tail fibre proteins - that can self assemble into nano-structure(s), useful as filters etc, also corresponding DNA
claim 7; Fig 7; Bipp; English.
A protein (R97371) of unspecified function is the product of open reading frame X of the tail fibre protein gene region (see also 1729053) of phage T4. This gene region also includes open reading frames for tail fibre proteins (see also R97370 and R97372-74).
Tail fibre proteins (active or modified) can be produced in large quantities in microbial cells and used as building blocks of strong, Stable nanostructures. 56 ö Length 65; Match 54.4%; Score 300; DB 19; Length 65 Local Similarity 82.1%; Pred. No. 1.22e-19; les 46; Conservative 3; Mismatches 7; Indels Query Match Best Local S Matches 4 셤 ò

1.22e-19 1.66e+00 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.09e+01 1.31e+01 1.31e+01 1.57e+01 2.72e+01 2.72e+01 3.26e+01 3.26e+01

Phage T4.ORFX gene pr Hepatitis E virus hol Amino acid sequence o HEV strain protein en Protein encoded by OR Hepatitis E virus str Protein encoded by OR Hepatitis E virus (HE Amino acid sequence o Protein encoded by OR Amino acid sequence o Hepatitis C virus gen HCV genomic amino aci Sequence encoded in t Sequence of hepatitis HCV NSS domain antige

R97371 W76368 W76368 W80196 W80196 W815109 W815109 W75774 W75774 R75774 R75774 R75774 R75775 R75775

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55.4.4 11.5.6 11.5.6 11.5.6 11.5.6 11.6.7

300 940 860 860 880 880 880 880 880 880 880

Pred.

SUMMARIES

ВВ

Length

Score

Result

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RESULT 2 ID W76368 standard; Protein; 1693 AA

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VIBRIO CHOLERAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
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                                                                                                                         Ouery Match 19.4%; Score 78; DB 14; Length 3011; Best Local Similarity 35.6%; Pred. No. 2.91e+00; Matches 16; Conservative 12; Mismatches 13; Indels 4
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Best Local Similarity 29.0%; Pred. No. 4.04e+00;
Matches 9; Conservative 14; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                           2116 IPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 2159
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-E7946 EL TOR;
FIORE A.E., KAPER J.B.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U50074; G1236642: -..
SEQUENCE 418 AA: 47600 MW; 408D6983 CRC32;
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01-NOV-1996 (TREWBLREL. 01, CREATED)
01-NOV-1996 (TREWBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREWBLREL. 08, LAST ANNOTATION UPDATE)
LECITHINASE.
POLYPROTEIN.
SEQUENCE 3011 AA; 327184 MW; BB4B08D3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 418 AA
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Search completed: Wed Sep 1 16:10:34 1999 Job time: 24 secs.

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SEQUENCE
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BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAXHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEPATITIS C VIRUS STRAIN H77.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
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MEDLINE; 97385173.
YANAGI M., PURCELL R.H., EMERSON S.U., BUKH J.;
TARASI M., PURCELL R.H., EMERSON S.U., BUKH J.;
"Transcripts from a single full-length cDNA clone of hepatitis C
virus are infectious when directly transfected into the liver of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H77;
MEDLINE; 97385177;
MEDLINE; 97385170;
YANAGI M., PURCELL R.H., EMERSON S.U., BUKH J.;
YANAGI M., PURCELL R.H., EMERSON S.U., BUKH J.;
"Transcripts from a single full-length cDNA clone of hepatitis C
virus are infectious when directly transfected into the liver of
                                                                                                                                                                                                                                                                                                                                                                      2;
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                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
EMBL; AEGOO137; G1786500; -
SEQUENCE 70 AA; 7854 MW; B754D938 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 14; Length 301
Pred. No. 2.91e+00;
12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                           Ouery Match 19.4%; Score 78; DB 2; Length 70; Best Local Similarity 44.0%; Pred. No. 2.91e+00; Matches 11; Conservative 9; Mismatches 3; Indels
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN.
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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EMBL; AF011751; G2327071; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chimpanzee.";
PROC. NATL. ACAD. SCI. U.S.A. 94:8738-8743(1997)
EEMBL, AF011753; 62327075; -.
PFAM; PF00998; HCV_RGRR; 1.
PFAM; PF01001; HCV_NS4b; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    47 QVYVQTSYLSQQSSIIRYT-AFTGP 70
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Local Similarity 35.6%;
les 16; Conservative
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036608;
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYPROTEIN.
HEPATITIS C VIRUS (HCV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE: FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEPATITIS C VIRUS STRAIN H77.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YANAGI M., PURCELL R.H., EMERSON S.U., BUKH J.;
Transcripts from a single full-length cDNA clone of hepatitis C virus are infectious when directly transfected into the liver of chimpanzee ";
PROC. NATL. ACAD. SCI. U.S.A. 94:8738-8743(1997).
BEMBL, AF0101752, G2327073; --
PFAM; PF01009; HCV_RGRP; 1.
PFAM; PF01000; HCV_NSAb; 1.
PFAM; PF01006; HCV_NS4b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE; 97373636.
KOLYKHALOV A.A., AGAPOV E.V., BLIGHT K.J., MIHALIK K., FEINSTONE
                                                                                                                                                                     4
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Pred. No. 2.91e+00;
                                                                                                                 Score 78; DB 14; Length 3011;
Pred. No. 2.91e+00;
                                                                                                                                                                   12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2116 IPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 2159
                                                                                                                                                                                                         2116 IPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 2159
                                                                                                                                                                                                                                   13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 13
03609
036609
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3011 AA; 327262 MW; 26388444 CRC32;
                                                                                 3011 AA; 327114 MW; A987CA50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08,
                                                                                                                          Query Match 19.4%;
Best Local Similarity 35.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 19.4%;
Local Similarity 35.6%;
hes 16; Conservative
PFAM; PF00998; HCV_RdRP; 1.
PFAM; PF01001; HCV_NS4b; 1.
PFAM; PF01006; HCV_NS4a; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97385173.
                                                              POLYPROTEIN. SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H77
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[2]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
DU Z., GATTUNG S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESCHERICHIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 9
059003
059003;
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               SPREER
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
HEPATITIS C VIRUS (HCV).
HEPATITIS C VIRUS (HCV).
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; META2OA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                          3,
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                                                                                                                         Score 80; DB 3; Length 802;
Pred. No. 1.50e+00;
                                                                                                                                                                                    10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1666 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
CHOO Q.L., RICHMAN K., HAN J.;
SUBMITTED (AMX-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
BLBMITTED (AMX-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
PFAM; PF00998: HCV_RGRP; 1.
PFAM; PF01001; HCV_NS4b; 1.
PFAM; PF01006; HCV_NS4b; 1.
                                                                                                                                                                                                                                                  663
                                                                                                                                                                                                                                                                                                             20
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO GLUTAMATE DECARBOXYLASE.
                                                                                                                                                                                                                                                                                 10 QGY-VQTPF-LSESNSVRYKISIAGSCPLSTAGPSYVKFQDNP
                                                                                                                                                                                                                                               622 QGYGSQPPIPMNQSYG-RYQTSIPPPPPQQQIPQGYGRYQAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
2436 2436
2436 AA; 264734 MW; 3CF4508C CRC32;
EMBL; D37935; D1007731; -.
PFAM; PF00076; rrm; 1.
SEQUENCE 802 AA; 90437 MW; 54BF0DFF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 19.9%;
Local Similarity 37.8%;
                                                                                                                         Query Match 19.9%;
Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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NATURE 368:32-38(1994).
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NON_TER
SEQUENCE
                                                              SEQUENCE
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017456
017456;
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081756
081756;
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KANARABATASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHPUKU Y.,
SUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KINGCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).
EMBL; AP000006; D1031349; -. SEQUENCE 860 AA: 95455 MW; B336F868 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P75688 PRELIMINARY; PRT: 70 AA. P75688 P75689 P75689 P75689 P75689 P75689 P75689 P7668 P7668
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19.7%; Score 79; DB 1; Length 860;
Best Local Similarity 28.0%; Pred. No. 2.10e+00;
Matches 7; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 79; DB 5; Length 542;
Pred. No. 2.10e+00;
11; Mismatches 10; Indels
DU 2., GATTUNG S.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                         STRAIN-BRISTOL N2;
WATERSTON R.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U50312; 61226312; -.
SEQUENCE 542 A3; 61133 MW; A7C148AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
860AA LONG HYPOTHETICAL PROTEIN.
PH1302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GFLL-PFLEE-DEIRYDFRVPGVSSISADSHKY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKFLTDFSNAFIRVAFKYNSYEAR 25
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Best Local Similarity 30.3%;
Matches 10; Conservative
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STRAIN-K-12;
MEDLINE; 97426617.
                                                                                                                          SEQUENCE FROM N.A.
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Gaps

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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
ANDERIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBLIN R., FAVELLO A., FULTON L.,
CRAXTON M., DEAR S., DU Z., DURBLIN R., FAVELLO M., TOHNSTON L.,
A GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
AMALDON N., SMITH A., SONHHAMMER E., STADEN R., SULSTON J.,
ANTONE JA., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T. 2.2 ND of CONTIGUOUS nucleotide sequence from chromosome III of C.
H. HIGHEN JASSE J., E1349927; -.
SQ SEQUENCE 357 AA; 41307 MW; D2FB4683 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SUGINOTO K., MATSUMOTO K., KORNBERG R.D., REED S.I., WITTENBERG C.;
SUGINOTO K., MATSUMOTO K., KORNBERG R.D., REED S.I., WITTENBERG C.;
"HMD1 of the yeast Saccharomyces cerevisiae encodes a putative
"NA/Single strand DNA-Dinding protein, whose overexpression reduces
the expression of a G1 cyclin, CLN3.";
SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METALOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA BINDING PROTEIN.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 5; Length 357;
Pred. No. 1.50e+00;
"".matches 6; Indels
                                                                              Pred. No. 1.50e+00;
11; Mismatches 13; Indels
                                                                                                                          140 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 183
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                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                           13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ
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(TREMBLREL. 09, LAST ANNOTATION UPDATE)
    1 1
275 275
275 AA; 30495 MW; 9BEIEE8B CRC32;
                                                                DB 14;
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007034 PRELIMINARY; PRT;
007034;
01-004-1996 (TREMBLREL: 01, CREATED)
01-NOY-1999 (TREMBLREL: 01, LAST SEO
01-JAN-1999 (TREMBLREL: 09, LAST SNN
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                                                             Match 19.9%;
Local Similarity 37.8%;
les 17; Conservative
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19.9%;
Best Local Similarity 45.8%;
Matches 11; Conservative
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01-JAN-1999 (TREMBLREL.
VC27A7L.1 PROTEIN.
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001993;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
HEPATITIS C VIRUS (HCV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
POLYPROTEIN (FRAGMENT).
POLYPROTEIN (FRAGMENT).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEVAITIIS C-LIKE VIRUSES.
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
HEPATITIS C VIRUS (HCV).
HEPATITIS C VIRUS (HCV).
HEPATITIS C-LIKE VIRUSES.
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Pred. No. 1.50e+00;
11; Mismatches 13; Indels
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Pred. No. 1.50e+00;
11; Mismatches 13; Indels
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STRAIN-PAITENT #2675;
VIZMANOS J.L.;
THESIS (1996), GENETICS DEPT., UNIVERSITY OF NAVARRA.
EMBL; U37645; G1173777; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-PATIENT #2675;
VIZMANOS J.L.;
THESIS (1996), GENETICS DEPT., UNIVERSITY OF NAVARRA.
EMBL; U37644; G1173775;
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THESIS (1996), GENETICS DEPT., UNIVERSITY OF NAVARRA
EMBL; U37646; G1173779; -.
                                                                                                                                                                                                1 1 275 275 275 275 AA; 6D967905 CKC32;
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30423 MW; 6DE9E548 CRC32;
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Best Local Similarity 37.8%;
Matches 17; Conservative
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Best Local Similarity 37.8%;
Matches 17; Conservative
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275 AA;
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protein - protein database search, using Smith-Waterman algorithm MasPar time 7.61 Seconds 401.470 Million cell updates/sec Wed Sep 1 16:10:10 1999; MPsrch_pp Run on:

Tabular output not generated.

> PCT-US99-13024-2 (1-56) from PCTUS9913024.pep (4 of 12) 402 1 MEKFWAEFGGGYVQTPFLSE......STAGPSYVKFQDNPVGSQTF 56 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 5:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 34.913; Variance 62.861; scale 0.555 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPTES

		•			SUMMARIES		
Result		Query					
No.	Score	Match	Match Length	DB	QI .	Description	Pred. No.
-	81	20.1	3011	14	003463	GENOME POLYPROTEIN.	1.08e+00
7	80	19.9	275	14	068468	POLYPROTEIN (FRAGMENT)	1.50e+00
Э	80	19.9	275	14	068467	POLYPROTEIN (FRAGMENT)	1.50e+00
4	80	19.9	275	14	068469		1.50e+00
S	80	19.9	357	ß	001993		1.50e+00
9	80	19.9	802	m	007034	RNA BINDING PROTEIN.	1.50e+00
7	80	19.9	2436	14	081756	POLYPROTEIN (FRAGMENT)	1.50e+00
80	79	19.7	542	Ŋ	017456	SIMILAR TO GLUTAMATE D	2.10e+00
σ	79	19.7	860	-	059003	860AA LONG HYPOTHETICA	2.10e+00
10	78	19.4	70	7	P75688	FROM BASES 311709 TO 3	2.91e+00
11	78	19.4	3011	14	036610	POLYPROTEIN.	2.91e+00
12	78	19.4	3011	14	036608	POLYPROTEIN.	2.91e+00
13	78	19.4	3011	14	036609	POLYPROTEIN.	2.91e+00
14	78	19.4	3011	14	036579	POLYPROTEIN.	2.916+00
15	77	19.2	418	~	056631	LECITHINASE.	4.040+00
16	77	19.2	470	~	087325	LECITHINASE.	4.040+00
17	77	19.2	266	7	084354	HYPOTHETICAL 63.5 KD P	4 040+00
18	77	19.2	696	~	054123		4.04e+00
19	77	19.2	1464	11	063728	N-METHYL-D-ASPARTATE R	4.04e+00
20	77	19.2	1464	11	008948	N-METHYL-D-ASPARTATE R	4.040+00

4.04e+00 4.04e+00	5.58e+00 5.58e+00	5.58e+00	5.58e+00	5.58e+00	7.70e+00	1.06e+01	1.06e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.98e+01	1.98e + 01	1.98e+01						
ω	SIMILARITY TO HUMAN GT FRUCTOFURANOSIDASE (EC	H	B120.	F25F2.2 (FRAGMENT).	MANNOSE-1-PHOSPHATE GU	HYPOTHETICAL 19.4 KD P	C34B7.2 PROTEIN.	L1 PROTEIN (FRAGMENT).	HYPOTHETICAL 49.3 KD P	TAIL PROTEIN.	PUTATIVE MEMBRANE PROT	COMPLETE GENOME SEQUEN	F13P17.19 PROTEIN.	HAEMAGGLUTININ (FRAGME	HAEMAGGLUTININ (FRAGME	HAEMAGGLUTININ (FRAGME	HEMAGGLUTININ HAI DOMA	HEMAGGLUTININ (FRAGMEN	HEMAGGLUTININ (FRAGMEN	HEMAGGLUTININ (FRAGMEN	POLYPROTEIN (FRAGMENT)	POLYPROTEIN (FRAGMENT)
Q12879 Q23388	P91315 002490	051735	014497	019785	074624	060074	P90770	072154	043411	938005	053784	981876	080784	082650	082658	082649	067383	067381	067363	967366	089483	089496
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1464 2219	535 550	821	1142	2660	364	178	921	92	442	286	964	1693	2301	347	347	347	362	362	379	379	447	447
19.2	18.9 18.9	18.9	18.9	18.9	18.7	18.4	18.4	18.2	18.2	18.2	18.2	18.2	18.2	•	17.9		17.9	•	17.9	17.9		17.9
77	76 76	92	26	92	75	74	74	73	73	73	73	73	73	72	72	72	72	72	72	72	72	72
122	53 54 3	25	26	27	88	53	30	31	32	33	34	32	36	37	38	33	4 0	41	42	43	44	45

ALIGNMENTS

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LT 1
003463
003463
003463
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 00, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 00, LAST SEQUENCE UPDATE)
GENOME POLYPROTEIN
HERPATITIS C VIRUS (ISOLATE HC-J1) (HCV).
HERPATITIS C-LIKE VIRUSES.
HERPATITIS C-LIKE VIRUSES.
                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE, 93117120.
OKAMOTO H., KANAI N., MISHIRO S.;
OKAMOTO H., KANAI N., MISHIRO S.;
"Full-length nucleotide sequence of a Japanese hepatitis C virus isolate (HC-J1) with high homology to USA isolates.";
NUCLEIC ACIDS RES. 20:6410-6410(1992).
                                                                                                                                                                                                                                                                                                           X MEDLINE; 91013116.
A OKAMOTO H., OKADA S., SUGIYAMA Y., YOTSUMOTO S., TANAKA T., OKAMOTO H., OKADA S., SUGIYAMA Y., YOTSUMOTO S., TANAKA T., YOSHIZAWA H., TSUDA F., MIYAKAWA Y., MAYUMI M.;
I The 5'-terminal sequence of the hepatitis C virus genome.";
I The 5'-terminal sequence of the hepatitis C virus genome.";
I The 5'-terminal sequence of the hepatitis C virus genome.";
I The 5'-terminal sequence of the hepatitis C virus genome.";
I FABL; D10749; G221587;
R PEFAM; PF01098; HCV_ARGRP; I.
R PFFAM; PF01001; HCV_NS45; I.
R PFAM; PF01006; HCV_NS45; I.
R PFAM; PF01006; HCV_NS45; I.
R PFAM; PF01006; HCV_NS45; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81; DB 14; Length 301
Pred. No. 1.08e+00;
10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2116 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHDYPVGSQ 2159
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ID Q68468 PRELIMINARY; PRT;
AC Q68468;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 20.1%;
Local Similarity 40.0%;
es 18; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 6.29 Seconds 314.294 Million cell updates/sec Wed Sep 1 16:17:15 1999; Run on:

not generated.

Pabular output

634 1 MEKFMAEFGGGYVQTPFLSE......DSKSYAFSTSNDTTSAAFVS 93 >PCT-US99-13024-2 (1-93) from PCTUS9913024.pep (6 of 12) Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq35 Database:

Variance 116.070; scale 0.235 Mean 27.254; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0,	Score	& Query Match	å Query Match Length DB	DB	ID	Description	Pred. No.
:	300	47.3	.3 65	19	R97371	Phage T4 ORFX gene or	1.866-18
	96	15.7	1693	35	W76368	Hepatitis E virus hol	3.010+00
	92	14.5	520		P94617	Neutral protease enco	6.200+00
	85	14.5	521	m	P51009	Sequence of neutral p	6.20e+00
	87	13.7	242	19	P95000	Bacillus subtilis lic	1.510+01
	87	13.7	623	35	W75773	Amino acid sequence o	1.510+01
	98	13.6	239	Н	R06621	Hybrid (1,3-1,4)-pre-	1.80e+01
	98	13.6	1693	34	W71209	Protein encoded by OR	1.806+01
	86	13.6	1693	19	R91813	Hepatitis E virus str	1.80e+01
	86	13.6	1693	10	R51264		1.80e+01
	86	13.6	1693	37	W81519	Hepatitis E virus (HE	1.80e+01
	98	13.6	1693	36	W80196	Protein encoded by OR	1.800+01
	82	13.4	633	35	W75774	Amino acid sequence o	2.14e+01
	84	13.2	1693	m	R14618	Protein encoded by OR	2.55e+01
	83	13.1	613	36	W73122	A. thaliana ethylene	3.04e+01
	83	13.1	613	15	R74632	OETR ethylene respons	3.04e+01

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	3.61e-01		4.29e+01				5.09e+01	5.09e+01	5.09e+01	5.09e+01	5.09e+01	5.09e+01					5.09e+01									5.09e+01	5.09e+01	5.09e+01	5.09e+01
	0)	GTP-cyclohydrolase II	ဗ္ဗ	rirus q	Sequence of hepatitis	HCV NS5 domain antige	HCV non-structural pr	Microspore-specific c 5.0	HCV NS5 encoded by pH	HCV CKS-NS5E recombin	CKS-NS5	HCV CKS-NS5E - pHCV-4	Sequence encoded in t	of	Sequence encoded in t	HCV polypeptide 1.	HCV amino acid sequen	encod	>	Hepatitis C virus pol		Composite hepatitis C		ťΩ	3 HCV seque	S C	HCV polyprotein.	Hepatitis C virus pol	HCV polyprotein.
	W75775	R52824	R40120	R66995	P90150	R90934	W67010	R06519	R33441	R33595	R33633	R21566	P92041	P90158	P92047	R25135	R28582	P92050	P90288	R08123	R34009	R70230	R24440	R08124	R21519	R31621	m	093	W40038
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	85	81	81	81	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80
	17	18	19	50	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT

New proteins derived from T4 phage tail fibre proteins - that can self assemble into nano-structure(s), useful as filters etc, also corresponding DNA
Claim 7: Fig 7: 83pp; English.
A protein (R97371) of unspecified function is the product of open reading frame X of the tail fibre protein gene region (see also frames for tail fibre proteins (see also R97370 and R97372-74).
Tail fibre proteins (ace also R97370 and R97372-74).
Tail fibre proteins (ace also R97370 and R97372-74).
Tail fibre proteins (ace also R97370 and R97372-74). 07-JAN-1997 (first entry).

Phage T4 ORFX gene product. gp34.

Phage T4; tail fibre protein; nanotechnology; nano-structure; filter; molecular sieve.

W09611947-A1. T R97371 standard; Protein; 65 AA. 25-APR-1996. 13-0CT-1995; U13023. 13-0CT-1994; US-322760. (GOLD/) GOLDBERG E B. GOLDBERG EB. WPI: 96-221942/22. N-PSDB; T29053 Sequence

Gaps ö Length 65; Score 300; DB 19; Length 65 Pred. No. 1.86e-18; 3; Mismatches 7; Indels Query Match 47.3%; Best Local Similarity 82.1%; Matches 46; Conservative

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RESULT 2 ID W76368 standard; Protein; 1693 AA

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Claimed replicon comprises a promoter and regulatory regions, capable of
expressing alkaline and neutral protease genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                               Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation

Claim 10: Page 17-24: 29pp: Japanese.

This sequence represents a Hepatitis E viral hollow particle protein. This polypeptides can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 frtsfvdgavleangperynlsfdasqstmaagpfsptyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
       03-DEC-1998 (first entry)
Hepatitis E virus hollow particle protein #1.
Hollow particle protein; virus; antibody; detection; immunoassay; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vectors for expression of polypeptide(s) in Bacillus -
contg. promoter and regulatory regions which control expression
and secretion of protease(s) in Bacillus.
Disclosure, p: English.
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21-JUN-1990 (first entry)
Neutral protease encoded by npr gene.
Protease; expression systems; substilin; neutral protease; ds.
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 96; DB 35; Length 1693; larity 26.9%; Pred. No. 3.01e+00; Conservative 21; Mismatches 25; Indels
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19; Mismatches 18; Indels
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                                                                                                                                                                             /note= "Partial sequence"
                                                                                                                                                                                                                                             28-FEB-1997; 062445.
28-FEB-1997; JP-062445.
(DENK-) DENKA SEIKEN KK.
(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
WPI: 98-535037/46.
N-PSDB; V61687.
                                                                                                                                  Location/Qualifiers
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Nagaratjan V. Rhodes CS, Banner CDB;
WPI: 89-053639/07.
N-PSDB; N91114.
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P94617 standard; protein; 520 AA.
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/note="Mature"
27..520
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ilarity 27.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1985; 717800.
29-MAR-1985; US-717800.
                                                                                                                                                       1..1693
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nes 18; Conser
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                                                                                                               Hepatitis virus.
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W76368;
03-DEC-1998
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Matches
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The lichenase gene from Bacillus subtilis Y-25 is used for transforming Bacillus hosts so that they show increased lichenase expression. The recombinant lichenase enzyme produced by the transformants is useful in beer production for decomposing beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Replicable plasmidic expression vector - for transformation of Bacillus to direct expression of poly:peptide
Disclosure; Fig 4; 37pp; English.
The inventors claim a vector comprising a replicable plasmid containing the promoter and regulatory region of a gene selected from apr[Bamp] and npr[Bamp], for transformation of Bacillus to direct expression of polypeptide.
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12-FEB-1997 (first entry)
Bacillus subtilis lichenase.
Beer production; fermentation; barley; beta-glucan; hydrolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                  Tr. 4
P51009 standard; Protein; 521 AA.
P51009.
(01-DEC-1991 (first entry)
Sequence of neutral protease encoded by the npr[BamP] gene.
Bacillus expression vector; secretion vector.
Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 3; Length 521;
Pred. No. 6.20e+00;
19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal
28..221
/label= Pro sequence
222..521
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08-JUN-1984; US-618902.
29-MAR-1985; US-717800.
(GENE-) GENEX CORP.
NAGARAJAN V. Banner CDB, Rhodes CS;
WPI: 85-057299/10.
N-PSDB; N50542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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P95000 standard; Protein; 242
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08-5EP-1987; 224615.
08-SEP-1987; JP-224615.
(ASAK ) ASAHI BREWERIES KK.
WPI; 89-119863/16.
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Best Local Similarity 27.8%;
Matches 15; Conservative
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06-JUL-1984; 304662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucan from barley
Sequence 242 AA;
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Hofemeister J, Thomsen KK, Olsen O, Vonwettstein
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W71209 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                              Match 13.6%;
Local Similarity 25.5%;
les 14; Conservative
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Best Local Similarity 25.4%;
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05-APR-1991; US-681078.
17-JUN-1988; US-208997.
11-APR-1989; US-336672.
19-JUN-1989; US-367486.
13-OCT-1989; US-420921.
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Borriss R, Hofemel:
WPI; 90-275129/36.
N-PSDB; Q05832.
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WPI; 98-446186/38.
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                                                                                                                                                                                                                                                               02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD573 toxin.
HD573 toxin: PCR: priner; amplification; Bacillus thuringiensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Heliotoverpa zea Claim 14: Pages 28-30: 50pp; English.
This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Heliotoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
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                                                              Gaps
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                                                                                                   77 laltspsynkfdcgenrsvqtygyglyevrm-kpakntgivssfftytgptdgtp 130
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09-JAN-1991 (first entry)
09-JAN-1991 (first entry)
Hybrid (1,3-1,4)-pre-beta-glucanase.
Hybrid pre-beta-glucanase; glucans; beer; animal feed; poultry.
Hybrid pre-beta-glucanase; Bacillus macerans.
Bacillus amyloliquefaciens, Bacillus macerans.
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Pred. No. 1.51e+01;
26; Mismatches 26; Indels
                 Score 87; DB 19; Length 242; Pred. No. 1.51e+01;
                                                         Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=carboxyl-terminal of B.macerans
                                                                                                                                                                                                                                                                                                                                                                                                                      MYCO) MYCOGEN CORP.
MILLET-Cohn J. Narva KE, Schnepf HE;
WPI; 98506734/43.
N PSDB: V52610.
                                                           19;
                                                                                                                                                                                                                             W75773 standard; Protein; 623 AA
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16-FEB-1989; DD-325800.
04-AUG-1989; DK-003848.
(CARL-) CARLSBERG A/S.
(DEAK ) AKAD WISSENSCHAFT DDR.
               13.7%;
larity 27.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 13.7%;
Local Similarity 18.2%;
nes 12; Conservative
                                     Local Similarity es 15; Conser
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16-FEB-1990; 1
16-FEB-1989; 1
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                 Query Match
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Matches
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New thermostable (1,3-1,4)-beta-glucanase - prepd. using hybrid gene obtd. using Bacillus amyloliquefaciens and B.macerans genes Disclosure; page 26; 84pp; Pagilsh.

This hybrid protein is encoded by the beta-glucanase-H1 gene. This hybrid protein is encoded by the beta-glucanase-H1 gene. Following processing of the signal peptide the mature protein is produced, comprising the amino terminus of the amyloliquefaciens beta-glucanase and the carboxyl-terminal half of the B.macerans beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glucanase. This hybrid protein is thermostable and hydrolyses beta-glucan and hydrolys
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W71209-11 represent the proteins encoded by the open reading frames W71209-11 represent the proteins encoded by the open reading frames transmitted nonA/nonB viral hepatitis agent (ET-NANE). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV). detecting ET-NANE in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - useful for e.g. virus detection and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 laltspsynkfdcgenrsvqtygyglyevrm-kpakntgivssfftytgptegtp 127
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Pred. No. 1.80e+01;
20; Mismatches 18; Indels
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05-APR-1990; US-505888.
25-JUL-1994; US-279823.
(GENE-) GENELABS TECHNOLOGIES INC.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam
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Pred. No. 1.80e+01;
22; Mismatches 25;
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Misc_difference 1514
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The present sequence is the protein prod. of ORF-1 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an entically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the protein ond anti-HEV antibodies (pref. 196 or 19M) in blood, plasma, care, cerebrospinal fluid, tissue, urine or pleural fluid. The protein and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV OKF-2 conty, baculovirus, i.e. the claimed recombinant
572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
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21-077-1994 (first entry)
HEV strain protein encoded by ORF-1.
Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF;
antibody; detection; diagnosis; primates; stool suspension.
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misc_difference 1455..1693

/note= "10 bp nucleic acid sequence TGGTNTTYGA has to be inserted between nucleotides 4390..4391 of T27394 before these amino acid residues can be decoded"
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26-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 ORF-1.
Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
structural region; antigen; detection; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86; DB 19; Length 1693;
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Best Local Similarity 25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection.
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                                                                                                                      fapgvsp 638
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                                                                                                                                                                               FDPSTGA 71
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N-PSDB; T27394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunisation;
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PF 22-05-1998; U07418.

PF 19-4RF-1999; U07418.

PR 19-4RF-1999; U07418.

11-4RF-1997; US-840316.

PR 1-4RF-1997; US-840316.

PR 1058 H | US DEPT HEALTH & HUMAN SERVICES.

PR 1 | Se-568733/48.

PR 25 | Se-568733/48.

PR 25 | Se-568733/48.

PR 27 | Se-568733/48.

PR 29 | Se-568733/48.

PR 29 | Se-568733/48.

PR 20 | Se-56873/48.

PR 20 | Se-56
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                                                                                                                                                                                                                                                     for use in detection, diagnosis, vaccines and therapy of hepatitis E virus infection Disclosure; Page 57-62: 114pp: English.

The sequences given in R51264-66 are encoded by the hepatitis E virus (HEV) strain SAR-55. The CDNA sequence contains three open reading frames (OREs). These proteins can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. The HEV SAR-55 CDNA was isolated from primates innoculated with stool
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Hepatilis B virus (HEV) ORF-1 protein.
Hepatilis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
Bassive Immunisation; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                  Emerson SU, Purcell RH, Tsarev SA;
WPI; 94-118462/14.
N-PSDB; 045197.
Purified hepatitis E strain SAR-55 virus - used to develop prods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 86; DB 10; Length 169
Pred. No. 1.80e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suspensions obtained from hepatitis E patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by CAG"
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W81519 standard; Protein; 1693 AA.
W81519;
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Misc_difference 1352
Hepatitis E virus strain SAR-55.
WO9406913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.68;
                                                31-MAR-1994.
17-SEP-1993; U08849.
18-SEP-1992; US-947263.
(USSH ) US SEC DEPT HEALTH.
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Matches 17; Conservative
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NerSubi yozoni.

New insecticidal Bacillus thuringlensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Hellothis virescens and Helicoverpa zea Claim 14; Pages 32-34; 50pp; English.

This is the amino acid sequence of a novel Bacillus thuringlensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                             02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD525 toxin.
HD525 toxin, PCR; primer; amplification; Bacillus thuringlensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringlensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 fisekfgngsdslrfegsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
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A positive clone ET1.1 was identified in a library prepared from bile of cynomolgus monkeys infected with the Burma strain of ET-NANE Both strands of ET1.1 were sequenced. Identity of the sequence with
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Protein encoded by ORF 1 of Burmese ET-NANB viral strain.
enterically transmitted non-A, non-B hepatitis virus; hepatitis HCV; E.coll strain BB4; ATCC deposit number 67717; Burma.
Enterically transmitted non-A, non-B hepatitis virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85; DB 35; Length 633; Pred. No. 2.14e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reyes GR, Yarbough PO, Bradley DW, Krawczynski K2, Tam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indeis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Le
2.55e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84; DB 3;
Pred. No. 2.55e+(
20; Mismatches
                                                                                                                                                                                                                                                                              13-MAR-1998; UO5081.
13-MAR-1997; US-040512.
(MYCO ) WICOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
WPI; 98-506734/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R14618 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-1991.
05-APR-1991; U02368.
05-APR-1990; US-505888.
(GEME-) GENELABS INC.
(USSH ) US DEPT HEALTH & HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.4%;
Best Local Similarity 23.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.2%;
Best Local Similarity 26.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91-325242/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q14412
                                                                                                                                                                                                                       WO9840490-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; V5261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R14618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä
      NEW TERM TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEV, and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HEV infection and disease in a mammal. The antibodies can be used for detection or for passive immunisation of
                                                                                                                                                                                                                                                                                     ň
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                            572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A recourse of the proteins - useful for diagnosis or vaccine production the Virus claim 22; Columns 57-66; 47pp; English.

Wally 6-98 are encoded by the genome of the Burma strain of wally 6-98 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodiase present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORFI sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       8 FGQGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQT-F-SAGLHLR-V 64
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Protein encoded by ORF1 of ET-NANB (HEV) Burma strain DNA sequence.
Enterically transmitted non A non B hepatitis virus; ET-NANB;
Hepatitis E virus; HEV; Burma HEV isolate; vaccine;
                                                                                                                                                                                                                                                                                     ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1693;
                                                                                                                                                                                                                       Length 1693;
                                                                                                                                                                                                                       Score 86; DB 37; Length 1693,
Pred. No. 1.80e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86; DB 36; Length 169
Pred. No. 1.80e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE.) GENELABS TECHNOLOGIES INC.
Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 1693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W75774 standard; Protein; 633 AA.
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ilarity 25.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non A non B Hepatitis virus
                                                                                                                                                                                                                   Query Match 13.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APK-1989; US-336672; 16-JUN-1989; US-367486; US-367486; US-367486; US-50541; US-505888; US-JUN-1995; US-475807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1998.
07-JUN-1995; 475807.
25-JUL-1994; US-279823.
17-JUN-1988; US-208997.
11-APR-1989; US-336672.
                                                                                                                                                         1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1693 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        632 fapgvsp 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V66321.
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                                                                                                                                                            Sequence
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                                                                                                                               mammals.
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W80196 :
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ID W7
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and development.

Example 5: Fig 12: 149pp; English.

This sequence is encoded by the Arabidopsis thaliana ethylene response. This sequence is encoded by the Arabidopsis thaliana ethylene response. (ETR) gene, designated OITR. The ETR gene is used in the antisense expression construct of the invention, which also contains a promoter. Expression of the construct in a plant cell results in a decreased production of plants which have a decrease in physiological responses to the presence of ethylene. Ethylene is a plant hormone which is involved in various positive plant controls e.g. growth, development and fruit ripening, and is also induced by environmental stresses wounding, pathogenic infection and flooding. Controllable, inducible expression of ethylene antisense constructs in transformed plant cells allows
                                                                                                                                                                                                                                                                                                                                                                                                        C'JAN-1959 (LIESC-EULY)

A thaliana ethylene response protein OITR.

Ethylene response gene; ETR; plant hormone; plant growth modulation;

Mabidopsis thaliana.

Saddewelopment control; fruit ripening.

MS824668-A.

US5824668-A.

DO OCT-1996.

PP 07-JUN-1995; US-484101.

PR 07-JUN-1995; US-484101.

PR 07-JUN-1995; US-68555.

PR 01-JUL-1993; US-086555.

PR 01-JUL-1993; US-086555.

PR 01-JUL-1994; US-086555.

PR 01-JUL-1994; US-086555.

PR 01-JUL-1995; US-086555.

PR 01-JUL-19
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572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83; DB 36; Length 613;
Pred. No. 3.04e+01;
17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Wed Sep 1 16:17:50 1999 Job time: 35 secs.
                                                                                                                                                                                                                                                                                      JT 15
W73122 standard; Protein; 613 AA.
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Best Local Similarity 31.4%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                            632 fapg 635
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:31:44 1999; MasPar time 5.61 Seconds 126.558 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 1 STSNDTTSAAFVS 13 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:Sp_archea 2:Sp_bacteria 3:sp_fungl 4:sp_human 5:Sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:Sp_plant 11:sp_rodent 12:sp_unclassified 13:Sp_vertebrate 14:sp_virus sptremb19

Mean 21.936; Variance 22.856; scale 0.960 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
				: :			
٦	24	79.4	101	11	088517	CALCIUM CHANNEL BETA 1	7.52e-02
7	54	79.4	579	4	015331	L-TYPE CALCIUM CHANNEL	7.52e-02
e	47	69.1	241	2	020870	SIMILAR TO GLUTAMATE R	4.20e+00
4	47	69.1	982	ഗ	009532	HYPOTHETICAL 110.9 KD	4.20e+00
ស	47	69.1	2100	٣	P87112	PUTATIVE TRANSCRIPTION	4.20e+00
9	46	9.79	268	S	094484	ORF DG1007 (FRAGMENT).	7.24e+00
7	45	66.2	337	ហ	019474	F15A2.4 PROTEIN.	1.24e+01
œ	45	66.2	583	٣	012372.	CHROMOSOME XII READING	1.24e+01
σ	44	64.7	37	S	026818	SURFACE ANTIGEN (FRAGM	2.09e+01
10	44	64.7	53	'n	023582	SIMILAR TO ADENOSINE A	2.09e+01
11	44	64.7	236	11	060000	POTASSIUM CHANNEL PROT	2.09e+01
12	44	64.7	371	10	065584	HYPOTHETICAL 40.8 KD P	2.09e+01
13	44	64.7	461	~	068923	GLYCERALDEHYDE-3-PHOSP	2.09e+01
14	44	64.7	488	Ŋ	044317	REVERSE TRANSCRIPTASE	2.09e+01
15	44	64.7	545	m	P87306	HYPOTHETICAL 62.5 KD P	2.09e+01
16	44	64.7	575	Ŋ	026040	SHAL 1 POTASSIUM CHANN	2.09e+01
17	44	64.7	611	11	063286	VOLTAGE-GATED K+ CHANN	2.09e+01
18	44	64.7	623	Ŋ	016992	WO3F9.4 PROTEIN.	2.09e+01
19	44	64.7	636	11	P70622	KV4.3 POTASSIUM CHANNE	2.09e+01
20	44	64.7	636	4	060576	KV4.3 POTASSIUM CHANNE	2.09e+01

ö

Gaps

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Score 54; DB 11; Length 101; Pred. No. 7.52e-02; 2; Mismatches 1; Indels

Query Match 79.4%; Best Local Similarity 75.0%; Matches 9; Conservative

|||:|||| :|| 81 STSNDTTSAAFV 92 36 STSSDITSNSFV 47

셤 ö CACNLEI.
HOMO SAPIENS (HUMAN),
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
(2ATARRHINI; HOMINIDAE; HOMO.
(1)

015331 PRELIMINARY; PRT; 579 AA. 015331; 01-3AN-1998 (TREMBLREL. 05, CREATED) 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) LITPE CALCIUM CHANNEL BETA SUBUNIT ISOFORM BETA-1B.

RESULT 1D DI DD DI DD O11 DD O11 DD CA CA CA RN CA

2.09e+01 2.09e+01 2.09e+01 2.09e+01 2.09e+01 2.09e+01 3.51e+01	3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01 3.51e+01		RODENTIA; al cDNA
SHAL-RELATED POTASSIUM KV4.3 POTASSIUM CHANNE KV4.3. FLAGELLIN (FRAGMENT). SIMILAR TO GTP-BINDING AGGLUTIMIN-LIKE ADHESI LAMININ ALPHA 2 CHAIN. CHROMOSOME XII READING	YDBO PROTEIN. CODED POR BY C. ELEGAN HYPOTHETICAL 52.3 KD P PHEROPHORIN III (FRACH POTASSIUM CHANNEL PROT GP5-LIKE PROTEIN (FRAG SIMILARITY TO A HOMEOB DPPE. SODIUM-DEPENDENT TRANS SHALI. IMMEDIATE EARLY PROTEI UBIQUITIN CARBOXYL-TER CODED FOR BY C. ELEGAN DJ332K4.1 (HYPOTHETICAL HYPOTHETICAL 141.7 KD PROTEIN-TYROSINE PROSEIN PROTEIN-TYROSINE PROSE	101 AA. ENCE UPI TATION ENT).	RATA; MAMMALIA; EUTHERIA; RO .A.; nnel beta 1 subunit, partial /DDBJ DATA BANKS. 9F3 CRC32;
Q62897 Q60577 Q08723 Q68385 Q18286 Q13368 Q12338	P96610 001681 0095249 P93694 087767 016749 01619 010619 020079 092185	N, 4	CHORDATA; VERTEBRATA; EE, MURINAE; MUSBRAIN; N H.P.T., WAHL M.A.; rated calcium channel 7 TO EMBL/GENBANK/DDBJ 72008; 11240 MW; 838619F3 C
.7 636 .7 655 .7 659 .7 132 .7 1419 .7 3110	290 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		US (MOUSE). METAZOA; CHORDATA; VERTEBRATA; MANMA HI; MURIDAE; MURINAE; MUS. ROM N.A. I; TISSUE-BRAIN; D J., AMARON H.P.T., WAHL M.A.; VOItage-gated calcium channel beta 1 [MAX-1998] TO EMBL/GENBANK/DDBJ DATA 8898; G3202008; 101 101 101 AA; 11240 MW; 838619F3 CRG32;
, 444444444 6000000	44444444444444444444444444444444444444	1 88517 88517: 1-NOV-1998 1-NOV-1998 1-NOV-1998	SCUL SCUL GNAT GNAT CE F CE F *NMR BRAN OUSE CC .*
2222222 12222222	Q m u u u u u u u u u u u u u u u u u u	RESULT ID OO DT OO DT OO	

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SEQUENCE FROM N.A.

XX MEDLINE; 9415018.

A WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
WILSON R., AINSCOUGH R., CONNELL M., COPERT T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., DYBBIN R., FAVELLO A., FULTON L.,
CRAXTON M., DERR S., DJ., DYBBIN R., FAVELLO A., FULTON L.,
A GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., KROPRA A., SAUNDERS D., SHOWNKEEN R.,
RAALDON N., SMITH A., SONNHAMERE E., STADEN R., WATERYON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
ELGGANS ".,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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Pred. No. 4.20e+00;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 4; Length 579;
Pred. No. 7.52e-02;
2; Mismatches 1; Indels
SEQUENCE FROM N.A.
POWERS P.A., GREGG R.G., HOGAN K.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U86953; Q2155256; JOINED.
EMBL; U86955; G2155256; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U39997; G1055122; -.
SEQUENCE 241 AA: 27445 MW; F0977197 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHĪSSOE S., WILSON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                651614EF CRC32;
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                                                                                                                                        EMBL, 086961, G2155256, EMBL, 086922, G2155256, JOINED. EMBL, 086992, G2155256, JOINED. EMBL, 086999, G2155256, JOINED. EMBL, 086960, G2155256, JOINED. EMBL, 086969, G2155256, JOINED. EMBL, 086958, G2155256, JOINED.
                                                                                                                                                                                                                                                                                                                                         PF00774; Ca_channel_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILAR TO GLUTAMATE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0%;
Matches 9: Correction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.18;
larity 80.08;
Conservative
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                                                                                                                                                                                                                                                                                                                  PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||:|||| :||
81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 STSSDTTSNSFV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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01-NOV-1996 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 3
Q20870
Q20870;
                                                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                              PFAM;
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                                                                                                                                                                                                                                   EUKARYOTA; METALOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972;
BADCOCK K., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1 SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1 SIMILARITY: TO YEAST NOT1.
EMBL: 295334; E315491;
-1 HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                  OL-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 110.9 KD PROTEIN F07F6.6 IN CHROMOSOME II.
F07F6.6.
                                                                                                                                                                                                                                                                                                                                                                      CHISSOE S.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.-1-SIMILARITY: TO GLUTAMATE RECEPTOR.
EMBL; U23486; G746452; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.7 5 PRELIMINARY; PRT; 2100 AA. P87112 P87112. 06. CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-JUN-1998 (TREMBLEEL. 06, LAST SEQUENCE UPDATE) PUTATIVE TRANSCRIPTIONAL REGULATOR C20G8.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAC20GB.06.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA: ARCHIASCOMYCETES:
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 5; Lv
Pred. No. 4.20e+00;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9A710DB4 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 3; LA
Pred. No. 4.20e+00;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               982 AA; 110892 MW; B4285770 CRC32;
                   982 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AA
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094484
094484;
01-4484;
01-EB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENC
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENC
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENC
01-FEB-1997 (FRAGMENT).
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY - ARG
                                                                       CREATED)
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237132 MW;
                                                                       (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.1%;
80.0%;
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WORMPEP; F07F6.6; CE01898.
PFAM; PF00060; lig_chan; l.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                   PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830
                                                                                                                                                                                                             CAENORHABDITIS ELEGANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                       Q09532;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
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T 4
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AC 099
DT 011
DT 011
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Best Loc Matches

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01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST SEQUENCE UPDATE)
SURFACE ANTIGEN (FRAGMENT).
TRYPANOSOMA BRUCEI.
BRUCEI.
FURARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94150718.
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 83169719.

MERRIT S.C., TSCHUDI C., KONIGSBERG W.H., RICHARDS F.F.;

"Reverse transcription of trypanosome variable antigen mRNAs initiated by a specific oligonucleotide primer.";

PROC. NATL. ACAD. SCI. U.S.A. 80:1536-1540(1983).

EMBL; V01391; G10560; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 5; Length 37;
Pred. No. 2.09e+01;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                         SEVENTE CONTROL OF THE CONTROL OF TH
                             WEDLER H., WEDLER E., SCHARFE M., WAMBUTT R.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                             SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) SIMILAR TO ADENOSINE A3 RECEPTOR. NCBI GI: 1072232.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 66.2%; Score 45; DB 3; Le Local Similarity 50.0%; Pred. No. 1.24e+01; es 6; Conservative 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551442D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, 01-NOV-1996 (TREMBLREL. 01, 01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 AA; 4068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZK721.5.
CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 SSSEDITASPFV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 TSNTTASNSFV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 TSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
     SEQUENCE FROM N.A.
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|:| |:::||
81 STSNDTTSAAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-GAMBIENSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LT 9
Q26818
Q26818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q23582
Q23582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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MEDLINE: 9415018.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPERT T., COOPER J., COULSON A.,

BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J., COULSON A.,

CRAXTON M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,

LIGHTNING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., KROPRA A., SAUNDERS D., SHOWNKEEN R.,

RAALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDWAN P.;

RAALDON S., WOHLDWAN P.;

RAALDON S., COLLIGUOUS NUCLEOIDE SEQUENCE FIOM ChICOMOSOME III of C.
                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ULT 8
012372
012372
012372
012372
01-372
01-372
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
CHROMOSOME XII REMBILE CORF YILOGIW
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
SACCHAROMYCETACEAE; SACCHAROMYCETALES;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 5; Length 337;
Pred. No. 1.24e+01;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                       Score 46; DB 5; Length 268;
Pred. No. 7.24e+00;
4; Mismatches 2; Indels
                                                                                            LOOMIS W.F.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U66911; G1519534;
NON TER 268 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREGORY J.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 368:32-38(1994).
EMBL: 270207; E1345607; -.
SEQUENCE 337 AA; 38483 MW; ABD004B8 CRC32;
                                                                                                                                                                                NON_TER 268 268
SEQUENCE 268 AA; 30503 MW; 04E723F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337 AA
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01,
01,
09,
                                                                                                                                                                                                                                                         Match 67.6%;
Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%;
66.7%;
                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
F15A2.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                            15 TINNNITPNKFVS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 SKHNSTTSATFV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | ||||:||
81 STSNDTTSAAFV 92
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Best Local Similarity
Matches 8; Conser
                                                SEQUENCE FROM N.A.
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                                                                                 STRAIN-AX4;
                                                                                                                                                                                                                                                            Query Match
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019474;
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RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURIDAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVERY THIRD POSITION.

HE AMINO TERMINIS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM CURRENT CLASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGING TO THE SHIV GENE SUBFAMILY, A HOMOLOGUE OF THE SHAKER GENE SHAL OF DROSOPHILA MELANOGASTER.
EMBL. MA1898; G205041; -.
PFAM; PFON520; ion_trans; 1.
IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; VOLTAGE-GATED CHANNEL;
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNREEN SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIGG J., THOMAS K., VAUGHAN K., WATERSTON R., WALKINSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATERSTON R.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U40951; G1072232; -...
SEQUENCE 53 AA: 5833 MW; C4DA122E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 5; L
Pred. No. 2.09e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
(BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA.
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$2
$3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.78;
58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                               elegans.";
NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSNSTSRVSFV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                              MILLER N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 11
000090
000090;
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BUKARYOTA; VIRIDIPLAMATAE; STREPTOPHYTA: EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 9427486.
MEDLINE; 9427486.
"Cloning, sequencing and deduced functions of a cluster of Streptomyces genes probably encoding biosynthesis of the polyketide antibiotic frenolicin.";
GENE 142:31-39(1994).
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE FROM N.A.
BEVAN M., VANDENBOL M., JALLET C., PORTETELLE D., HOHEISEL J.,
BEVER H.W., MAYER K., SCHUELLER C.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                          Length 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 10; Length 371
Pred. No. 2.09e+01;
6; Mismatches 2; Indels
                                                                                                                                                         2; Indels
  SEGMENT S5 (BY SIMILARITY). SEGMENT S6 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
REEVES C.D., SOLIDAY C.L.;
SUBMITTED (APR.1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF058302; G3170587; -.
EMBL; AF058302; G3170587; -.
Af1 AA; 49966 MW; 26EC2672 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AL022223; E1283943;
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 40.8 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLYCERALDBHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG.
                                                                                                        Score 44; DB 11; I
Pred. No. 2.09e+01;
4; Mismatches 2;
173 SEGMENT S5 (BY SIN
234 SEGMENT S6 (BY SIN
236
26261 MW; C4A458FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40833 MW; 5B0F5AA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 AA.
                                                                                                                                                                                                                                                                                                                                       371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 64.7%;
Local Similarity 38.5%;
les 5; Conservative
                                                                                                             Ouery Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREPTOMYCES ROSEOFULVUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 SSSGESSESSFVS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                       108 TNNEDVSGAFVT 119
                                                                                                                                                                                                                                                 82 TSNDTTSAAFVS 93
  152
213
213
236
236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA;
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81 STSNDTTSAAFVS
  TRANSMEM
TRANSMEM
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                  o65584
065584
065584;
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068923
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUGESIELLA SP.
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE;
MYGALOMORPHAE; THERAPHOSIDAE; DUGESIELLA.
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Score 44; DB 2; Length 461;
Pred. No. 2.09e+01;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 15
P87306
P87306
P87306
P87306;
OL-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 62.5 KD PROTEIN C31F10.04C IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 3; Length 545;
Pred. No. 2.09e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 5; Length 488;
Pred. No. 2.09e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
SERAIN-972;
WOOD V., RAJANDREAM M.A., BARRELL B.G., POHL T.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 297204; E322252;
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
BURKE W.D., MALIK H.S., EICKBUSH T.H.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF015813; G2736044; -.
RNA-DIRECTED DNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                          01-JÜN-1998 (TREMBLREL. 06, CREATED)
01-JÜN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
REVERSE TRANSCRIPTASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPBC31F10.04C.

CENTZOSACCHAROMYCES POMBE (FISSION YEAST).

EUKARYOTA, FUNGI, ASCOMYCOTA, ARCHIASCOMYCETES;

SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 AA; 55092 MW; FA67B24C CRC32;
                                                                                                                                                                                                                                                                                                        488 AA
                                                                                                                                                                                                                                                                                                        PRT;
uuery Match 64.7%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 64.7%;
Local Similarity 58.3%;
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                         394 TTSADAVSSDFVG 406
                                                                                                                                                           :|| |: |: ||:
81 STSNDTTSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 SKTSDGTGAAFV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 SNEDISTNFVT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||: ||: ||:
83 SNDTTSAAFVS 93
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SEQUENCE
                                                                                                                                                                                                                                                                            LT 14
044317
044317;
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AC 004
AC 004
DT 001
DT 011
DT
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Search completed: Wed Sep 1 16:32:18 1999 Job time : 34 secs.

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SACCHAROMYCETACEAE; SACCHAROMYCES
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Q57981;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97449781.

DANIELSON P.B., FOGLEMAN J.C.;

"Isolation and sequence analysis of cytochrome P450 12B1: the first
mitochondrial insect P450 with homology to 1 alpha, 25 dlhydroxy-D3
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         24-hydroxylase.";
INSECT BICCHEM. MOL. BIOL. 27:595-604(1997).
-!- FUNCTION: PROBABLY INVOLVED IN STEROID HORMONES BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (PROBABLE).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                        ö
                                                                                                                                                                                                                                                               DOGSOPHILA ACANTHOPTERA (FRUIT FLY).
EUKARYOTA: METAZOA; ARTHROPODA: TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 119.3 KD PROTEIN IN PIPI-GLN3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION (BY SIMILARITY).
CYTOCHROME P450 12B1.
HEME (POTENTIAL).
5 53F97355 CRC32).
                            Length 1036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1; Length 532;
Pred. No. 3.44e+00;
2; Mismatches 0; Indels
                       Score 48; DB 1; Length 1036
Pred. No. 1.11e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLYBASE; FBGN0022933; Daca\Cyp12b1.
PROSITE: PS00086; CYTOCHONE_P456; 1.
OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; HEME;
MITOCHONDRION; TRANSIT PEPTIDE.
1036 AA; 109310 MW; CCDE5BE8 CRC32;
                                                                                                                                                                                                          15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CYTOCHROME P450 12B1 PRECURSOR (EC 1.14.-.-).
                                                                                                                                                                     532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1076 AA.
                                                                                                                                                                                                15-DEC-1998 (REL. 37, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62031 MW;
                          70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.6%;
77.8%;
                                                                                                                                                                                                                                                                                                            DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U78485; G2674278; -.
                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532
                                                                                                 |:||: || :||:
81 STSNDTTSAAFVS 93
                                                                                 87 SSSNNNTSNGFVA 99
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 DTTSSAFVT 343
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 DITSAAFVS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              480
                                                                                                                                                      LT 11
CPP1_DROAC
044220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEM3_YEAST
P40021;
                                                                                                                                                                                                                                                                                                                                                       STRAIN-A584
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
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                                                      Matches
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ID YE
AC P4
AC P4
DT 01
DT 01
DT 01
DT YE
CN YE
OS SF
OC EU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGRAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGGYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                      DIETRICH F.S., MULLIGAN J.I., HENNESSEY K.M., ALLEN E., ARAUJO R., AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M. CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S., MOSEDALE D., NAKAHARA A., KOMP C., LASHKIN D., LEW H., LIN D., NOSEDALE D., NAKAHARA A., NAMATH A., NORGREN R., OEFNER P., OH C., PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V., TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.; SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: GTP + IMP + L-ASPARTATE - GDP + ORTHOPHOSPHATE + ADENYLOSUCCINATE.
-!- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
-!- SIMILARITY: WITH OTHER ADENYLOSUCCINATE SYNTHETASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076 AA; 119349 MW; 9FED783D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 1; L. Pred. No. 3.44e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
STRAIN-S288C / AB972;
DIETRICH F.S., MULLIGAN J.T., HENNESSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCIENCE 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.6%;
Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U18796; G603266; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 TSTNOTTSNSFV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
6ENOME POLYPROTEIN (PL. 37, LAST ANNOTATION UPDATE)
COMPONENT PROTEINASE (EC 3.4.22..) (HC-PRO); PROTEIN P3; 6 KD PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R., HORGINELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETI J.A., HORGINELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovitus strain AD169;".

CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 5.97e+00;
5; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (REL. 15, CREATED)
1-AUG-1990 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN IRL12 (TRL12).
HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRUSES: DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
BETAHERESVIRINAE; CYTOMEGALOVIRUS.
                                                                        PROSITE: PSO1266; ADENYLOSUCCIN_SYN_1; 1.
PROSITE: PSO0513; ADENYLOSUCCIN_SYN_2; FALSE_NEG.
PFAM: PFO0709; Adenylsucc_synt; 1.
HSSP; P12283; 1ADI.
PURINE BIOSYNTHESIS; LIGASE; GTP_BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.97e+00;
                                                                                                                                                                  GTP-BINDING.
GTP (POTENTIAL).
: E15BE2C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47416 MW; 8289EB89 CRC32;
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or send an email to license@isb-sib.ch).
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SEQUENCE 345 AA; 37820 MW;
                                                                                                                                                                                                                                                    Query Match 66.2%;
Best Local Similarity 50.0%;
Matches 6; Conservative
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Similarity 50.0%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                      EMBL; U67505; G1591267;
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82 TSNDTTSAAFVS 93
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HYPOTHETICAL PROTEIN.
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82 TSNDTTSAAFVS 93
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Q65399;
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FANG G.W., ALLISON R.F., ZAMBOLIM E.M., MAXWELL D.P., GILBERTSON R.L.;

"The complete nuclectide sequence and genome organization of bean common mosalc virus (NL3 strain).";

VIRUS RES. 39:13-23(1995).

- I- FUNCTION: HILPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

- I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT MAY BE INVOLVED IN REPLICATION PROTEIN HAS HELICASE ACTIVITY. IT DAYS BE INVOLVED IN REPLICATION PROTEIN HAS HELICASE ACTIVITY.

- I- FUNCTION: WUCLEAR INCLUSION PROTEIN HAS PROTEOLYTIC ACTIVITY.

- I- PUNCTION: WUCLEAR INCLUSION PROTEIN HAS PROTEOLYTIC ACTIVITY.

- I- PUNCTION: WUCLEAR INCLUSION PROTEIN HAS PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ r send an email to license@isb-sib.ch).
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1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOWELLINKED PROTEIN A (NI-A) (NIA) (EC 3.4-12.-) (49 KD PROTEINASE) (49 KD PROTEIN B (NI-B) (NIB) (RNA-BIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)].

BEAN COMMON MOSAIC VIRUS (STRAIN NI-3 / MICHIGAN) (BCMV), VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00271; helicase_C; 1.

PFAM; PF00680; RNA_dep_RNA_pol; 1.

PFAM; PF00767; Poty_coat; 1.

PFAM; PF00851; Peptidase_C6; 1.

HYDROLASE; TRANSFERASE; THIOL PROTEASE; RNA-DIRECTED RNA POLYMERASE; COAT_PROTEIN; POLYPROTEIN; COVALENT PROTEIN-RNA LINKAGE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 5.97e+00;
5; Mismatches 0; Indels
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MW; 67B875D6 CRC32;
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PROTEIN P3.
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larity 54.5%;
Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 9.45 Seconds 450.572 Million cell updates/sec Wed Sep 1 16:13:05 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 1 MEKFWAEFGQGXVQTPFLSE.....GLHLRVFDPSTGALVDSKSY 78

Title: Description: Perfect Score: Sequence:

Scoring table:

179066 seqs, 54579741 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human
5:sp_invertebrate 6:sp_namma1 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 37.051; Variance 67.149; scale 0.552 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		đ			SUMMAKIES		
Result		Query					
NO.	Score	Match	Match Length DB	88	ID	Description	Pred. No.
-	100	18.1	1693	14	081876	COMPLETE GENOME SECTION	00.000
7	96	17.4	114	14	041088		2 00e-03
٣	92	16.7	299	7	065574	HYPOTHETICAL 32 4 KP D	8 159-02
4	92	16.7	300	14	065581	9	158-02
S	89	16.2		7	084354	HYPOTHETICAL 63.5 KD P	2.28e-01
9	98	15.6		14	081862	1	6.276-01
7		15.6	1693	14	081344	HEPATAITIS E VIRUS COM	6.27e-01
œ	86	15.6		14	089444	UNNAMED PROTEIN PRODUC	6.27e-01
6	86	15.6	1693	14	069410	METHYL TRANSFERASE	6.276-01
10	84	15.2	622	~	045743	CRYIIC DELIA-ENDOTOXIN	1.216+00
11	84	15.2	921	2	P90770	C34B7.2 PROTEIN.	1.216+00
12	83	15.1	180	10	049984	PUTATIVE ETHYLENE RECE	1.68e+00
13	83	15.1		σ	038022	ORF 1.	1.68e+00
14	83	15.1		~	054178	GLUCOSYLTRANSFERASE.	1.68e+00
15	83	15.1	_	14	039221	NONSTRUCTURAL POLYPROT	1.68e+00
16	81	14.7	196	14	065847	PUTATIVE COAT PROTEIN.	3.21e+00
17	81	14.7	216	7	609290	FLAGELLAR L-RING PROTE	3.21e+00
18	81	14.7	633	7	052764	INSECTICIDAL CRYSTAL P	3.21e+00
19	81	14.7	642	14	065848	PUTATIVE READTHROUGH P	3.21e+00
20	81	14.7	3011	14	003463	GENOME POLYPROTEIN.	3.216+00

NT) 4.41e+00 NT) 4.41e+00 NT) 4.41e+00	44000	80 80 80 80 60		
POLYPROTEIN (FRAGMENT POLYPROTEIN (FRAGMENT POLYPROTEIN (FRAGMENT VC2747L.)	RNA BINDING PROTEIN. POLYPROTEIN (FRAGMENT) D9461.24P. SIMILAR TO GLUTAMATE D 860AA LONG HYPOTHETICA	311709 ESPONSE N. N. N.	OSACCHA L 145.0 ASPARTAT ASPARTAT ASPARTAT OTEIN. ANE PROT	ENTS; 1693 AA.; 1693 ED; SEQUENCE UPDATE; ANNOTATION UPDATE)
Q68467 Q68468 Q68469 Q01993	007034 007034 004083 017456 059003	P75688 Q38846 Q36609 Q36608 Q36610 Q36579	087325 065322 084123 086617 008948 063728 012879 023388	ALIGNM PRT CREAT LAST LAST
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ALLGUMENIS	PRT; 1693 AA.	01, CREATED) 01, LAST SEQUENCE UPDATE) 09, LAST ANNOTATION UPDATE)	GENOME SEQUENCE. ; E VIRUS (HEV). SERNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE; US.	111 STRAIN-UIGH179; UCHIDA T.; EMBL, D11093; D1002342; SEQUENCE 1693 AA; 184840 MW; 8952DD38 CRC32;	 Score 100; DB 14; Length 1693; Pred. No. 4.78e-03; 22; Mismatches 24; Indels 3; Gaps 	572 FRTSFVDGAVLEANGPERYNLSFDASGSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631		PRT: 114 AA. 05, CREATED) 05, LAST SEQUENCE UPDATE) 08, LAST ANNOTATION UPDATE)	RELLA VIRUS 1 (PBCV-1). 40 RNA STAGE; PHYCODNAVIRIDAE; PHYCODNAVIRUS.
	RESULT 1 ID Q81876 PRELIMINARY; AC O81876.	1996 (TREMBLREL. 1996 (TREMBLREL. 1999 (TREMBLREL.	COMPLETE GENOME SEQUENCE. HEPATITIS E VIRUS (HEV). VIRUSES: SSRNA POSITIVE-S CALICIVIRUS.	SEQUENCE FROM N.A. STRAIN-UIGH179; UCHIDA T.; SUBMITTED (MAY-1992) TO E EMBL; DI1093; D1002342; SEQUENCE 1693 AA; 1848	Query Match Best Local Similarity 26.9%; Matches 18; Conservative	572 FRTSFVDGAVLEANGPERYN :: :: :: :: : FGGGYVQTPFLSESNSVRYK	632 FAPGVSP 638 ::: 65 FDPSTGA 71	PRELIMINARY; ; -1998 (TREMBLREL1998 (TREMBLREL1998 (TREMBLREL. PROTEIN.	A606L. PARAMECIUM BURSARIA CHLORELLA VIRUS 1 VIRUSES; DSDNA VIRUSES, NO RNA STAGE; [1] SEQUENCE FROM N.A. MEDLINE; 98022962.
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LETCHWORTH G.J., SCHWYZER M.;
"Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus I genome which exhibits a collinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus.";
                                                                                                                                                                                     5 FSSMSSNISFRVRLTASCAI - - LNPSYGRGRKSRNNSLNFTMSLSLMVFVISIKPSMSIK 62
                                                                                                                                             Gaps
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LI Y., LU Z., SUN L., ROPP S., KUTISH G.F., ROCK D.L.,
VAN ETTEN J.L.;
"Analysis of 74 kb of DNA located at the right end of the 330-kb
chlorella virus PBCV-1 genome.";
VIROLGGY 237:360-377(1997).
EMBL: U42580; G2447164; -.
SEQUENCE 114 AA; 13257 MW; 1B75BE43 CRC32;
                                                                                                                                             'n
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                                                                                                             17.4%; Score 96; DB 14; Length 114; arity 27.4%; Pred. No. 2.00e-02; Conservative 18; Mismatches 25; Indels
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                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 32.4 KD PROTEIN.
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA; 32379 MW; A3897D4A CRC32;
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                                                                                                                                                                                                                                                                                                            299 AA.
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Best Local Similarity 47.2%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-COOPER, AND JURA;
MEDLINE; 95313343.
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Matches 17; Conser
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Q65581
Q65581;
01-NOV-1996 (
01-NOV-1996 (
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STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
DAVIS R.W.;.... 1000 M. DE DE MENDRAL DATA BANKS.
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                                                                                   SEQUENCE FROM N.A.
STRAIN-SCHOENBOEKEN;
MEDLINE; 96135223.
SCHMITHS; 96135224.
"Identification and characterization of the bovine herpesvirus 1 UL7
gene and gene product which are not essential for virus replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 FGGGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDP 67
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAVIS R.W.;
"Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
SCIENCE 0:0-0(1998).
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                                                                                                                                                                                                                                                    Length 300;
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Pred. No. 2.28e-01;
25; Mismatches 18; Indels
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EMBL; AE001308; G3328711; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 566 AA; 63508 MW; CIALC491 CRC32;
                          BOVINE HERPESVIRUS TYPE 1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 63.5 KD PROTEIN.
                                                                                                                                                                                                                                                Score 92; DB 14; Le
Pred. No. 8.15e-02;
9; Mismatches 6;
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BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA
                                                                                                                                                                           in cell culture.";
J. VIROL. 70:1091-1099(1996).
BEBL: X9151; GLO06630; -.
SEQUENCE 300 AA: 32450 MW; 86377347 CRC32;
                                                                                                                                                                                                                                                                                                          PRT; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      566 AA
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ID Q81862 PRELIMINARY; PRT;
AC Q81862;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
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                                                         ALPHAHERPESVIRINAE; VARICELLOVIRUS
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Best Local Similarity 47.2%;
Matches 17; Conservative
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Best Local Similarity 26.2%;
Matches 17; Conservative
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SEQUENCE FROM N.A.
STRAIN-K52-87;
MEDLINE; 95176571.

YIN S., PURCELL R.H., EMERSON S.U.;
"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 FRISFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
UNNAMED PROTEIN PRODUCT.
HEPATITIS E VIRUS (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HEPATAITIS E VIRUS COMPLETE GENOME.
HEPATITIS E VIRUS (HEV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
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MEDLINE; 9348763.
MEDLINE; 9348763.

"The Sequence of hepatitis E virus isolated directly from a single source during an outbreak in China.";

EMBL: M94177; G1209364;
                                                                                                                                                                                                                                                                                                                                                                             572 FRISFVDGAVLEINGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV
                                                                                                                                                                                                                                                                                                  Score 86; DB 14; Length 1693; Pred. No. 6.27e-01;
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Pred. No. 6.27e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                          22; Mismatches 25; Indels
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SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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LAST SEQUENCE UPDATE)
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EMBL; L25547; G1209366; -.
EMBL; L25595; G784878; -.
SEQUENCE 1693 AA; 185122 MW; 0E56663A CRC32;
                                                                                                                                                                                                                                                                 185271 MW; EF762F9E CRC32;
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Local Similarity 25.4%;
les 17; Conservative
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les 17; Conservative
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                                                                           CALICIVIRUS
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089444;
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SEQUENCE FROM N.A.
MEDILNE: 92261377.
UCHIDA T., SUZUKI K., HAYASHI N., IIDA F., HARA T., OO S.S.,
WANG C.K., SHIRATA T., ICHIKAMA M., RIKHHISA T., MIZUNO K., WIN K.M.;
"Hepatitis E virus: CDNA cloning and expression.";
MICROBIOL. IMMUNOL. 36:67-79(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE: 92271465.
FRY K.E., TAM A.W., SMITH M.M., KIM J.P., LUK K.C., YOUNG L.M., PIATAK M., FELDAMN R.A., YUN K.Y., PURDY M.A., ET AL., "Hepatitis E virus (HEV): strain variation in the nonstructural gene region encoding consensus motifs for an RNA-dependent RNA polymerase and an ATP/GTP binding site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 FRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
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VIRUSES; SSRNA POȘITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
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BI S.L., PURDY M.A., MCCAUSTLAND K.A., MARGOLIS H.S., BRADLEY D.W.;
The sequence of hepatitis E virus isolated directly from a single source during an outbreak in China.";
VIRUS RES. 28:233-247(1993).

EMBL; LO8816; G330009;
EMBL; LO8816; G330009;
SEQUENCE 1693 AA; 185052 MW; 30A917E1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of a hepatitis E virus isolated from the Xinjiang epidemic (1986-1988) of China."; NUCLEIC ACIDS RES. 20:3512-3512(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSAREV S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEGTERS L.J.,
MALIK I.A., 100BAL M., PURCELL R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).
                                                                                                                                                                                                     "Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome."; VIROLOGY 185:120-131(1991).
                                                                                                                                                                  TAM A.W., SMITH M.M., GUERRA M.E., HUANG C.C., BRADLEY D.W., FRY REYES G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 14; Length 1693;
Pred. No. 6.27e-01;
22; Mismatches 25; Indels 3;
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SEQUENCE FROM N.A.
MEDLINE; 92335008.
AXE T.T., UCHIDA T., MA X.Z., IIDA F., SHIKATA T., ZHUANG
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQ
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01-NOV-1996 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
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Best Local Similarity
Matches 17; Conserv
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Length 1693;

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SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
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08,
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Local Similarity 36.0%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.2%;
Best Local Similarity 24.7%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 QI-VWDMASSGNVADGR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | | :|:| : |::
61 HLRVFD-PSTGALVDSK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL. (TREMBLREL. (TREMBLREL. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIOPHAGE PHI-C31.
    SEQUENCE FROM N.A.
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 13
Q38022
Q38022;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
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SEQUENCE
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049984;
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                                                                                                                                                                                                                                                                                                                                                                                                                     572 FRISFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLIYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                HEPATITIS E VIRUS (HEV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
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EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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m
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BACILLUS.
                                                                                                                                                                                                                                                                                                                            Length 1693;
                                                                                                                                                                                                                                                                                                                          Score 86; DB 14; Length 169
Pred. No. 6.27e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84; DB 2; Length 622;
Pred. No. 1.21e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches 26; Indels
                                                                                                                                                          STRAIN=HEV037;
DONNTI M.C., FAGAN E.A., HARRISON T.J.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, x98292; E1175751; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
07, LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                1693 AA; 185190 MW; 287742F6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69729 MW; 65E72171 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 AA
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STRAIN=SHANGHAI 1 (S-1);
WU D., CAO X.L., BAI Y.Y., ARONSON A.I.;
FEMS MICROBIOL. LETT. 81:31-36(1991).
EMBL; X57252; G40286; -
PFAM; PF00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
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05,
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Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 15.2%;
Local Similarity 18.2%;
les 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
01-AUG-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRYIIC DELTA-ENDOTOXIN. BACILLUS THURINGIENSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 AA;
                      METHYL TRANSFERASE
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 FAPGVSP 638
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                                                                                        CALICIVIRUS
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                                                                                                                                                                                                                                                                                SEQUENCE
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Q45743
Q45743;
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P90770
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WEDLINE: 94150718.
WILSON R., AINDERSON K., BAYNES C., BERKS M.,
BONFIELD J. BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.
LIGHTNING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PECK C., RIFKEN L., ROPERA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
"2.2 Mb of contiguous nucleotide sequence from chromosome 111 of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRASSICA OLERACEA (CAULIFLOWER).
EUKARYOTA; VIRIDIPLAMTRE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; BRASSICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 ERWFVEIVHGYVRQEYIFLPIG-RISLTIIGRRSTKYAGTRFLKRGANPTGNVANYVETE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EKFMAEFGOGYVOTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGS-QTFSAGL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
CHARNG Y.Y., SUN C.W., YAN S.L., CHOU S.J., CHEN Y.R., YANG S.F.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U87239; G2738025; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83; DB 10; Length 180;
Pred. No. 1.68e+00;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB 5; Length 921;
Pred. No. 1.21e+00;
22; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                  NATÜRE 368:32-38(1994).
EMBL; 283220; E1344511; -.
SEQUENCE 921 AA; 106698 MW; 21DE4C35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 AA; 19859 MW; D9B072C1 CRC32;
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01-JUN-1998 (TREMBLEEL. 06, LAST SEQUEN
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTY-
PUTATIVE ETHYLENE RECEPTOR (FRAGMENT).
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                                      MEDLINE; 94374705.
HARTLEY N.M., MURPHY G.O., BRUTON C.J., CHATER K.F.;
HARTLEY N.M., MURPHY G.O., BRUTON C.J., CHATER K.F.;
"Sequence of the essential early region of phi C31, a temperate phage of Streptomyces spp. with unusual features in its lytic development.":
GENE 147:29-40(1994).
EMBL; X75288; G579071; -.
SEQUENCE 281 AA; 31680 MW; 0E734629 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                               194 AYMNADFIIDPDGNREPMPEFDGAAVLHVTDETWA-FKPVETGPDVFAQFLHLRQTFD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                               BACTERIA: FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS.
                                                                                                                                                                                            DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                             VICKERMAN M.M., SULAVIK M.C., CLEWELL D.B.; "Molecular analysis of Streptococcus gordonii glucosyltransferase
                                                                                                                                                             3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1577;
                                                                                                                                     Score 83; DB 9; Length 281;
Pred. No. 1.68e+00;
                                                                                                                                                            17; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83; DB 2; I
Pred. No. 1.68e+00;
                                                                                                                                                                                                                                              PRT; 1577 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 QDDGTVKKNFAVELNGKILYFDAETGALVDSNEY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phase variants.";
DEV. BIOL. STAND. 85:309-314(1995).
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01,
08,
                                                                                                                                      / Match 15.18;
Local Similarity 24.18;
les 14; Conservative
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Local Similarity 41.2%;
les 14; Conservative
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                                                                                                                                                                                                                                 ULT 14

Q54178 PRELIMINARY;

Q54178; O54247;

O1-NOV-1996 (TREMBLREL. 0

01-NOV-1998 (TREMBLREL. 0

01-NOV-1998 (TREMBLREL. 0

GLUCOSYLTRANSFERASE.
                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      STREPTOCOCCUS GORDONII.
 VIRUSES; DSDNA VIRU
LAMBDA PHAGE GROUP.
                               SEQUENCE FROM N.A. MEDLINE; 94374705.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92276337.
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CHALLIS;
MEDLINE; 96157084.
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                                                                                                                                      Query Match
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039221
039221;
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572 FRISFVDGAVLEINGPERHNLSFDASOSTMAAGPFSLIYAASAAGLEVRYVGAGLDHRAI 631
                                                                                                                                                                                                                                                                                                                                                                                           SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                           ω
;
                                                                                                                                      STRAIN-HYDERABAD, INDIA;
ANSARI I.H., NANDA S.K., DURGAPAL H., JAMEEL S., PANDA S.K.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                        Length 1693;
                                                                                                                                                                                                                                                                                                  Score 83; DB 14; Length 169
Pred. No. 1.68e+00;
23; Mismatches 25; Indels
                                                                                                                                                                                                                                                                   1693 AA; 185620 MW; E8D755D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: Wed Sep 1 16:13:32 1999 Job time: 27 secs.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.9%;
Matches 16; Conservative
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              632 FAPGVSP 638
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                  CALICIVIRUS.
                                                                                                                                                                                                                                                 POLYPROTEIN.
SEQUENCE 1
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:29:24 1999; MasPar time 5.26 Seconds 145.242 Million cell updates/sec Tabular output not generated. Run on:

>PCT-US99-13024-2 (66-79) from PCTUS9913024.pep (11 of 12) 86 Title: Description: Perfect Score:

1 DPSTGALVDSKSYA 14 Sequence: 179066 seqs, 54579741 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 24.488; Variance 26.991; scale 0.907 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Pred. No.	7.85e-02	4.07e-01	4.07e-01	3.35e+00	3.35e+00	3.35e+00	5.58e+00	5.58e+00	5.58e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	9.22e+00	1.51e+01	1.51e+01
			Description	GLUCOSYLTRANSFERASE.	HEAT SHOCK PROTEIN/SER	SERINE PROTEASE.	KIAA0574 PROTEIN (FRAG	RADIAL SPOKEHEAD.	KIAA0563 PROTEIN.	PHOTOLYASE.	POLYPROTEIN (FRAGMENT)	POLYPROTEIN.	ENVELOPE GLYCOPROTEIN	MONOCARBOXYLATE TRANSP	W-AMINO-TRANSFERASE-LI	CMP-N-ACETYLNEURAMINAT	MONOCARBOXYLATE TRANSP	MONOCARBOXYLATE TRANSP	RETINAL EPITHELIAL MEM	SIMILARITY TO MYOSIN H	PATERNALLY EXPRESSED P	YCDH.	HEMAGGLUTININ (FRAGMEN
SUMMARIES			ar ar	054178	046094	046120	060320	046178	060309	Q24281	088274	039734	087600	035308	Q44188	P72097	070461	013151	090632	004626	061138	034966	092324
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			Match Length DB	1577	368	472	405	552	870	240	1340	3493	142	156	262	371	492	542	542	1133	1378	319	327
	æ	Query	Match	68.6	65.1	65.1	60.5	60.5	60.5	59.3	59.3	59.3	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	58.1	57.0	57.0
			Score	59	26	26	52	52	22	51	51	51	20	20	20	20	20	20	20	20	20	49	49
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### ALIGNMENTS

66 DPSTGALVDSKSY 78 à

RESULT

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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUECHINOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                              MEDLINE; 98290545.
NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE; 98119758.

MEDILINE; 98119758.

GINGRAS D., GAGNON C.;

Molecular cloning and characterization of a radial spoke head protein of sea urchin sperm axonemes: involvement of the protein in the regularion of sperm motility. "; MOL. CELL 9:513-522(1998).

EMBL; 073123; G2905895; -. EMBL; 073123; G2905895.
                                                                                                                                                                                       "Prediction of the coding sequences of unidentified human genes. 1) The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA RES. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
RADIAL SPOKEHEAD.
STRONGYLOCENTRATOUS PURPLUS (PURPLE SEA URCHIN).
EUKARYOTA: METAZOA: ECHINODERMATA: ECHINOZOA: ECHINOIDEA: EUECH ECHINACEA; ECHINOIDEA: EUECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.5%; Score 52; DB 5; Length 552; imilarity 50.0%; Pred. No. 3.35e+00; 6; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                  Score 52; DB 4; Length 405; Pred. No. 3.35e+00; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
KIAAOS74 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                       DUM RES. 3:31-39(1998).
EMEL; ABO11146; D1026430; -.
NOW TER 1 1 1
SEQUENCE 405 AA; 42409 MW; 09BA9932 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                        552 AA.
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07,
08,
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Similarity 77.8%;
7; Conservative
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060309
060309;
01-AUG-1998 (TREMBLREL: 0'
01-AUG-1998 (TREMBLREL: 0'
01-NOV-1998 (TREMBLREL: 0'
KIAAO563 PROTEIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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67 PSTGALVDSKSY 78
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Best Local Similarity
Matches 7; Conser
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Best Local Similarity
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                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       LISSUE-BRAIN;
                                                                                                                                                                             OHARA O.;
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046178
046178;
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Matches
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                                                                                           CAMPYLOBACTER JEJUNI.
BACTERIA: PROTEOBACTERIA: EPSILON SUBDIVISION; CAMPYLOBACTER GROUP;
CAMPYLOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; CAMPYLOBACTER GROUP; CAMPYLOBACTER.
                                                                                                                                                                                       TAYLOR D.E., HIRATSUKA K.; "Use of non-radioactive DNA probes for detection of Campylobacter jejuni and Campylobacter coli in stool specimens."; MOL. CELL. PROBES 4:261-271(1990).
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EMBL; X82628; E315368; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB 2; Length 472;
Pred. No. 4.07e-01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                  HIRATSUKA K.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U27271; 6881375; -.
PRAM: PPG0089; trypsin; 1.
PFAM: PF00595; PDZ; 2.
                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN/SERINE PROTEASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 4.07e-01;
2; Mismatches 1;
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  368
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  PRT;
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046120;
01-NOV-1996 (TREMBLREL. 01, CR
01-70L-1997 (TREMBLREL. 04, LA
01-NOV-1998 (TREMBLREL. 08, LA
SERINE PROTEASE.
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Local Similarity 72.7%;
hes 8; Conservative
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Best Local Similarity 72.7%;
Matches 8; Conservative
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PFAM; PF00595; PDZ; 2.
PROTFAST
  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMPYLOBACTER JEJUNI.
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68 STGALVDSKSY 78
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                           MEDLINE; 90384493.
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SEQUENCE
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060320
060320;
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VIROL. 140:1473-1482(1995).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         POTYVIRUS.
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                 MEDLINE; 98290545.

NAGASE T., ISHIKAWA K., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N., OHARA O.;

Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA RES. 5:31-39(1998).

EMBL; ABO11135; D1026419; -.

SEQUENCE 870 AA; 94665 MW; EB9CD3F4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                        "Similarity among the Drosophila (6-4)photolyase, a human photolyase hombiog, and the DNA photolyase-blue-light photoreceptor family."; SCIENCE 272:109-112(1996).
EMBL: D83701; D1012739; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence analysis of two nuclear inclusion body and coat protein genes of a sweet potato feathery mottle virus severe strain (SPFMV-S) genomic RNA.";
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PHR: TISSUE-CVARY;
MEDLINE; 96178677.
TODO I., RYO H., YAMAMOTO K., TOH H., INUI T., AYAKI H., NOMURA T.,
IKENAGA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        088274;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
POLYPROPEIN (FRAGENENT).
SWEET POTATO FEATHERY MOTTLE VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                       ;
0
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MEDLINE; 95390803.
MORI M., SAKAI J., KIMURA T., USUGI T., HAYASHI T., HANADA K.,
NISHIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                            DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTENYGOTA: DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                Score 52; DB 4; Length 870; Pred. No. 3.35e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 540;
                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 5; Length 540;
Pred. No. 5.58e+00;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
PHOTOLYSES (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOTOLYSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 AA; 62548 MW; 62F139EE CRC32;
                                                                                                                                                                                                                                            540 AA.
                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                             PRT;
                                                                                                                               60.5%;
imilarity 42.9%;
6; Conservative
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Similarity 35.7%;
5; Conservative
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66 DPSTGALVDSKSYA 79
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SEQUENCE FROM N.A.
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           TISSUE-BRAIN;
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                                                                                                                                 Query Match
                                                                                                                                                                                                                                          Q24281
Q24281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 8
Q88274
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence and genome organization of sweet potato
feathery mottle virus (S strain) genomic RNA: the large coding region
of the P1 gene.":
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-ON-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN.
SWEET POTATO FEATHERY MOTILE VIRUS.
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; POTYVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S STRAIN;
MEDILINE; 98336489.
SAKAI J., MORI M., MORISHITA T., TANAKA M., HANADA K., USUGI T.,
NISHIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                               Score 51; DB 14; Length 1340; Pred. No. 5.58e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 14; Length 3493;
Pred. No. 5.58e+00;
4; Mismatches 3; Indels 0
                                                                                                                                     CYTOPLASMIC INCLUSION PROTEIN
                                                                                                                                                                                                                            B.
                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
GENOME-LINKED VIRAL PROTEIN
                                                                                                                                                     17 69 6K2 PROTEIN.
70 261 VPG PROTEIN.
504 NIA PROTEASE.
505 1025 NUCLEAR INCLUSION PROTEIN
1026 1340 COAT PROTEIN.
1340 AA; 151873 MW; 12C01867 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 664 POTENTIAL.
665 1122 POTENTIAL.
1123 1474 POTENTIAL.
11475 1526 POTENTIAL.
1527 2169 POTENTIAL.
2223 2414 GENOME-LINKED VIRAL PR
2415 2657 PROTENTIAL.
2418 CENTIAL.
2419 CONDITION OF PROTENTIAL.
2419 A4; 393818 MW; AOZEFAOS CRC32;
                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 3493 AA.
EMBL; D38543; D1008127;
PFAM; PF0068; RNA_dep_RNA_pol; 1.
PFAM; PF00863; Peptidase_C4; 1.
PFAM; PF00863; Peptidase_C4; 1.
NON_TER 1 1 1 CYTOPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCH. VIROL. 142:1553-1562(1997).

EMBL; D86371; D1023570; -.

PFAM; PF00680; RNA_dep_RNA_pol; 1.

PFAM; PF00851; Peptidase_C6; 1.

PFAM; PF00851; Peptidase_C6; 1.

PFAM; PF00851; Peptidase_C6; 1.

PLYPROTEIN. 1 664

CHAIN 665 1122 POTENTI
                                                                                                                                                                                                                                                                                                             59.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                           Conservative
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Gaps

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SEQUENCE FROM N.A.

STRAIN-MCS8 / NRCC 4728, 406Y / NRCC 4030, AND M982B / NRCC 4725;

STRAIN-MCS8 / NRCC 4728, 406Y / NRCC 4030, AND M982B / NRCC 4725;

GILBERT M., HATSON D.C., CUNNINGHAM A.-M., JENNINGS M.P., YOUNG N.M.,

J. BIOL, CHEM. 271:28271-28276(1996).

-I-FUNCTION: TRANSFERS SIALIC ACID FROM THE SUBSTRATE CMP-SIALIC
ACID DONOR TO THE TERMINAL
BETA-D-GALACTOSYL-1, 4-ACETYL-BETA-D-GLUCOSAMINE ON THE
LACTO-N-NEDTETRAGOSE BRANCH OF THE LIPOOLIGOSACCHARIDE.

-I-CATALYTIC ACTIVITY: CMP-N-ACETYLNEURAMINATE +
BETA-D-GALACTOSYL-1, 4-ACETYL-BETA-D-GLUCOSAMINE - CMP +
ALPHA-N-ACETYLLNEURAMINYL-2, 3-BETA-D-GALACTOSYL-1, 4-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALPHA-N-ACETYL-BETA-ALP
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N -> K
(IN STRAINS 406Y / NRCC 4030 AND M982B /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEISSERIA MENINGITIDIS.
BACTERIA; PROTEOBACTERIA; BETA SUBDIVISION; NEISSERIACEAE; NEISSERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN STRAINS 406Y / NRCC 4030 AND M982B NRCC 4725).
E -> D
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L -> *: (IN STRAIN M982B / NRCC 4725;

LOSS OF ACTIVITY).

T -> A (IN STRAIN 406Y / NRCC 4030).

K -> N (IN STRAIN 406Y / NRCC 4030).

73DB83A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> S (IN STRAIN M982B / NRCC 4725).
Q -> H
  BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHI2OBIACEAE GROUP;
RHIZOBIACEAE; AGROBACTERIUM.
                                                                    SEQUENCE FROM N.A.
STRAIN-T1305 LAC9;
MEDLINE; 96429889.
TIBURIUS A., DE LUCA N., HUSSAIN H., JOHNSTON A.W.B.;
"Expression of the exoY gene, required for exopolysaccharide synthesis in Agrobacterium, is activated by the regulatory ros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIALYLTRANSFERASE (EC 2.4.99,-)
(BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST)
(LIPOOLIGOSACCHARIDE SIALYLTRANSFERASE) (LST).
                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 2; Length 262;
Pred. No. 9.22e+00;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 13
P72097
P72099; P72009; P72101;
D720997; P72099; P721001;
D1-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-
                                                                                                                                                                                                                                                                                                                                  262 AA; 28124 MW; DF7A4568 CRC32;
                                                                                                                                                                                                                           gene. .;
MICROBIOLOGY 142:2621-2629(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: GLYCOSYLATION.
EMBL; U60660; G1546004; -.
EMBL; U60661; G1546009; -.
EMBL; U60662; G1546009; -.
EMBL; U60665; G1546011; -.
TRANSFERASE; GLYCOSYLTRANSFERASE.
                                                                                                                                                                                                                                                              EMBL; X95394; E220383; -.
PFAM; PF00202; aminotran_3; 1.
TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42611 MW;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 STGVLVPPKGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 STGALVDSKSY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
273
371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-GLUCOSAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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VARIANT
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01-JAN-1998 (TREMBLELEL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
MONOCARBOXYLATE TRANSPORTER MCT3 (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MUSIDAE: MUSALOA; MONDAE: MORTOAE; MUSALOA;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-POB1;
BIBOLLET-RUCHE F., BRENGUES C., GALAT-LUONG A., GALAT G., POURRUT X., VIDAL. N., VESS F., DURAND J.P., CUNY G.;
J. VIROL. 71:307-313(1997).
EMBL; U37209; G1353456; -.
PFAM; PF00517; GP41; 1.
ENVELOPE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 14; Length 142;
Pred. No. 9.22e+00;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 11; Length 156;
Pred. No. 9.22e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHILP N.J., YOON H.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF019111; G2407664; -
                                                                                     LT 10
087600 PRELIMINARY; PRT; 142 AA.
087600;
01-00V-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
044188 PRELIMINARY; PRT; 262 AA.
044189; 044189; 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
W-AMINO-TRANSFERASE-LIKE PROTEIN.
                                                                                                                                                                                                                                                                               SIMIAN IMMUNODEFICIENCY VIRUS (SIV-AGM).
VIRUSES; RETROID VIRUSES; RETROVIRIDAE; LENTIVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 142 142
SEQUENCE 142 AA; 16852 MW; C58A9A91 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB394B9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 156 AA; 16253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match
Local Similarity 61.5%;
hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.1%;
Similarity 46.7%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGROBACTERIUM RADIOBACTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :|:| ||:||:
DPSTGALV-DSKSYA 79
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 PSAGRLVDALKNY 49
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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LT 11 035308 035308;

99

Query Match

Matches

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29

Match

Query

Matches

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01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
MONOCARBOXYLATE TRANSPORTER MCT3.
RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA; EUTHERIA: RODENTIA;
SCIUROGNATHI: MURIDAE: MURINAE: RATTUS.
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEGGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.1%; Score 50; DB 13; Length 542; Best Local Similarity 61.5%; Pred. No. 9.22e+00; Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 58.1%; Score 50; DB 11; Length 492; Local Similarity 61.5%; Pred. No. 9.22e+00; hes 8; Conservative 3; Mismatches 1; Indels
      Length 371;
Score 50; DB 2; Length 371;
Pred. No. 9.22e+00;
3; Mismatches 3; Indels
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINA;
STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINA;
PHILP N.J., YOON H.;
SUBMITTED (ARR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; APOS9288; G3170609; -.
SFOUENCE 492 AA; 51590 MW; 20F051C1 CRC32;
SFOUENCE 492 AA; 51590 MW; DB 11; Lengt
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PHILP N.J., YOON H.;
SUBMITIED (ADDOLADE) DATA BANKS.
EMBL; AFDOO240; G2198807; -.
SEQUENCE 542 AA; 58085 MW; 836DA7B1 CRC32;
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013151
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01-301-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-A01-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
MONOCARBOXYLATE TRANSPORTER 3.
                                                                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                PRT;
Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                    164 DDGTGNLIQSSSY 176
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66 DPSTGALVDSKSY 78
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Search completed: Wed Sep 1.16:29:45 1999 Job time : 21 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.43 Seconds 62.340 Million cell updates/sec Wed Sep 1 16:33:07 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 Description: Perfect Score:

1 STSNDTTSAAFVS 13 Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part14 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part34 35:part33 36:part36 37:part37 38:part38 39:part39

Mean 15.573; Variance 46.313; scale 0.336 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Watch Length DB ID Descri
Human calcium	
Human calcium	
Human calcium	
Human calcium	219 33 W63158 Human Ce
Myasthenic antiqenic	240 8 R39697 Myasther
Human neuronal VDCC	478 8 R39563 Human n
Human calcium channe	33 W63143 Human
Human calcium channel	478 14 R72611 Human ca.
Sequence of splice va	6 R33551
Human calcium	479 14 R72604 Human cal
Human calcium	33 W63156 Human
Human calcium channel	
Human neuronal	
Human calcium channel	33 W63144 Human
Human calcium channe	
Sequence of splice va	598 6 R33552 Segmence

Human neuronal calciu 1.78e+01 Human Kv potassium ch 2.29e+02 Merosin major subunit 2.29e+02 Merosin major subunit 2.29e+02 Merosin major subunit 2.29e+02 Bovine poly-immunoglo 2.9ae+02 C. japonica phosphoen 3.74e+02 AFP-1 (Ala 2460 Val). 3.74e+02 AFP-1. DP10 VH region. 3.74e+02 AFP-1. DP10 VH region. 4.76e+02 CEA-specific antibody 4.76e+02 Achromobacter lyticus 4.76e+02 Achromobacter lyticus 4.76e+02 Achromobacter lyticus 4.76e+02 Achromobacter lyticus 4.76e+02 B-t. alkaline proteas 4.76e+02 Srotease encoded by c 4.76e+02 Srotease encoded by C 4.76e+02 Crystal protein CryET 4.76e+02	PERSULT 1  W63157 standard; Protein; 216 AA.  Human calcium channel beta-4 subunit.  W6127-1998
R72613 W79589 W79590 W79590 W772990 R113436 W72564 W72564 W77568 W27568 W27568 W27568 W2756 W27136 W27136 W27136 W27136 W27136 W27136 W27136 W27136 W27136	ALIGNMENT 216 AA.  216 AA.  4 subunit cium chann Eaton Synd duction of san of Lam Sis of Lam Sents the channel equired for the nucleic equired for the nucleic says for the channel. Then transcript hen transcript her reactive for it and indiv gnostic for grant of the reactive her reactive the reactive for it and indiv gnostic for grant for the reactive for the reactive for the reactive for the reactive for it and indiv gnostic for grant for the reactive for the reactiv
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N-FSDB; QR/823.

The encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for developing prods. for studying calcium channels, e.g. for obtainhing agonists and antagonists.

To isolate DNA encoding the Beta I subunit, a human hippocampus con the product of the Beta I subunit, a bush is selected and was in turn used to isolate encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate converlaping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were isolated and sequenced. Five alternatively spliced forms of the beta I subunit have been identified. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-2, expressed in the calls. Full-length DNA clones encoding the beta 1-2 and beta 1-3 subunits have been constructed. The subunits beta 1-1 and beta 1-2 and beta 1-2, expressed in milling subunit. Sequences of the beta 1 spliced forms of the calls and pilication analysis as alternatively spliced forms of the beta subunit. Sequences of the beta 1 splice variants are set forth in QBT88172611, QBT839/R72612 and QQBT831-QBT833 and
                                                Gaps
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                        Length 216;
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                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.78e+01;
2; Mismatches 1; Indels
                                                                                                                                                                            Human calcium channel subunit beta 1-4.
Calcium channel subunit; antagonist; agonist; diagnosis;
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1995 (first entry)
Human calcium channel subunit beta 1-5.
Calcium channel subunit; antagonist; agonist; diagnosis;
                                78e+01;
                        Score 54; DB 33;
Pred. No. 1.78e+01
                                              2; Mismatches
                                                                                                                                                                                                                                       16-FEB-1995.
11-AUG-1994; U09230.
11-AUG-1993: US-105536.
05-NOV-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB. Gillespie A, Harpold MM, McCU
WPI; 95-090900/12.
                                                                                                                               T 2
R72605 standard; Protein; 216 AA.
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                     79.4%;
Similarity 75.0%;
9; Conservative
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01-DEC-1995 (first entry)
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11-AUG-1994; U09230.
11-AUG-1993; US-105536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambert Eaton Syndrome
                                                                     44 stssdttsnsfv 55
                                                                                         81 STSNDTTSAAFV 92
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                                  Local Similarity
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 216 AA;
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WO9504822-A.
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WO9504822-A.
Sequence
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DNA encoding human calcium channel alpha 1B sub:unit protein - useful for recombinant production of the channel for screening of its modulators, and diagnosis of Lambert Eaton Syndrome Disclosure; Columns 27-230; 166pp; English.

The present sequence represents the beta-5 subunit of a human calcium channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can
                                                                                                                                                                                                                                                                                              DNA encoding human calcium channel sub-unit(s) - used for developing prods. for studying calcium channels, e.g. for developing prods. for studying calcium channels, e.g. for obtaining agonists and antagonists.

PT developing prodists and antagonists

Disclosure; Page 258-259, 285pp; English.

CT oisolate DNA encoding the Beta I subunit, a human hippocampus comparing the arabit sweletal muscle calcium channel beta subunit.

CA hybridising clone was selected and was in turn used to isolate cancoding the entire human calcium channel beta subunit.

A hybridishing clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were concoling the entire human calcium channel beta 2 subunit were beta 1-1, expressed in sheletal muscle, beta 1-2, expressed in the CNS, beta 1-1, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3 subunits have been constructed. The subunits beta 1-3 subunits have been constructed. The subunits beta 1-3 beta 1-2, cancoding the beta 1-3 beta 1-2, cancoding the beta 1-3 beta 1-2, expressed in the CNS beta 1-4 and beta 1-5 have been identified by nucleic acid beta 1-4 and beta 1-5 have been identified by nucleic acid beta subunit. Sequences of the beta 1 splice variants are set forth in QR7808/R72611, QR7883/R72612 and QQR881-QR888/R72611, QR7884/R72612 and QQR881-QR888/R72611, QR7884/R72612 and QQR881-QR888/R72611, QR7884/R72612 and QQR881-QR888/R72611, CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR888-CR8
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
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Beta-5 subunit; human; calcium channel; assay; detection;
characterisation; Lambert Eaton Syndrome; LES; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1989; US-603751.
04-APR-1989; US-603751.
20-FBE-1990; US-603751.
20-NOV-1990; US-620250.
15-AUG-1991; US-745206.
31-ANG-1995; US-755543.
SIBIA NURROSCIENCES INC.
Brenner R. Ellis SB, Feldman DH, Harpold MM, McCue
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Ellis SB, Gillespie A, Harpold MM, Mccue AF,
WPI: 95-099900/12.
DNA ACCUE A.
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Best Local Similarity 75.0%;
Matches 9; Conservative
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81 STSNDTTSAAFV 92
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04-APR-1994; US-2233
04-APR-1988; US-1768
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N-PSDB; V42707.
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be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha I subunit with Igg molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mer purified myasthenic antigenic polypeptide and its corresp. antibody - useful for diagnosing and treating proliferation of neoplastic cells in patient with Lambert-Eaton myasthenic syndrome claim 5; Page 26-27, 48pp; English.

The sequence is that of myasthenic antigenic polypeptide (MAP) encoded by the cDNA clone p mysB. MAP can be used to detect antibodies associated with paraneoplastic sensory neuronopathy such as Lambert-Eaton myasthenic syndrome (LEMS). These antibodies are used to determine if a patient with neurological symptoms has a fumour expressing MAP, to inhibit proliferation of neoplastic cells in LEMS
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Myssthenic antigenic polypeptide.
MAP: antibody detection; LEMS; Lambert-Eaton myasthenic syndrome;
paraneoplastic sensory neuronopathy; p mys B; mysB; ss.
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                                                                                                                                                     Score 54; DB 33; Length 219;
Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 8; Length 240; Pred. No. 1.78e+01;
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09-FEB-1994 (first entry)
Human neuronal VDCC beta-subunit encoded by clone HBB1.
Voltage-dependent calcium channel; VDCC; beta-subunit;
calcium flux; ss.
                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUL-1993. U00227. 11-JAN-1993. U00227. 10-JAN-1992. US-820312. (SLOK ) SLOAN KETTERING INST CANCER. Furneaux HM, Posner JB; WPI; 93-243126/30. N-PSDB; Q46673.
                                                                                                                                                                                                                                                                                                                                                     T
R39697 standard; Protein; 240 AA.
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R39563 standard; Protein; 478 AA.
                                                                                                                                                     Match 79.4%;
Local Similarity 75.0%;
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Local Similarity 75.0%;
                                                                                                                                                                                                  9; Conservative
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06-JUL-1992; 222126.
17-FEB-1992; DE-204716.
06-JUL-1992; DE-222126.
                                                                                                                                                                                                                                           44 stssdttsnsfv 55
                                                                                                                                                                                                                                                                                 81 STSNDTTSAAFV 92
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                                                                                                            219 AA;
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81 STSNDTTSAAFV
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Spreyer P, Unter
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WO9314098-A.
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DE4222126-A.
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The present sequence and the channel alpha lb sub:unit protein - useful for recombinant production of the channel for screening of the useful for recombinant production of the channel for screening of the medialacries, and diagnosis of Lambert Eaton Syndrome Claim 3; Columns 217-220; Löfep; English.

The present sequence is encoded by a splice variant of the beta subunit of an achieum channel. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into contraction. The recombinant subunit, when expressed with nucleic acids contraction and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribed, giving more than one form of the protein from the same transcribt, each having slightly different properties. In addition, the rection and variance and alternatively from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a diagnostic for the disease.
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                    for agonists and antagonists of calcium channels for agonists and antagonists of calcium channels.

A first oligonucleotide probe (Q46075) complementary to nucleotides 361-400 of the VDCC beta-subunit from rabbit skeletal muscle was used to screen a human hippocampus cDNA library. A 1.9kb cDNA fragment was isolated for further screening to isolate human VDCC beta-subunit coding sequences. Clone HBB1 was sequenced and found sequence R39563 was deduced from the open reading frame.

See also Q46077-Q46078.
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      and screening systems
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 8; Length 478; Pred. No. 1.78e+01; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human calcium channel beta subunit splice variant beta2. Beta subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-1990; US-482384.
30-000Y-1990; US-482384.
31-MG-1991; US-745206.
31-MAY-1995; US-455543.
(SIBI-) SIBIA NEUROSCIENCES INC.
WHILLAMS R. Ellis SB, Feldman DH, Harpold MM, McCue AF, Williams R.
useful in calcium-flux studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W63143 standard; Protein; 478 AA.
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Similarity 75.0%;
9; Conservative
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Best Local Similarity 75.0%;
Matches 9; Conservative
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12-OCT-1998 (first entry)
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04-APR-1994; US-223305.
04-APR-1988; US-176899.
04-APR-1989; US-603751.
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Best Local Similarity
Matches 9; Conserv
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US5792846-A.
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Sequence
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                                                                                                                                                                                                                                                                                                                               developing proces. For studying calcium channels, e.g. Lor obtaining agonists and antagonists

Disclosure: Page 160-162; 285pp; English.

Disclosure Page 160-162; 285pp; English.

To isolate DNA encoding the Beta I subunit, a human hippocampus converted by hybridisation to a DNA fragment encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate overlapping clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were sociated and sequenced. Five alternatively spliced forms of the beta 1 subunit have been identified. These forms are designated beta 1 subunit have been identified. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-1, expressed in the CNS beta 1-4 expressed in the CNS beta 1-4 and beta 1-5 have been identified by nucleic acid subunits have been constructed. The subunits beta 1-1, beta 1-2, and beta 1-2 and beta 1-3 an
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Lambert Eaton syndrome.
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                                                                                                                                                               16-FEB-1995.
11-Add-1994. U09230.
11-Add-1993: US-105536.
05-NOV-1993: US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Elis SB, Gillespie A, Harpold MM, Mccue AF, Williams ME; WPI: 95-090000/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 14; Length 478; Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                           for
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Sequence of splice variant beta 1-2 of beta human calcium
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                                                          01-DEC-1995 (first entry)
Human calcium channel subunit beta 1.
Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                   N-PSDB; Q87838.
DNA encoding human calcium channel sub-unit(s) - used
developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-701-1992; U06903.
15-AUG-1992; US-745206.
10-APR-1992; US-868354.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Brenner R, Ellis SB, Feldman DH, Harpold MM,
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                             R72611 standard; Protein; 478 AA.
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Best Local Similarity 75.0%;
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                                                                                                Calcium channel subunit
Lambert Eaton Syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 stssdttsnsfv 55
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N-PSDB; 037819.
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WO9304083-A.
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                                               R72611;
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The developing prods. for studying calcium channels, e.g. for obtainfng agonists and antagonists

To isolate DNA encoding the Beta I subunit, a human hippocampus

CODNA library was screened by hybridisation to a DNA fragment encoding a rabbit skeletal muscle calcium channel beta subunit.

A hybridising clone was selected and was in turn used to isolate coverlapping clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were isolated and sequenced. Five alternatively spliced forms of the beta I subunit have been identified. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-3, also expressed in the CNS, beta 1-1, expressed in the CNS, beta 1-2 and beta 1-3 subunits have been constructed. The subunits beta 1-2 beta 1-2, beta 1-2, cannot an an an an an an allysis as alternatively spliced forms of the beta 1-4 and beta 1-5 have been identified by nucleic acid amplification analysis as alternatively spliced forms of the beta subunit subunit
Disclosure; Page 129-131; 150pp; English.

Five alternatively spliced forms of the human calcium channel beta I subunit have been identified and DNA encoding a number of forms have been identified and DNA encoding a number of forms have been isolated. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-3, also expressed in the CNS, beta and HEK 293 cells, and beta 1-5, expressed in HEK 293 cells.
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Pred. No. 1.78e+01;
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Lambert Eaton Syndrome.
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11-AUG-1993; US-105536.
05-NV-1993: US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
E111s SB. G11Lespie A, Harpold MM, Mccue AF,
WPI: 95-090900/12.
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Pred. No. 1.78e+01;
                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1995 (first entry)
Human calcium channel subunit beta 1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .T 11
W63156 standard; Protein; 523 AA.
W63156.
12-0CT-1998 (first entry)
Human calcium channel beta-1 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 10
R72604 standard; Protein; 479 AA.
                                                                                                                                                                                                                                                                                        79.48;
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Similarity 75.0%;
9; Conservative
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81 STSNDTTSAAFV 92
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Best Local Similarity
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Matches 9; Conser
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WO9504822-A.
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PCT-US99-13024-2-12.rag

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Dividing human calcium channel alpha 1B sub:unit protein -

useful for recombinant production of the channel for screening of

useful for recombinant production of the channel for screening of

useful for recombinant production of Lambert Eaton Syndrome

claim 3: Columns 223-226; 166pp; English.

The present sequence represents the beta-1 subunit of a human calcium

channel, calcium channels are membrane-spanning, multi-subunit proteins

that allow controlled entry of calcium ions into cells. This leads

to depolarisation events required for muscle contraction. The recombinant

subunit, when expressed with nucleic acids encoding the complete calcium

channel, can be used in assays for the detection and characterisation of

compounds that modulate the channel. The DNA encoding the subunits can

be alternatively spliced when transcribed, giving more than one form of

the protein from the same transcribe, each having slightly different

properties. In addition, the reactivity of the alpha 1 subunit with IgG

molecules from the serum of an individual with Lambert Eaton Syndrome

(LES) can be used as a diagnostic for the disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human calcium channel alpha 1B sub:unit protein - useful for recombinant production of the channel for screening of its modulators, and diagnosis of Lambert Eaton Syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 33; Length 523; Pred. No. 1.78e+01;
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Beta subunit; human; calcium channel; assay; detection;
characterisation; Lambert Eaton Syndrome; LES; diagnosis.
   detection;
                  characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                      (SIBI-) SIBIA NEUROSCIENCES INC.
Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SIBI-) SIBIA NEUROSCIENCES INC.
Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF,
Beta-1 subunit; human; calcium channel; assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 530 AA:
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Best Local Similarity 75.0%;
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04-APR-1994; US-223305.

04-APR-1989; US-603751.

04-APR-1989; WO-U01408.

04-APR-1989; WO-U01408.

20-FEB-1990; US-482384.

30-NOV-1990; US-45206.

15-AUG-1991; US-745206.
                                                                                   31-MAY 1995; 455543.
04-APR-1994; US-223305.
04-APR-1988; US-176899.
04-APR-1989; WO-U01408.
20-FEB-1990; US-462384.
30-NOV-1990; US-42206.
15-AUG-1991; US-745206.
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81 STSNDTTSAAFV 92
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WPI; 98-456192/39.
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USS792846-A.
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W63147
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Disclosure; Columns 125-130; 166pp; English.

The present sequence represents the beta subunit of a human calcium channels are membrane-spanning, multi-subunit channel. Calcium channels are membrane-spanning, multi-subunit mortaling that allow controlled entry of calcium ions into cells.

This leads to depolarisation events required for muscle contraction. The recombinant subunit, when expressed with nucleic acids encoding the complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding the subunits can be alternatively spliced when transcribed, glving more than one form of the protein from the same transcript, each having alightly different properties. In addition, the cactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert Eaton Syndrome (LES) can be used as a individual with Lambert Eaton Syndrome (LES) can be used as a squence 530 AA;
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Claim 2: Page 11-13; 13pp; German

A first oligonucleotide probe (046075) complementary to nucleotides 361-400 of the VDCC beta-subunit from rabbit skeletal muscle was used to screen a human hippocampus CDNA library. A 1.9kb cDNA beta-subunit coding sequences. Clone HBB3 was sequenced and nucleotides 1-1288 were found to have 92% homology to the rabbit The anino acid sequence and coding sequence is no detectable homology. The anino acid sequence R39565 was deduced from the open reading frame. See also 046076 and 046077.
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                                                                                                                                                                                                                                                                                                                                  Score 54; DB 33; Length 530; Pred. No. 1.78e+01;
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W63144;
L2-OCT-1998 (first entry)
Human calcium channel beta subunit splice variant beta3.
Beta subunit; human; calcium channel; assay; detection; characterisation; Lambert Eaton Syndrome; LES; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R39565 standard; Protein; 571 AA.
R39565;
09-FEB-1994 (first entry)
Human neuronal VDCC beta-subunit encoded by clone HBB3.
Voltage-dependent calcium channel; VDCC; beta-subunit;
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                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                Query Match 79.4%;
Best Local Similarity 75.0%;
Matches 9; Conservative
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Similarity 75.0%;
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               44 stssdttsnsfv 55
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81 STSNDTTSAAFV 92
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81 STSNDTTSAAFV 92
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Best Local Similarity
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DE4222126-A.
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PCT-US99-13024-2-12.rag

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N'ENDIS' Vacobo.

N'ENDIS' Vac
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Disclosure; Page 163-165; 285pp; English.

To isolate DNA encoding the Beta I subunit, a human hippocampus CDNA library was screened by hybridisation to a DNA fragment ancoding a rabbit skeletal muscle calcium channel beta subunit. A hybridising clone was selected and was in turn used to isolate overlapping clones until the overlapping clones encompassing DNA encoding the entire human calcium channel beta 2 subunit were isolated and sequenced. Five alternatively spliced forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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11-AUG-1994; U09230.
11-AUG-1993; US-105536.
05-NOV-1993; US-149097.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
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Pred. No. 1.78e+01;
2; Mismatches 1; Indels
                                                       Human calcium channel subunit beta 1-3.
Calcium channel subunit; antagonist; agonist; dlagnosis;
Lambert Eaton Syndrome.
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Best Local Similarity 75.0%;
Matches 9; Conservative
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Sequence 598 AA;
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N-PSDB; V42688.
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WPI; 95-090900/
N-PSDB; Q87839.
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16-FEB-1995.
                                                                                                                                                                                                                                                                                                                                 Williams ME;
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beta 1 subunit have been identified. These forms are designated beta 1-1, expressed in skeletal muscle, beta 1-2, expressed in the CNS, beta 1-4, expressed in the CNS, beta 1-4, expressed in acorta tissue and HEK 293 cells, and beta 1-5, expressed in HEK 293 cells. Full-length DNA clones encoding the beta 1-2 and beta 1-3 subunits have been constructed. The subunits beta 1-1, beta 1-2, amplification analysis as alternatively spliced forms of the beta subunit. Sequences of the beta 1 splice variants are set forth in QNF038/R72611, QNF039/R72612 and QQNF031-QNF033 and
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                                                                                                                                                                                                                                                                        Score 54; DB 14; Length 598;
Pred. No. 1.78e+01;
2; Mismatches 1; Indels
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Best Local Similarity 75.0%;
Matches 9; Conservative
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81 STSNDTTSAAFV
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:32:35 1999; MasPar time 4.57 Seconds 113.947 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 1 STSNDTTSAAFVS 13 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 22.122; Variance 24.813; scale 0.892 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred	•	1.44e-01	1.440-01	1.446-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	1.44e-01	3.61e+00	3.61e+00	3.61e+00	9.97e+00	1.64e+01	1.64e+01	1.64e+01	2.67e+01	2.67e+01		2.67e+01	2.67e+01
	Description		voltage-dependent cal	L-type voltage-gated	calcium channel beta-	voltage-dependent cal	L-type voltage-gated	calcium channel prote	myasthenic syndrome a	voltage-dependent cal	calcium channel prote	L-type voltage-gated	calcium channel prote	long polar fimbrial o	probable hormone rece	nitrogen requiatory p	hypothetical protein	adenylosuccinate synt	hypothetical protein	probable membrane pro	variant surface glyco	potassium channel pro	potassium channel pro	probable helicase (EC	
SUMMARIES	ID		A44461	165766	JH0566	B44461	165767	A41347	A48895	C44461	S18304	152859	S21048	D56271	A57172	A34755	S50536	A64370	S09761	820929	A21112	157681	A35312	A39624	ммномн
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	Length		475	477	478	478	522	524	267	296	597	597	632	355	886	1036	1076	345	416	583	37	236	490	588	1751
æ	Query Match	1 1	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4	9.07	70.6	9.07	9.79	66.2	66.2	66.2	64.7	64.7	64.7	64.7	64.7
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##residues 1-478 ##label WIL
##cross-references GB-M76560; NID:g179743; PID:g179744
##experimental_source hippocampus
VT This protein is a subunit of the voltage dependent calcium channel.
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Neuron (1992) 8:71-84
Structure and functional expression of alphal, alpha2, and beta subunits of a novel human neuronal calcium channel
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Circ. Res. (1993) 72:1337-1344
Molecular cloning of three isoforms of the L-type
voltage-dependent calcium channel B subunit from normal
            L-type voltage-gated calcium channel B subunit - human #formal_name Homo sapiens #common_name man 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
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Powers, P.A.; Liu, S.; Hogan, K.; Gregg, R.G.
J. Biol. Chem. (1992) 267:22967-22972
Skeletal muscle and brain isoforms of a beta-subunit of human
voltage-dependent calcium channels are encoded by a single
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Caltc. Res. (1993) 72:1337-1344
Molecular cloning of three isoforms of the L-type
voltage-dependent calcium channel B subunit from normal
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B44461 #type complete
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##molecule_type nucleic acid
##cresidues 1-478 ##label POW
##cross-references GB:M92302; NID:g179803; PID:g179804
##experimental_source hippocampus
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##residues 1-522 ##label RES
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Powers, P.A.; Liu, S.; Hogan, K.; Gregg, R.G.
J. Biol. Chem. (1992) 267:22967-22972
J. Biol. muscle and brain isoforms of a beta-subunit of human voltage-dependent calcium channels are encoded by a single
            #authors Ruth, P.; Roehrkasten, A.; Biel, M.; Bosse, E.; Regulla, S.; Meyer, H.E.; Flockerzi, V.; Hofmann, F. Science (1989) 245:1115-1118
#journal Science (1989) 245:1115-1118
#title Primary structure of the beta subunit of the DHP-sensitive calcium channel from skeletal muscle.
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Ann. Neurol. (1993) 33:113:120
Cloning and characterization of a Lambert-Eaton myasthenic
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#length 524 #molecular-weight 57868 #checksum 8438
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                                                                                                                                                                                                                                            Score 54; DB 2; Length 544;
Pred. No. 1.44e-01;
....matches 1; Indels
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Pred. No. 1.44e-01;
2; Mismatches 1; Indels
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##residues 1-567 ##label ROS
##cross references GB:S60415; NID:g300416; PID:g300417
##experimental_source fetal brain
                                                                                                                                                                                                                                                                                                                                                                                                                           A48895 #type complete
myasthenic syndrome antigen B - human
MysB
                                                                                                                                                                     ##residues 1-524 ##label RUT
##cross-references GB:M25817
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##molecule_type mRNA
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larity 75.0%;
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Local Similarity 75.0%;
es 9; Conservative
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81 STSNDTTSAAFV 92
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Best Local Similarity
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#journal FEBS Lett. (1991) 291:253-258
#title Cloning and tissue-specific expression of the brain calcium cannot beta-subunit.
#cross-references MUID:92038046
#accession S18304
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#formal_name Rattus norvegicus #common_name Norway rat
22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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Glrc. Res. (1993) 72.1337-1344
Molecular cloning of three isoforms of the L-type
yoltage-dependent calcium channel B subunit from
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##cross-references GB:X61394; NID:955893; PID:955894
Y #holecular-weight 557 #molecular-weight 65679 #checksum
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Pred. No. 1.44e-01;
....matches 1; Indels
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##cross-references GB:L06110; NID:g187014; PID:g187015
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#accession 152859
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larity 75.0%; Conservative
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Best Local Similarity 75.0%;
Matches 9; Conservative
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81 STSNDTTSAAFV 92
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44 STSSDTTSNSFV 55

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Baud, V.; Chissoe, S.L.; Viegas-Pequignot, E.; Diriong, S.; N'Guyen, V.C.; Roe, B.A.; Lipinski, M. Genomics (1995) 26:334-344
EMRI, an unusual member in the family of hormone receptors with seven transmembrane segments.
A57172
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#superfamily nitrogen regulatory protein nit-2; GATA-type zinc finger homology
DNA binding; transcription regulation; zinc finger
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Rauthors Fu, Y.H.; Marzluf, G.A.
Fournal Mol. Cell. Biol. (1990) 10:1056-1065
Fille nit-2, the major nitrogen regulatory gene of Neurospora crassa, encodes a protein with a putative zinc finger DNA-binding domain.

#cross-references MUID:90158568
#accession A34755
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#formal_name Neurospora crassa
13.Jul-1990 #sequence_revision 26.Jul-1996 #text_change
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*region zinc finger GATA motif
*length 1036 *molecular-weight 109295 *checksum 235
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28-May-1993 #sequence_revision 24-Feb-1995 #text_change
21-Nov-1997
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#map_position 19p13.3-19p13.3
KEYWORDS transmembrane protein
SUMMARY #length 886 #molecular-weight 97679 #checksum 2055
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hypothetical protein YER033c - yeast (Saccharomyces
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##cross-references GB:X81479; NID:9784993; PID:9784994
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Pred. No. 3.61e+00;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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##residues 1-88
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81 STSNDTTSAAFVS 93
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81 STSNDTTSAAFVS 93
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N.; Hofmann, F.; Flockerzi, V.
#journal EMBO J. (1992) 11:885-890
#title Calcium channel beta subunit heterogeneity: functional
expression of cloned cDNA from heart, aorta and brain.
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10-Sep-1997
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03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
09-Sep-1997
D56271
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XX #length 632 #molecular-weight 70943 #checksum 1583
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long polar fimbrial operon protein LpfD - Salmonella
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#length 355 #molecular-weight 37714 #checksum
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Pred. No. 3.61e+00;
4; Mismatches 0; Indels
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Pred. No. 1.44e-01;
2; Mismatches 1;
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imilarity 63.6%;
7; Conservative
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Best Local Similarity 75.0%;
Matches 9; Conservative
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rabbit
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81 STSNDTTSAAFV 92
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ORGANISM
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 2.98 Seconds 123.152 Million cell updates/sec Wed Sep 1 16:31:14 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (81-93) from PCTUS9913024.pep (12 of 12) 68 Title: Description: Perfect Score: Sequence:

1 STSNDTTSAAFVS 13

PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 22.697; Variance 22.190; scale 1.023 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADIES

	Pred. No.	3.036-02	3.03e-02	3.03e-02	3.03e-02	3.03e-02	3.03e-02	3.03e-02	1.11e+00		1.11e+00	3.446+00	3.44e+00	5.97e+00		5.97e+00	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.03e+01	1.75e+01	1.75e+01	1.75e+01
	Description	DIHYDROPYRIDINE-SENSIT	LPFD PROTEIN PRECURSOR	CELL SURFACE GLYCOPROT	NITROGEN CATABOLIC ENZ	CYTOCHROME P450 12B1 P	HYPOTHETICAL 119.3 KD	ADENYLOSUCCINATE SYNTH	HYPOTHETICAL PROTEIN I	GENOME POLYPROTEIN [CO	VOLTAGE-GATED POTASSIU	PRE-MRNA SPLICING FACT	HYPERSENSITIVITY RESPO	LAMININ ALPHA-2 CHAIN	LAMININ ALPHA-2 CHAIN	DNA-DIRECTED RNA POLYM	METHYLENETETRAHYDROFOL	HYPOTHETICAL 38.2 KD P						
SUMMARIES	01	CCBB_HUMAN	CCBC_HUMAN	CCBC_RABIT	CCB2_HUMAN	CCBA_HUMAN	CCBA_RAT	CCB2_RABIT	LPFD_SALTY	EMR1_HUMAN	NIT2_NEUCR	CPP1_DROAC	YEM3_YEAST	PURA_METJA	IR12_HCMVA	POLG_BCMVN	CIKL_DROME	PR28_YEAST	HRA1_XANCV	LMA2_MOUSE	LMA2_HUMAN	RPC9_YEAST	FOLD_MYCPN	YEB7_YEAST
	DB	-	-	-	-	н	~	Н	Н	~1	-	-	-	-	Н	-	-	H	-	н	-	-	-	
	Query Match Length	478	523	524	567	296	597	632	355	886	1036	532	1076	345	416	3066	490	588	607	3106	3110	142	269	337
œ	Ouery Match	79.4	79.4	79.4	79.4	79.4	79.4	79.4	70.6	70.6	9.07	9. 79	67.6	66.2	66.2	66.2	64.7	64.7	64.7	64.7	64.7	63.2	63.2	63.2
	Score	54	54	54	54	54	24	24	48	48	48	46	46	45	45	45	44	44	44	44	44	43	43	43
	Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

PROBABLE AMMONIUM TRAN DEVELOPMENTAL PROTEIN HYPOTHETICAL 63.7 KD P	N POLIMERIC - IMMUNOS COBUL L HYPOTHETICAL 84.3 KD P L HYPOTHETICAL 124.8 KD E TRANSIENT - RECEPTOR - POT	1 JANUAROSE JUMONJI PROIEER. 1 YEAA_BACSU HYPOTHETICAL 31.8 KD P 2.94e+01 1 JYAU3_YEAST HYPOTHETICAL SUGAR KIN 2.94e+01 1 YHU3_YEAST HYPOTHETICAL 33.4 KD P 2.94e+01	1 PERX_SOLTU SUBERIZATION-ASSOCIATE 2.94e+01 1 PERZ_LYCES SUBERIZATION-ASSOCIATE 2.94e+01 1 PERL_LYCES SUBERIZATION-ASSOCIATE 2.94e+01 1 HISX_METUA HISTIDINOL DEHYDROGENA 2.94e+01	1 TBB1_PORPU TUBULIN BETA CHAIN 1. 2.94e+01 1 AMTZ_LYCES HIGH AFFINITY AMMONIUM 2.94e+01 1 YA7D_SCHPO HYDCTHETICAL 98.4 KD P 2.94e+01 1 YAY5_SCHPO PROBABLE ATP-DEPENDENT 2.94e+01 1 PS91_HUWAN 26S PROTEASOME REGULAT 2.94e+01 1 NS91_ERAT PROBABLE ATP-DEPENDENT 2.94e+01 1 N153_HUWAN NUCLEAR PORE COMPLEX P 2.94e+01
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## ALIGNMENTS

PCT-US99-13024-2-12.rsp

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MEDLINE; 93265672.
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no wath modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ALTERNATIVE PRODUCTS: THREE, TISSUE-SPECIFIC, FORMS OF THE BETA-1 SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE. SIMILARITY: CONTAINS I SH3 DOWAIN.
SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                   CALCIUM CHANNEL;
SH3 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POWERS P. A., LIUS., HOGAN K., GREGG R.G.;
"Skeletal muscle and brain isoforms of a beta-subunit of human voltage-dependent calcium channels are encoded by a single gene.";
J. BIOL. CHEM. 267:22967-22972(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 2
CCBC_HUMAN STANDARD: PRT; 523 AA.
Q0263-9.
Q0263-9.
Q1-304-1994 (REL. 29, CREATED)
O1-304-1996 (REL. 34, LAST SEQUENCE UPDATE)
D15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
D14VDROPPKRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-1M SUBUNIT CACNEI OR CACNEI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      E -> G (IN REF. 2).
QG -> R (IN REF. 3).
AA -> RR (IN REF. 1 AND 4).
6011892D CRC32;
                                                                                                                                                                                                                                                                                          PIR; B44*...
MIM; 114207; -..
PROSTIE: PS50002; SH3; 1.
PRAM; PF00018; SH3; 1.
PFAM; PF00018; Ca_channel_B; 1.
PFAM; PF00774; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 1; L
Pred. No. 3.03e-02;
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                                                                                                                                                                      EMBL, L06111, G187017;

EMBL, U86950, G2155254;

EMBL, U86952, G2155254;

EMBL, U86954, G2155254;

EMBL, U86955, G2155254;

JOINED.

EMBL, U86955, G2155254;

JOINED.

EMBL, U86955;

EMBL, U86956;

EMBL, U86957;

EMBL, U86957;

EMBL, U86959;

EMBL, URED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        53006 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                  EMBL; M92302; G179804; -. EMBL; M76560; G179744; -.
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TISSUE-SKELETAL MUSCLE;
MEDLINE; 93054616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
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STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                               189
425
21
28
434
478 AA;
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TISSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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hyperthermia susceptibility.";

L HUM. MOL. GENET. 2:863-868(1993).

L HUM. MOL. GENET. 2:863-868(1993).

L FUNCTION. THIS PROTEIN IS THE BETA SUBUNIT OF THE DIHYDROPYRIDINE.

C HONDENSTITYE CALCIUM CHANNEL. PLAYS A ROLE IN EXCITATION.

C CONTRACTION COUPLING. THE SKELETAL MUSCLE DHP-SENSITIVE CA(2+)

C CHANNEL MAY FUNCTION ONLY AS A MULTIPLE SUBUNIT COMPLEX.

C HONDEL MAY FUNCTION ONLY AS A MULTIPLE SUBUNIT. COMPOSED OF RIVE SUBUNITS: ALPHA-1, ALHA-2, BETA, GAMMA AND DELTA.

THE CYTOPLASMIC ASPECT OF THE SARCOLEMMA.

THE CYTOPLASMIC ASPECT OF THE SARCOLEMMA.

C HOSSUB SPECIFICITY: SKELETAL MUSCLE.

C HISSUE SPECIFICITY: SKELETAL MUSCLE.

C HISSUE SPECIFICITY: SKELETAL MUSCLE.

SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE.

SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE.

SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PFAM; PF00774; Ca_channel_B; 1.

IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
COLLIN T., WANG J., NARGEOT J., SCHWARTZ A.;
"Modecular cloining of three isoforms of the L-type voltage-dependent calcium channel beta subnit from normal human heart.";
CIRC. RES. 72:1337-1344(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93372845.

ILES D.E., SEGERS B., SENGERS R.C.A., MONSIEURS K., HEYTENS L.,
HALSALL P.J., HOPKINS P.M., ELLIS F.R., HALL-CURRAN J.L.,
STEWART A.D., WIERINGA B.,
"Genetic mapping of the beta 1- and gamma-subunits of the human
skeletal muscle L-type voltage-dependent calcium channel on
chromosome 17q and exclusion as candidate genes for malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Pred. No. 3.03e-02;
2; Mismatches 1; Indels
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MISSING (IN REF. 4).
AA -> RR (IN REF. 1 AND 3).
32CBEE9D CRC32;
                                                                                                                                                                   SEQUENCE FROM N.A.
POWERS P.A., GREGG R.G., HOGAN K.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH3.
POTENTIAL.
POTENTIAL.
QG -> R (IN
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1086960; 62155255; --
1086950; 62155255; --
1086954; 62155255; JOINED.
1086954; 62155255; JOINED.
1086955; 62155255; JOINED.
1086957; 62155255; JOINED.
1086957; 62155255; JOINED.
1086959; 62155255; JOINED.
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                                                                                                                                                                                                                                                                                                             SEQUENCE OF 146-209 FROM N.A.
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Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M92301; G179802; -.
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189
470
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183
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567 AA.

PRT;

STANDARD;

(REL. 30, CREATED)

Thu

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ROSENFELD M.R., WONG E., DALMAU J., MANLEY G., POSNER J.B.,
SHER E., FURNEAUX H.M.;
"Cloning and characterization of a Lambert-Eaton myasthenic syndrome
                                                              01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-2 SUBUNIT
(LAMBERT-EATON MYASTHENIC SYNDROME ANTIGEN B) (MYSB).
CACNB2 OR CACNLB2 OR MYSB.
                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                    HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                TISSUE-FETAL BRAIN;
MEDLINE; 93263585.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NOTE THE THE TRANSPORT OF THE PROCESS OF THE PROCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1-SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
ALPHA-1, ALPHA-2, BETA AND GAMMA.
-1-SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH
THE CYTOPLASMIC ASPECT OF THE SAFCOLEMMA.
-1-ALTERNATIVE PRODUCTS: THREE, TISSUE-SPECIFIC, FORMS OF THE BETA-1
SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE (BY
SIMILARITY:
-1-SIMILARITY: CONTAINS I SH3 DOMAIN.
-1-SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUCKERZI V., ROEHRKASTEN A., BIEL M., BOSSE E., REGULLA S., MEYER H.E.,
FLOCKERZI V., HOFFMANN F.;
"Primary structure of the beta subunit of the DHP-sensitive calcium
channel from skeletal muscle.";
SCIENCE 245:1115-1118(1989).
-!- FUNCTION: THIS PROFEIN IS A SUBUNIT OF THE DIHYDROPYRIDINE (DHP)
SENSITYPE CALCIUM CHANNEL.
                                                                                                                                                                        01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-1M SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50002; SH3; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00714; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHA GLXCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
                                                                                                                                                                                                                                                                                                                               ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 1; Length 524;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (IN G598370).
8AAC8B67 CRC32;
                                                                                                                                                     524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 89368946.
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POTENTIAL.
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57825 MW;
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                                                                                                                                                     STANDARD;
              44 STSSDTTSNSFV 55
                                        524 AA;
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                                                                                                                                                CCBC_RABIT
P19517;
01-FEB-1991 (
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CARBOHYD
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Matches
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MIDIOATGLDAEUDIPANHRSPKPSANSVTSPHSKEKRMP
FFKK -> GARSADEQDQWKTAGLFWRFT (IN
ALTERNATE FORM 1).
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ANN. NEDROL. 33:113-120(1993).

-I- FUNCTION: THIS PROTEIN IS A SUBUNIT OF THE DIHYDROPYRIDINE (DHP) SERNSTIVE CALCIUM CHANNEL (BY SIMILARITY).

-I- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

-I- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.

-I- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.

-I- TISSUE SPECIFICITY: TYPE FORMS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE.

-I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

-I- SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
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PFAM; PF00774; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 3.03e-02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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(REL. 29, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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Llarity 75.0%;
Conservative
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122
203
523
268
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MIM; 600003; -.
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81 STSNDTTSAAFV 92
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Best Local Similarity
Matches 9; Conser
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01-JUN-1994 (
15-JUL-1998 (
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CCBA_HUMAN
Q02641;
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                                                                                                                                                                                                                                                                                                                                                                                                          ACCILINT., WANG J., NARGEOT J., SCHWARTZ A.;

MEDLINE; 93265672.

A COLLIN T., WANG J., NARGEOT J., SCHWARTZ A.;

COLLIN T., WANG J., NARGEOT J., SCHWARTZ A.;

T. Molecular cloning of three isoforms of the L-type voltage-dependent at molecular cloning of three isoforms of the L-type voltage-dependent at molecular cloning of three isoforms of the L-type voltage.

C cle ES. 72:1337-1344(1993).

C IRC. RES. 72:1337-1344(1994).

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EMBL; L06110; G187015; --
EMBL; L06110; G187015; --
PIR; --
PA4461; --
MIM; 114207; --
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
PRAM; PF00018; SH3; 1.
PFAM; PF00018; SH3; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
                                                                                                                                                                   SEQUENCE FROM N.A.
ISSUE-HIPPOCAMPUS;
MEDLINE: 93054616.
POWERS P.A., LIU S., HOGAN K., GREGG R.G.;
FOWERS P.A., LIU S. HOGAN K., GREGG R.G.;
Valtage-dependent calcium channels are encoded by a single gene.";
J. BIOL. CHEM. 267:22967-22972(1992).
                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CHANNEL BETA-1-B2 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TS -> SG (IN REF. 2).
G -> R (IN REF. 2).
H -> D (IN REF. 2).
KL -> TV (IN REF. 2).
G -> S (IN REF. 2).
T -> S (IN REF. 2).
SNTR -> LOHT (IN REF. 2).
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A -> R (IN REF. 1).
E -> D (IN REF. 1).
B -> D (IN REF. 2).
A -> V (IN REF. 2).
A -> V (IN REF. 2).
S -> N (IN REF. 2).
C -> P (IN REF. 2).
L -> P (IN REF. 2).
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MISSING (IN REF. 2)
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POTENTIAL.
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CACNB1 OR CACNLB1.
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MEDLINE; 92038046.

MEDLINE; 92038046.

PRAGNELL M., SARAMOTO J., JAY S.D., CAMPBELL K.P.;

"Cloning and tissue-specific expression of the brain calcium channel beta-subunit.";

"EBS LETT. 291:253-258(1991).

"FEBS LETT. 291:253-258(1991).

"FEBS LETT. 291:253-258(1991).

"FEBS LETT. 291:253-258(1991).

"INTERPRETATIVE CALCIUM CHANNEL.

"SENSITIVE CALCIUM CHANNEL.

"SENSITIVE CALCIUM CHANNEL.

"SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

ALPHA-1, ALPERA-2, BETA AND GAMMA.

"THE CYTOPLASMIC ASPECT OF THE SARCOLEMMA.

"THE CYTOPLASMIC ASPECT OF THE SETA-1

"SIMILARITY: COUTAINS 1 SH3 DOMAIN.

"THE GENE (BY

SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
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PROSITE; PS50002; SH3; 1.
PFAM; PF00018; SH3; 1.
IONIC CHANNEL; SH3; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL;
GLYCOPROTEIN; PHOSPHORYLATION; ALTERNATIVE SPLICING; SH3 DOMAIN;
DOMAIN 100 161 SH3.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CHANNEL BETA-1-B2 SUBUNIT
                                                                                                                                                  Score 54; DB 1; Length 596;
Pred. No. 3.03e-02;
2; Mismatches 1; Indels
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Pred. No. 3.03e-02;
2; Mismatches 1; Indels
-> M (IN REF. 2).
                     L -> M (IN REF. 2).
WP -> CA (IN REF. 2).
R -> Q (IN REF. 2).
; OCC447D4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
23B08C47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                   557 557 L
571 572 WP
591 591 R
596 AA; 65638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65679 MW;
                                                                                                                                                  Match 79.4%;
Local Similarity 75.0%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.4%;
Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BETA-1 ISOFORM A).
CACUBI OR CACULBI.
RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                          44 STSSDTTSNSFV 55
                                                                                                                                                                                                                                                                                                           81 STSNDTTSAAFV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 STSSDTTSNSFV 55
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STSNDTTSAAFV 92
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Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                       JT 6
CCBA_RAT
P54283;
                   CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
MEDLINE, 95324926.
BAUD V., CHISSOE S.L., VIEGAS-PEQUIGNOT E., DIRIONG S., N'GUYEN V.C.,
ROE B.A., LIPINSKI M.;
"ERKI, an unusual member in the family of hormone receptors with
seven transmembrane segments.";
GENOMICS 26:334-344(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TECHNICATION: PROBABLY INVOLVED IN CELLULAR RESPONSE TO A HORMONE OR N INTERACTION WITH A PROTEIN LIGAND.

1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1 TISSUE SPECIFICITY: WIDE EXPRESSION; INCREASED LEVELS IN PERIPHERAL BLOOD MONONCLEAR CELLS.

1 PIN: N - AND O-GLYCOSYLATED; (POSSIBLE).

1 FIM: N - AND O-GLYCOSYLATED; (POSSIBLE).

1 SIMILARITY: CONTAINS 6 GEF-LIKE DOMAINS.

1 SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
CELL SURFACE GLYCOPROTEIN EMRI PRECURSOR (EMRI HORMONE RECEPTOR).
                                                                                                                  BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                  Identification and sequence analysis of lpfABCDE, a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1; Length 355;
Pred. No. 1.11e+00;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  fimbrial operon of Salmonella typhimurium.*;
J. BACTERIOL. 177:2087-2097(1995).
-1- SIMILARITY: BELONGS TO THE FIMH / LPFD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 POTENTIAL.
355 LPFD PROTEIN.
37714 MW; 20D529B5 CRC32;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 886 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYGENE; SG10560; LPFD.
PFAM; PF00419; Fimbrial; 1.
FIMBRIA; SIGNAL.
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 14028;
MEDLINE; 95238281.
BAUEMLER A.J., HEFFRON F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U18559; G829374; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                           LPFD PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24
355
                                                                                              SALMONELLA TYPHIMURIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TSKNTTGATFV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||::||:||:||
82 TSNDTTSAAFV 92
                                                                                                                                      SALMONELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMR1_HUMAN
Q14246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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MNQASGLDLLKISYGKGARRKNRFKGSDGSTSSDTTSNSFV
RQ -> MLDRHLAAPHTQGLVLE (IN CAB2A).
                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS: THREE FORMS OF THE BETA-2 SUBUNIT ARE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE: CAB2A, CAB2B (SHOWN HERE) AND CAB2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X64298; G1500; -.
EMBL; X64297; G1498; -.
EMBL; X64299; G1502; -.
PROSITE: PS50002; S13; 1.
PFAM: PF00018; S13; 1.
PFAM: PF00774; Ca_channel_B; 1.
IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; CALCIUM CHANNEL; GLYCOPROPEIN; PHOSPHORYLATION; S13 DOMAIN; MULTIGENE FAMILY;
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-2 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                         ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFKK -> KOKOKS (IN CAB2C)
DF97DA5D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER CALCIUM CHANNEL BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 1; Lv
Pred. No. 3.03e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN CAB2C)
MPFFKK -> KOKOKS (
                                                       632 AA.
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                                                       PRT;
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ilarity 75.0%;
Conservative
                                                       STANDARD;
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81 STSNDTTSAAFV 92
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235 2
632 AA;
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        MEDLINE; 92192022.
                                                                                                                                                                                       CACNB2 OR CACNLB2
                                                                                                                                                                                                                                                                                                        TISSUE-HEART
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LPFD_SALTY
P43663;
                                                       CCB2_RABIT
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SEQUENCE
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Gaps

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355 AA.

PRT;

STANDARD;

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Matches

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OR

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                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                               CELL SURFACE GLYCOPROTEIN EMR1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                           EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (1
EGF-LIKE 3, CALCIUM-BINDING (1
EGF-LIKE 4, CALCIUM-BINDING (1
EGF-LIKE 5, CALCIUM-BINDING (1
EGF-LIKE 6, CALCIUM-BINDING (1
                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
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                                                        EMBL; X81479; G784994; -.
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MOL. MICROBIOL. 4:1847-1852(1990).
-!- FUNCTION: MAJOR NITROGEN REGULATORY PROFEEN. DURING CONDITIONS OF NITROGEN LIMITATION IT TURNS ON THE EXPRESSION OF GENES FOR ENZYMES WHICH ARE REQUIRED FOR THE USE OF A VARIETY OF SECONDARY NITROGEN SOURCES, INCLUDING NITRATES, PURINES, AMINO ACIDS, AND
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                               STRAIN*74-0R23-1A;
MEDLINE; 90158568.
FU Y.-H., MARZLUF G.A.;
"nit-2, the major nitrogen regulatory gene of Neurospora crassa,
encodes a protein with a putative zinc finger DNA-binding domain.";
MOL. CELL. BIOL, 10:1056-1065(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- INDUCTION: BY LACK OF A PRIMARY NITROGEN SOURCE.
-!- SIMILARITY: HIGH TO OTHER FUNGAL NITROGEN REGULATORY PROTEINS.
-!- SIMILARITY: TO GATA TRANSCRIPTION FACTORS IN THE ZINC-FINGER REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HASE, TO0627; -:
TRANSFAC, TO0627; -:
TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING; ZINC-FINGER;
NUCLEAR PROTEIN; NITRATE ASSIMILATION; REPEAT.
DOMAIN 49 110 3 X APPROXIMATE REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING.
                                                                                                                                                                                                                                                                                               EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES; SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATA-TYPE.
CINC-STNG: ABOLISH DNA-BINDIN
RR-SG: ABOLISH DNA-BINDING.
RA-DV: ABOLISH DNA-BINDING.
GL->DV: ABOLISH DNA-BINDING.
KR->NS: ABOLISH DNA-BINDING.
Length 886
                                  Indels
Score 48; DB 1; Lence Pred. No. 1.11e+00; 2; Mismatches 3;
                                                                                                                                               10

NIT2_NEUCR STANDARD: PRT; 1036 AA.

NIT2_12:
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SANDATATION UPDATE)
NITROGEN CATABOLIC ENZYME REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A34755; A34755.
PROSITE; PS00344; GATA_ZN_FINGER; 1.
PFAM; PF00320; GATA; 1.
HSSP; P17429; 5GAT.
70.6%;
ilarity 61.5%;
Conservative
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92
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767
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769
                                                                 470 SESTETTGVAFVS 482
                                                                                          81 STSNDTTSAAFVS
 Query Match
Best Local Similarity
Matches 8; Conser
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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25:9b_est25
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	4.05e-63	1.58e-57	7.72e-54	2.26e-48	7.60e-31	1.70e-10	1.19e-09	4.19e-09	2.00e-06	2.00e-06
	Description	97SN1787 Rice Immature		97SN1784 Rice Immature	97SN1784 Rice Immature	AF034173 Human mRNA (T	AF034173 Human mRNA (T	vm55e09.xl Stratagene	Ī		yb26a12.rl Stratagene
	ΙΩ	AA754459	AA754459	AA754458	AA754458	AF034173	AF034173	A1506433	AA596420	AA032210	T58089
	DB	17	11	17	17	20	20	28	15	35	æ
	Query Match Length DB	252	252	247	247	2275	2275	507	565	369	517
<b>*</b>	Query	5.3	5.0	4.8	4.6	3.7	2.5	2.4	2.4	2.5	2.2
	Score	59	26	54	51	41	28	27	27	25	25
	Result No.	7	~	m	4	S	9	7	ထ	σ	10
	Res		υ		U		U		U	U	ပ

2.1 251 24 AL205893 qf60a07.x1 Soares_test 6.63e- 2.1 318 37 B96187 T18ETFE TAWN Arabidop 6.63e- 2.1 325 17 AA739545 310 PtFG2 Pinus taeda 6.63e- 2.1 381 41 AQ284757 RPCIII-87A4 TJ RPCIII 6.63e- 2.1 383 38 AQ028887 CIT-HSP-2313A16.TR CIT 3.82e- 2.1 396 10 AA234431 ZT72EL7.rl Soares_LMHM 3.82e- 2.1 447 39 AA13344 CIT-HSP-2313A16.TR CIT 6.63e- 2.1 441 39 AA113314 CIT-HSP-2313A10 3.82e- 2.1 441 39 AQ113314 CIT-HSP-237B1UJIA mal 6.53e- 2.1 441 39 AQ113314 CIT-HSP-237B1TJR CIT 6.63e- 2.1 441 39 AQ113314 CIT-HSP-237B1TJR CIT 6.63e-	2.1 447 19 109700	2.1 637 33 W03126 255303.r1 Soares feta 6 654 39 A011972 CIT-HSP-2377B1.TR CIT-3 82 2.1 654 39 A011972 CIT-HSP-2377B1.TR CIT-3 82 2.1 654 39 A011972 CIT-HSP-2377B1.TR CIT-3 82 2.1 764 14 A0264072 hbxb0066K14r CIGIR Rice 3 82 2.1 764 14 A0251506 hbxb00256G1f CIGIR Rice 3 82 2.1 769 41 A0291506 hbxb00256G1f CIGIR Rice 3 82 2.0 331 17 AA704953 zj95a01.s1 Soares_feta 1.03 2.0 360 32 D75694 CELKRO9AZE viji Kohara 1.03 2.0 360 32 A175673 EST218591 Normalized r 1.03 2.0 449 23 A175673 EST218591 Normalized r 1.03 2.0 609 25 A1294174 LP07487.5prime LP Dros 1.03 2.0 812 41 AQ291855 hbxb0040K19f CIGIR Rice 1.03 2.0 42 41 AQ291855 hbxb0040K19f CIGIR Rice 1.03 2.0 ALIGNMENTS	AA754459 252 bp mRNA EST 20-JAN-1998 SYN1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa AA754459 SAB01165 AA754459.1 GI:2801165 EST. Oryza sativa. Oryza sativa. Oryza sativa. Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Tobases 1 to 252)  Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.  Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)  On Jan 14, 1998 this sequence version replaced gi:1797457.	1 Tech, RDA 1 Tech, RDA 2 t of Biological 728 bhnahm@biose 7a"
44444464			1 10N 99 NO 1 S S E P A O O O O O O O O O O O O O O O O O O	RS II	×
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES

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a 21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA/54458 247 bp mRNA FST 20-JAN-1998
975N1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA clone 975N1784, mRNA sequence.
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/knote-"rectional cDNA library inserted into lambda ZAPII
/ector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref-"taxon:4530"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
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University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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1 (bases 1 to 247)

Nahm,B.H., Klim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R. Moon,E.P., Kim,W.T., Klim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y., Lee,M.C. and Eun,M.Y.

Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)

On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                                                                                                 91 NHTRCSRWRBVTRWAHYHDYTNCBBYNNNDYHWWHB-BMYBBTGCMTCTWWCWBHYNTKC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TA-SGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRK 208
                                                                                                                                                                                                                                                                                                                                                       31 WVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTWTWGTVNWBNVSGDWHYWBVBNTKVDVG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 252;
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                            / Match 5.0%; Score 56; DB 17; I Local Similarity 12.1%; Pred. No. 1.58e-57; nes 26; Conservative 109; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 YCVMWMTKKVVK-KYHVVBBGCHBTDSKCKTMWM 241
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                              /db_xref="taxon:4530"
/map="6"
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AA754458.1 GI:2801164
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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AA754459
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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21 c 12 g 35 t 179 others
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: MI3 Reverse Primer.
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1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 agtgttgagcaattcatgtcggcagttggtggaactaatgacgaaattgcgagattgcca 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMT-WGTVNWBNVSGDWHYWBVBN 84
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 YNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYT
                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                    Length 252
                                                                                                                                                                                                                                                                                                                                                5.3%; Score 59; DB 17; Length 252 Similarity 11.8%; Pred. No. 4.05e-63; 24; Conservative 109; Mismatches 66; Indels
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Department of Cytogenetics
National Inst. of Agri. Sci. and Tech,
Swon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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KEYWORDS
SOURCE
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1487 RKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKK-YTSTYYKSW 1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon2 contig, mRNA sequence.
                                                                                                                                                 61 HCRYTVBWYYARSKYGYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBT 120
                                                                                                                                                                                                                                                                                   121 AYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKV 180
                                                                                                                                                                                                                                                                                                                                                                                     616 ggaactaatgacgaaattgcgagattgccaacttcagctgctataagtaaattatctgat 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                       Gaps
                                                                                                                                                                                                                              181 TYGSSBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRRSRVHYGRWMBNKKRGMSRNWTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 19, 1998 this sequence version replaced gi:2045115.
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599 t 149 others
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                                                 Length 247;
                                          Query Match
4.6%; Score 51; DB 17; Length 247
Best Local Similarity 14.7%; Pred. No. 2.26e-48;
Matches 36; Conservative 107; Mismatches 100; Indels
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Pred. No. 7.60e-31;
85; Mismatches 55; Indels
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Division of Medical and Molecular Genetics
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7th floor, Guy's Tower, London SE1 9RT, UK
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/map-"6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="ntcon2 contig"
/clone_lib="Human mRNA
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Best Local Similarity 13.9%;
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Unpublished (1997)
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97SN1784 Rice Immature Seed Lambda 2APII cDNA Library Oryza sativa
CDNA Clone 97SN1784, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
Poaceae; Oryza.
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/coganism="oryza sativa"
/cultivar="Wilyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
*Not: Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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Nahm, B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797455.
                                                                                                                                                                                                                                                                                                      84 WNVDINIGGIGVGKTIVNVHSGWNNRCSNSVYYWBTAYCDYBHYBDRANHYDDTRCIND 143
                                                                                                                                                                                                                                                                                                                                                                                 25 HMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYGYGTBYY-S 83
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                         144 RGYCNYTASDNGTSA--TKRVTGYDKTDSDCGG-GCWRKVTYGSSBYBRCGVNVMVRTTS
                                                                                                                                                               4
                                                                                                                        Length 247;
                                                                                                                  Query Match
4.8%; Score 54; DB 17; Length 247
Best Local Similarity 15.5%; Pred. No. 7.72e-54;
Matches 35; Conservative 106; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       201 MWIDKSTKMBSMDMSRRSRVHYGRWMBNKKRGMSRNWIDTKTWRTR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
a 16 c 21 g 34 t 169 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Swon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA754458.1 GI:2801164
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The WashU-NCI Mouse EST Project 1999
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1493 RMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTSTYYKSWSRWYWYT 1552
                                                                                                                            AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens CDNA clone ntcon2 contig, mRNA sequence.
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1 (bases I to 2275)
Tripodis, N. and Ragoussis, J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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199 t 149 others
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               1605 YRYSWIGWIKWIIWWYMWSMIRWIMTIYIIWWIWRIIKIWWWWW 1649
                                       336 ttacttgctcttggaactacaaatatatctatcgtttttataat 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guys Hospital
7th floor, Guy's Tower, London SEl 9RT,
Email: nikos@nki.nl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .2275
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human mRNA
619 c 470 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ntcon2 contig"
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AF034173.1 GI:2707735
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Best Local Similarity 16.7%;
Matches 12; Conservative
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480 tttaacatgctc 469
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Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Parkway, Box 8501. St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watcon.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
MGI:566400
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: polyT not found
High quality sequence stopp: 464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..507

/organism="Mus musculus"

/note="Organ: blook Vector: pBluescript SK-; Site_1:

ECORI: Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;

Oligo dT. M30 cD4+ cells. Average insert size: 1.0 kb;

Oligo dT. Sequence: 5' adaptor sequence: 5' GAATTCGCACGAG

/db_xref="taxon:10090"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Medentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 595)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,R., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Materston,R.
The WashU-HHMI Mouse EST Project
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IMAGE:1002184 5', mRNA sequence.
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Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gi:1397738
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SolR (kanamycin resistant)"
127 c 106 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 507;
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Pred. No. 4.19e-09;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="8"
/clone="IMAGE:1002184"
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AA596420.1 GI:2411855
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Best Local Similarity 78.7%;
Matches 37; Conservative
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:S6400
Seg primer: -28ml3 revl ET from Amersham High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zk19d04.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone NAA672317, mRNA sequence.
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 
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1 (bases I to 369)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultnan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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On May 9, 1995 this sequence version replaced g1:802460.
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                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1002184"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
135 c 119 g 182 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 595;
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Pred. No. 4.19e-09;
0; Mismatches 10; Indels
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Location/Qualifiers
1. 595
/organism="Mus musculus"
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AA032210.1 GI:1502218
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Local Similarity 78.7%;
nes 37; Conservative
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/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
CoR1; Site_2: Xho!; Cloned uniditactionally. Primer:
Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
' -3' adaptor sequence: 5' CTCCAGTTTTTTTTTTTTTTT 3'"
/db_xref="GDB:49351"
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Insert Size: 887
High qality sequence stops: 312 Source: IMAGE Consortium, LLNL Th
clone is available royalty free through LLNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 887 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 TAAATAGCCATCAGAATACAATGGAATTTTAAGAATGAGATTAACTANTCCAAGTATATT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T58089 517 bp mRNA EST 08-FEB-1995 yb26a12.rl Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72286 5' similar to similar to gb:M31468 RAS-LIKE PROTEIN TC21 (HUMAN), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 517)
Hillacr.L., Clark.N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
              Library
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="IMAGE:72286"
/clone_lib="Stratagene fetal spleen (#937205)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
went through one round of normalization. Liconstructed by M. Fatima Bonaldo."

(db_xref="GDB:3756985"

(db_xref="taxon:9606"

/map="12p"

/clone="Inberes, pregnant_uterus_NöHPU"

/sex="female" adult"

/lab_host="dbH10B"

/ a 69 c 58 g 107 t lothers
                                                                                                                                                                                                                                                                                                                                                                            Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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0; Mismatches 26;
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    .517
    /organism="Homo sapiens"

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Location/Qualifiers
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Best Local Similarity 65.8%;
Matches 50; Conservative
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T58089.1 GI:659950
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High quality sequence stop: 245.
Location/Qualifiers
1. .251
/organism="Homo sapiens"
/organism="Homo sapiens"
/ore="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Ecc RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                             AI205893 251 bp mRNA EST 16-OCT-1998
qf60a07.xl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754388
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 251)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ATGAGCCTGCCAATCTGGACATTTTGGATACAGCTGGACAGGCAGAGTTTACAGCCATGC 157
                                                                                                                                                       Gaps
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151858
                                                                                                                                                     ;
;
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
1 98 c 135 g 145 t 9 others
                                                                                                                  Length 517;
                                                                                                                                                     30; Indels
                                                                                                            Score 25; DB 8; L. Pred. No. 2.00e-06; 0; Mismatches 30
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/clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                 367 ttaaccaagatactacttcaggag 344
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34 c 27 c
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AI205893.1 GI:3764565
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                                                                                                              Match 2.2%;
Local Similarity 64.3%;
les 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               3', mRNA sequence
AI205893
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;
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Rounaley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
Unpublished (1997)
Orber_GSSs: T18E5TR
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                B96187 318 bp DNA GSS 30-MAR-1998
T18E5TFB TAMU Arabidopsis thaliana genomic clone T18E5, genomic
                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thallana
Bukaryocta; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta: Tracheophyta; seed plants; Magnoliophyta;
eudicotyledons; Roslade; Capparales; Brassicaceae; Arabidopsis.
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/strain="Columbia"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2:
/haldIII; Produced by Rod Wing"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA739545 325 bp mRNA EST 15-JAN-1
310 PtIFG2 Pinus taeda cDNA clone 8507M 3', mRNA sequence.
AA739545
                                                                                                            125 TACAGICICAAAIAIGAAÁ-CIAAAAAGTICGAIAAICAITIAAGCAIIIICI 177
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  DB 24; Length 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 37; Length 318
Pred. No. 6.63e-04;
0; Mismatches 2; Indels
                                             0; Mismatches 12; Indels
  Score 23; DB 24;
Pred. No. 6.63e-04;
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Location/Qualiflers
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42 c 51 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 ATAATCGAATTTTTGCTATAATAACTA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_T18E5"
/clone_lib="TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rounsley@tigr.org
Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA739545.1 GI:2778096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%;
llarity 92.6%; Conservative
Query Match
Best Local Similarity 75.9%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                     g2998663
B96187.1 GI:2998663
                                                                                                                                                                                                                                                             survey sequence.
B96187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends
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Best Local Similarity 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              loblolly pine.
                                                                                                                                                                                                                                                                                                                                                                       thale cress.
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Gaps

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Indels

PCT-US99-13024-1.rst

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Unpublished (1997)
Other_GSSs: CIT-HSP-2313A16.TF
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primares; Catarrhini; Hominidae; Homo.
1 (bases 1 to 383)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                           Location/Qualifiers

1. 381

Arganism="Homo sapiens"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

/Ab_xref="GDB:7533027"

/db_xref="taxon:9606"

/clone="R-*RPA4"

/clone=lb="RPCIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ028987 383 bp DNA GSS 29-JUN-1998 CIT-HSP-2313A16.TR CIT-HSP Homo sapiens genomic clone 2313A16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                             Length 381;
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Pred. No. 3.82e-05;
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Pred. No. 6.63e-04;
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                                                                                                                                                                                                                                                                                     /cell_type="Lymphocytes"
56 c 64 g 14

    .383
    /organism="Homo sapiens"

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/clone="2313A16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualiflers
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74 c 50 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%;
Best Local Similarity 79.5%;
Matches 31; Conservative
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Best Local Similarity 71.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Pinus taeda"
/note-"Vector: lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/note-"Vector: lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
The tissue source for this library is xylem. The xylem
tissue was harvested in spring and summer from branches
of seed orchard trees which are clones of the same
genotype. Branches were 4-6 inches in diameter. The cDNAs
were directionally cloned into Lambda Zap and were
rescued as a Bluescript derivative in the EcoRI and XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 381)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                  Email: csk@s27w007.pswfs.gov
The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation.
Seq primer: M13.Universal.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ284757 381 bp DNA GSS 22-NOV-1998
PWC111-87A4.TJ RPCI11 Homo sapiens genomic clone R-87A4, genomic
AQ284757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
For clone availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                               Contact: Claire S. Kinlaw
USDA IFG Dendrome Project
Institute of Forest Genetics
Dendrome Project, Institute of Forest Genetics, P.O. Box 245,
Berkely, CA 94701
Tel: 51055596429
Fax: 5105556440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 TITGCTGTGTAATCTGCGGAATGGAAGTTGAACGATTAATATATCGTTTTTCCCGAAAA 307
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                                    Kinlaw,C.S.
Loblolly pine cDNAs
Unpublished (1995)
On Jan 7, 1998 this sequence version replaced g1:948055.
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Pred. No. 6.63e-04;
0; Mismatches 18; Indels
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="8507M"
/clone_lib="PtIFG2"
/tissue_type="xylem"
a 41 c 63 g
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2.1%;
Best Local Similarity 69.5%;
Matches 41; Conservative
                  (bases 1 to 325)
Pinaceae; Pinus
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                                        AUTHORS
TITLE
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g ô PCT-US99-13024-1.rst

ö Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps

Search completed: Thu Sep 2 14:51:10 1999 Job time: 2695 secs.

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25-APR-1996.
13-OCT-1995; U13023.
13-OCT-1994; US-322760.
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l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
ls:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part37 38:part38
39:part39 40:part46 41:part41 42:part42 43:part43
44:part44 50:part50 51:part41 42:part47 43:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part59 60:part66 5:part56 57:part57 58:part58
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962.282 Million cell updates/sec
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8.60e-09
3.23e-08
1.20e-07
1.20e-07
4.41e-07
2.50e-04
8.57e-04
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                                                                                                                                                                      . n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                          Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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Base substituted E.co
Oligonuclectide probe
Base substituted E.co
Mammalian DNA replica
Generic DNA sequence
Mammalian DNA replica
Generic DNA sequence
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(1-1119) from PCTUS9913024.seq
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Q51746
N81164
Q51746
N81164
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Q70465
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Listing first 45
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91
204
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Perfect Score:
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Comp:
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Generic DNA sequence
Generic DNA sequence
Generic DNA sequence
Generic DNA sequence
Mixed oligonuclectide
Generic DNA sequence
Sequence encoding new
Sequence e
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Phage T4 tail fibre genes.
Phage T4; tail fibre protein; nanotechnology; nano-structure; filter; molecular sieve; ss.
Bacterlophage T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product- unidentified product 4127..5014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/label= Gene_34
/product= gp34 protein
3894..4091
/*tag= b
/label= ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product- gp35 protein 5077..5742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= gp36 protein
5751..8831
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   /*tag= c
/label= Gene_35
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T29053 standard; DNA; 8855 ;
T29053;
07-JAN-1997 (first entry)
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Score 39;
Pred. No.
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01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CC
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Q51746 standard; cDNA; 91
Q51746;
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N81164;
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WPI; 93-378844/48.
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Best Local Similarity
Matches 1; Conser
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                                                                                                                                                                             corresponding DNA

Disclosure: Fig 7: 83pp; English.

Cenomic DNA (179053) from phage T4 includes open reading frames

Cenomic DNA (179053) from phage T4. Sp36 and gp37 (R97370, R97372-74), that comprise the tail fibres of the phage, as well

R97372-74), that comprise the tail fibres of the phage, as well

S an open reading frame encoding an unknown protein (R97371).

Cene sequences encoding native, modified or recombined tail fibre proteins can be incorporated into expression vectors to allow mass proden of the proteins in microbial hosts. Tail fibre proteins

C including fusion proteins) having novel structures are useful as building blocks for nanostructures having defined, adjustable, dimensions for use e.g. in filters and molecular sieves.

Sequence 8855 BP; 2731 A; 1624 C; 1859 G; 2641 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 aaactgagtaatagaaaaagcacagatgattatcaaactattttagatgttgtatttgac
                                                                    P-PSDB; R97371;
P-PSDB; R97372;
P-PSDB; R97373;
P-PSDB; R97374
P-PSDB; R97374
New proteins derived from T4 phage tail fibre proteins - that can self assemble into nano-structure(s), useful as filters etc, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttcatttaagagtttttgacccttccaccggagcattagttgatagtaagtcatatgctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1078; DB 24; Length 8855;
Pred. No. 0.00e+00;
0; Mismatches 8; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                               96.3%;
larity 98.9%;
Conservative
 B
 GOLDBERG E
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                 Goldberg EB;
WPI; 96-221942/22.
                                                      P-PSDB; R97370;
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                                                                                                                                                                                                      tgggaattaaaggaagattatgtagttgttccagaaaacgcagtaggatttacgatatac
                                                                                                                                                                                                                                                                                      gcacagagaactgcacaagctggccaaggtggcatgacaaatttaagcttttctgaagta
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but
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
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44; Mismatches 6;
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Mismatches 10;
                                                                                                                                                                                      Location/Qualifiers
  41;
                                                                                          T 5
N81164 standard; DNA; 204 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 6
V44650 standard; DNA; 91 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 A;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                           30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 11; Conser
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                                                                                                                                                                                                  misc_feature
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                                                                                                                    N81164;
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                                                                                                                                                                                                                 Disclosure; p: English.

Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable j' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 difft base substitutions, most of which
cocurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 759 atttgtagttccaagagcaagtaaatcagcatcagcatataactgagctttaagataaag 700
                                                                                                                                                      Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; WPI; 88-279927740.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 rttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhn 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             47 C; 17 G; 11 T; 108 Others;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14*A consists of nucleotides 5-95 of 10510315). It hybridized to all spp. of mycobacteria tested, 1 cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q517475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
Shank DD, Spears PA;
WPP: 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria - used
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 204;
Pred. No. 3.23e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 91;
                                    /*tag= a
/function=multiple cloning site
187.204
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 hnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 9; L
Pred. No. 1.20e-07;
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%;
Local Similarity 11.2%;
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             21 A;
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                                                                                                     05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
                                                                                                                                                                                                                                                                                                                                                                                             204 BP;
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Sscherichia coli
                          misc_feature
                                                                primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 aayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 aagtcatatgccttttcgacttcaaatgatactacatcagctgcttttgttagtttcatg 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; WPI; 88-279927/40.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Random point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                        08-NoV-1990 (first entry)

Base substituted E.coli beta-galactosidase alpha-fragment.

E.coli beta galactosidase alpha-fragment; base substitutions; ss.

Escherichia coli.
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                                                     2 gctccggcgssvhsyyvvhvvshhhsvhhvvhvsvvvvhhvvhvvhhvhyhvyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 ddhyvybbbvynvhnhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 mattetttgaegaataategaattgttgetatattaaetagtggaaaggttaa 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 204; Pred. No. 1.20e-07;
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     Indels
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/*tag= a
/function=multiple cloning site
/*tag= b
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See also P80575.
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21-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV MCGILL.
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This sequence represents a human or mammalian DNA replication origin

This sequence represents a human or mammalian DNA replication origin

Consensus sequences of the invention, designated uniorsconsensus.

Consensus sequences of the invention, designated uniorsconsensus.

Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication

In vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned human telomeres and maintained as bacterial plasmids, circular or artificial chromosomes and maintained as bacterial plasmids, circular or an analyse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; page 35, 255pp; English.

070465 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.

WPI; 98-362770/31.

Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2%; Score 36; DB 46; Length 91; Best Local Similarity 17.8%; Pred. No. 4.41e-07;
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G;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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WPI; 94-279739/34.
P-PSDB; R65150 and R65151.
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01-FEB-1994; U00977
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This sequence represents a human or mammalian DNA replication origin
Consensus sequences of the invention, designated uniorsconsensus.
Consensus sequences of the invention, designated uniorsconsensus.
Consensus sequences of the invention, designated uniorsconsensus.
Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication of the vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene the essential mammalian elements required for maintenance of corrections and large centromeric blocks for assembly of human conservation of the consensus sequence can be combined with cloned the consensus and large centromeric blocks for assembly of human conservation. The consensus assembly of successions of the consensus and antitained as bacterial plasmids, circular or incompleted.
Other specific peptides generated by these generic sequences are shown in RS5151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active they may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radiolisotope, peptide, toxin or enzyme, to the specific target or on the monoclonal or polyclonal antibodies and therefore circumvent the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inear, large or small yeast artificial chromosomes (YACs) or as episomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-1998 (first entry)
Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 gaattgttgctatattaactagtggaaaggttaattttcctcctgaagtagtatcttggt 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 12; Length 114
Pred. No. 2.50e-04;
29; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 banbanbanbanbanbanbanbanbanbanbtgcanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 taagaaccgccggaacgtctgcctttccatctgattctatatt 407
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C;
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Best Local Similarity 4.9%;
Matches 5; Conservative
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21-MAY-1997; US-047322.
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Tractioning a recombinant vector library expressing fusion proteins proceeding a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins of the processing a binding domain and an effector domain proteins by a comprising a binding domain and an effector domain proteins of 20068 is a generic DNA Sequence used to generate random TSAR (Totally C 70468 is a generic DNA Sequence STALS generic formula can also be represented as follows: X(NNB)11(TGC) (NNB)7(TGC) (NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in G7046-68.

C and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in G85151-54. TSARs are concatenated by these generic sequences are shown in G85151-54. TSARs are concatenated by these generic sequences are shown in a fiffility for a ligand and a second effector peptide portion that is chemically or a ligand and a second effector peptide portion that is chant the expressed peptide contains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues correspond and ascending a TSARs binding demain can be used in vivo to deliver a chemically or biologically active modety, eg. metal ion, and also replace the function of macromoleales.

C compression and rapid detection or in vivo antibody activity callowing direct and rapid detection in a screening process.
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                                                                                                                  vgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrkmwwtwkawsdatakwwwk 80
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                                          Gaps
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Length 91;
                                      38; Mismatches 20; Indels
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/note* "this sequence represents 'z'; z
sequence of 6, 9 or 12 nucleotides (see
Score 30; DB 46;
Pred. No. 8.57e-04;
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2.78;
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                                      Conservative
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US-176500.
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39/34.
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Best Local Similarity
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WPI; 94-279739/
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                                      12;
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01-FEB-1993;
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070468 s
070468;
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  Length 114;
                    77; Indels
 Score 30; DB 12;
Pred. No. 8.57e-04;
                    31; Mismatches
2.7%;
larity 3.6%;
Conservative
         Local Similarity
 Query Match
Best Local Si
Matches
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gaattgttgctatattaactagtggaaaggttaattttcctcctgaagtagtatcttggt 364

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Marifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins or comprising a binding domain and an effector domain proteins comprising a binding domain and an effector domain proteins by a binding domain and an effector domain proteins by a binding domain and an effector domain proteins by a binding domain and an effector domain proteins of 70469 is a generic DNA sequence used to generate random TSAR peptides (TAIS generic formula can be represented as follows: X(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)2(TGC)(NNB)10-CC (TGC)(NNB)10-CC (TGC)(NNB) 356 tatcttggttaagaaccgccggaacgtctgcctttccatctgattctatattgtcaagat 415 Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. 6 banbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbanban 65 ø þe ö taagaaccgccggaacgtctgcctttccatctgattctatattgtcaagatt 416 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114 can Score 29; DB 12; Length 114; 416 ttgacgtatcatatgctgctttttatacttcttctaaaagagctatcgc 464 74; Indels /*tag= a
//tote= "this sequence represents'2'; 2
sequence of 6,9 or 12 nucleotides (see
comments)" 4 T: Pred. No. 2.89e-03 28; Mismatches **4** G; Location/Qualifiers **4** n a screening process. BP. CUXNC-) UNIV NORTH CAROLINA. larity 6.4%; Conservative 2.68; T 10 Q70469 standard; DNA; 114 (first entry) US-176500. /*tag= US-013416 Best Local Similarity Matches 7; Conse WPI; 94-279739/34 misc_feature 30-DEC-1993; detection in 07-APR-1995 WO9418318-A Synthetic. Seguence Query Match 365 ద ð ð 윱 ò

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Synthetic.
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PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure: Page 35: 255pp: English.

COV466 is a generic DNA Sequence used to generate random TSAR (Totally COV466 is a generic DNA Sequence used to generic formula can also be represented as follows:X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4Z(NNB)8 (TGC)(NNB)

COVAGE SPECIFICATION STEEN (X IS NOT the Same as Y)

COVAGE SPECIFICATION STEEN (X IS NOT THE SAME AS Y)

COVAGE SPECIFICATION STEEN (X IS NOT THE SAME AS Y)

COVAGE SPECIFICATION STEEN (X IS NOT THE SAME AS Y)

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                                                                             Generic DNA sequence to generate a random TSAR-9 petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; reffector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                         can be
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Pred. No. 2.89e-03;
....matches 75; Indels
                                                                                                                                                                                                                                                                                                 sequence represents 'Z'; Z
), 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   direct and rapid detection in a screening process Sequence 114 BP; 0 A; 4 C; 4 G; 4 T
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55..60
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sequence of 6, 9
comments)"
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Q70467 standard; DNA; 114 BP.
Q70467;
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larity 8.1%;
Conservative
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Q70466 standard; DNA; 114
Q70466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
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WPI; 94-279739/34.
P-PSDB; R65152.
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Best Local Similarity
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01-FEB-1994;
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PPERBB: R65153.

PT 4724/395/34.

PPERBB: R65153.

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins per screening a binding domain and an effector domain bisclosure; Page 35: 255pp; English.

PR COMPAISING a binding domain and an effector domain bisclosure; Page 35: 255pp; English.

CC 70467 is a generic DNA sequence used to generate random TSAR (Totally Spirthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16/FCC)(NNB)12/NNB)16/FCG(NNB)17. X and Y are flanking restriction sites (X is not the same as Y) that are cont specified further. Other specified further. Other specified further. Other specified peptides generated by these are shown in 070466-68.

CC official signal and a second effector peptide portion that is comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides are also designed conformational rigidity to the specific target or on the cell. They can also replace the function of macromolecules, eg. conformational antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing director areas and an antipodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                 /*tag= a
/note= *this sequence represents 'Z'; Z can
sequence of 6, 9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946 agcttaaatttctcatgccaccttggccagcttgtgcagttctctgtgc 898
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Location/Qualifiers
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31-JAN-1994; US-189331.
(UNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
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Synthetic
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                                                                                                                                                                                                Disclosure; wedge 35, Jospp; tenglish.

C (7069) is a generic DNA sequence used to generate random TSAR peptide

C (TGC) (NMB) (TMB) (TGC) (NMB) (TGC) (NMB) 10-

C (TGC) (NMB) (TGC) (NMB) (TGC) (NMB) 10-

C (TGC) (NMB) (TGC) (NMB) (TGC) (NMB) 10-

Sites (X is not the same as Y) that are not specified further. This

Sequence generates peptides that are cloverleaf in structure. Other

Sequence generates peptides that are cloverleaf in structure. Other

C generic sequences are shown in (70465-68. Other specific peptides

C generated by these generic sequences are shown in R65150-54. TSARs are

C concatenated heterofunctional proteins or peptides, comprising at least

C concatenated heterofunctional proteins or peptides, comprising at least

C second effector peptide portion that is chemically or biologically

C a ctive. They may further comprise a linker peptide between the 2 domains.

C a ctive. They may further comprise a linker peptide between the 2 domains.

C contains 2 or 4 cysteine residues positioned in, or flanking, the

C conformational rigidity to the peptides. The TSARs or compsise.

C conformational rigidity to the peptides. The TSARs or compsise.

C conformational rigidity to the peptides. The TSARs or also replace

C conformation of macromolecules, eq. monoclonal or polyclonal antibodies

C formation or in vivo antibody production. The TSARs are easily

C formation in a screening process.

C detection in a screening process.

S sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                         Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.
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/note= "this sequence represents '2'; 2 can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
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                                                          30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
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larity 6.6%;
Conservative
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01-FEB-1993; US-013416.
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WPI; 94-279739/34.
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31-JAN-1994;
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Proceeding a recombinant vector library expressing fusion proteins
Promorising a pendinant vector library expressing fusion proteins
Disclosure; Page 35, 255pp; English.

C 070466 is a generic DNA Sequence used to generate random TSAR (Totally
Disclosure; Page 35, 255pp; English.

C 070466 is a generic DNA Sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
represented as follows: X(NNB)[TGC](NNB)10[TGC](NNB)4Z(NNB)8[TGC](NNB)

OY 0406 is a tare flanking restriction sites (X is not the same as Y)

C 1 that are not specified further other generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins

CC are shown in R65151-54. TSARs are concatenated heterofunctional proteins

CC domain with affinity for a ligand and a second effector peptide portion

C that is chemically or biologically active. They may further comprise a

CC linker peptide between the 2 domains. The oligonucleotides are also

designed so that the expressed peptide contains 2 or 4 cysteine residues

CC clinker peptide between the 2 domains. The oligonucleotides are also

designed so that the expressed peptide contains 2 or 4 cysteine residues

CC residues confer some degree of conformational rigidity to the peptides.

CT or The TSARs or compens. comprising a TSAR binding domain can be used in

C vivo to deliver a chemically or biologically active moiety, eg. metal

CC on the cell. They can also replace the function of macromolecules, eg.

CM on the cell. They can also replace the function of macromolecules.

CC complex methods of hybridoma formation or in vivo antibody production.

CC The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 ttgctatattaactagtggaaaggttaattttcctcctgaagtagtatcttggttaagaa 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 btgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnnnnn 62
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/note= "can be repeated y times, where y is 4-11,
provided that y+z is 6-12"
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/note= "can be repeated z times, where z is 1-4,
provided that y=z is 6-12; N stands for
identical or different nucleotides,
excluding stop codons"
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Mixed oligonucleotide #19 encodes ballast constituent.
Fusion protein; ballast constituent, pro-insulin production;
recombinant protein production; HMG CoA reductase;
human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase;
mixed oligonucleotide; ss.
                                                                                      Identifying proteins or peptide(s) which bind a ligand - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 12; Length 114;
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27; Mismatches 71; Indels
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Q51787 standard; DNA; 39 BP
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13-JUL-1993.
29-AUG-1989; 399874.
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Matches 8; Conser
Fowlkes DM, Kay Br
WPI; 94-279739/34.
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7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
genbank111
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                       Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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Sequence 5 from patent
Oxytricha fallax 57kD
Sequence 22 from paten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGAGSFASONNEDVRAPFYMNIDRTDASAYVPILKORYVOGNGCYSLGTLINNGNFR
VYHGGGDNGSTGPOTADFGMEFIRNGDFISPRDLIAGKVRFDRTGHITGGSGNFANL
NSTIESLKTDIMSSYPIGAPIPWPSDSVPAGFALMEGGTFDKSAYPKLAVAYPGGVIP
DMRQOTIKGRFSGRAYLSARDAGVRAHSHSASASSTDLGTKTTSSFDYGTKGTNSTGG
HTHSGSGSTSTNGEHSHYIEAMNGTGVGGNKMSSYAISYRAGGSNTNAAGNHSHFSF
                                                                                                                                                                                                                                                                                                                                                                                       bacteriophage T4
                                                                                                                                                    coliphage T4.
coliphage T4
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. 178
/note-"reading frame ? (1 is 3rd base in codon)"
/codon_start-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4022. .>4418
/note="gene 38 (4418 is 1st base in codon)'
                                                                                                                                                                                                                                                                                                                                                                                    genes 36 and 37 of (1981)
          and 38).
       Phage T4 tall fiber genes (numbers 36, 37 V00863 J02508 J02509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"gene 36"
/codon.start-1
/transl_table-11
/protein_id-"CAA24227.1"
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/db_xxef-"Fp15.913.3"
/db_xxef-"SWISS-PROT:P03743"

    4418
    organism="coliphage T4"
    db_xref="taxon:10665"

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/protein_id="CAA24229.1"
/db_xref="PID:915375"
                                                                                                                                                                                                                                                                              14-like phages.
1 (bases 1 to 4418)
0liver,D.B. and Crowther,R.A.
DNA sequence of the tail fibre
J. Mol. Biol. 153 (3), 545-568
82170495
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/codon_start-1
                                                                               g15371
V00863.1 GI:15371
                                                                        NID
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
       DEFINITION
ACCESSION
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TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MATURO OF KRSKIAGTRPAASVLAEGELAINLKDRTIFTKDDS /translation="MATURO OF KRSKIAGTRPAASVLAEGELAINLKDRTIFTKDDS SVIIDLGFAKGGOVDGNYTINGLLRINGDY VOTGGWYNGPIGSTDGYTGKIFRSTQG SFYARAT NDTSNAHLWFENADGTERGVIY TARDGTTTDGFIRLSTDGYTGGTGTANSEFYF RSINGSEFQARRILASDSLYTKRIAVDTVIHDAKAFGQYDSHSLYNYYPGTGETNGY NY LAKVRAKSGGT IYHEIVTAQTGLADEVSWYSGDPYFKLYGIRDDGRMIIRNSLAL GTFTNFSSDF GNGVWGDKYLVLGDTVTGLSYKKTGYFDLVGGGTSYAALITPDSFR STRKGIFGSREDGATWINFOTNAALLSVQTGADNNNAGDGGTYHGITPDSFR STRKGIFGSBDGATWINFOTNAALLSVQTGADNNNAGDGGTYHGIRLDNEIFLTKSNNTA GLAGONIN INTOQGMETNPGILKLYGSNNVOFYAACTISSIQPIKLDNEIFLTKSNNTA GLKFGAP SOVDGTRTIOWNGGFREGNNNYYVIIKMAGNSFNATGESRSPEYFOKSDS GYFFARRARATGDFITGRERDAKTWARSTGATSTOFT STOPTNAGGESTDHSSLF VOGGSSTITGOWY GGGTANALTHWARSTGATSTOFT IPTNONSGESDDHSSLR PVRIGLNDGWYGLGTANALTHWARSTGATSTROFT IPTNONSGESDDHSSLR PVRIGLNDGWYGLGTANALTHUNARSTGATSTROFT IPTNONSGESTDHSSLR PARTICUNGGNOSTAGTTINNGNFR NATURGANTUNGGRANDEN PAGAGSFASONNED VAR THE TRYNDEI TRANSKIT NANFRAUGGSAVIDAGCRANDEN PAGAGSFASONNED VAR THE TRYNDE TRANSKIT NANFRAUGGSAVIDAGFRAUT.
/db_xref="PID:9215885"
/db_xref="GI:215885"
/translation="SFSEVSRNGGISKPAEFGVNGIRVNYICESASPPDIMVLPTQAS
                                                                                                                                                                                                                                                                                                                                                                            /translation="MADLKVGSTTGGSV;WHQGNFPLNPAGDDVLYKSFKIYSEYNKP
AGANDHOFVSGNGGTYASKYTENAGLQVPYAPUNAGLYGGNGGGATFDTKNIDIV
SWYCVGFKSSFGSTGGTVVINTNODINTKQVSAAGQVRSGAAAPIAANDLTKKDYV
DGAINTVANANSRVLRSGDTWTGNLTAPNFFSQNPASQPSHVPRFDQIVIKDSVQDF
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MYRGOTIKGKRSGRAVLASBAGACVKAHSISASASSTDLGTYTTSSPYDTJKGTNBTGG
PHTGGSGSTSTNGBENYIEAMNGTCVGGNKSSYALSYRAGGSNTNAAGNHSHTFSF
GTSSAGDHSHSVGIGAHTHTVAIGSHGHTITVNSTGNTENIYKNIAFNYIVRLA"
//note-"tail fiber protein 38"
//codon_start=1
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VVFDERTQDWIYEEDHRGKRAWTFNKEEIFISDIGSPVGITFDEPGEFDIWTDDGWKE
DETYKRVLIRNRKIEELYKEFQVLNNMIEA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="tail fiber protein 37"
/codon_start=1
/transl_table=11
                                                                                                                                                                  /note="tail fiber protein 36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                    /protein_id="AAA32513.1"
/db_xref="PID:9215886"
/db_xref="GI:215886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA32514.1"
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/db_xref="GI:215887"
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/protein_id="AAA32515.1"
/db_xref="PID:9553025"
/db_xref="GI:553025"
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                                                                                                                                                                                                                                          /transl_table=11
                                                                                                     SKTGKVFGQEFREV"
                                                                                                                                                                                                             /codon_start=1
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Best Local Similarity 99.4%;
Matches 177; Conservative
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LOCUS
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/transl_table=11
/protein_id='CaA25991.1*
/db_xref="PID:915123"
/db_xref="GI:151213"
/db_xref="GI:15123"
/
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1 (bases 1 to 91).
Riede, I., Drexler, and Eschbach, M.L.
The nucleotide sequences of the tail fiber gene 36 of bacteriophage 12 and of genes 36 of the T-even type Escherichia coli phages K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CGGTATTCGCGTTAATTATGTCTGCGAATCGGCTTCACCTCCAGATATAATGGTACTTCC 120
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Submitted (18-NOV-1985) to the EMBL/GenBank/DDBJ databases
Data kindly reviewed (18-Nov-1985) by Riede I.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 902;
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                              (aa 1-216)"
                                                                                  (aa 1-216)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.83e-102;
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85215500
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Bacterlophage T2 tail fiber gene 36.
X01755
                                                                                                                                                                                                                                                                                                                                                     900. .902
/gene-"tail fiber gene 37"
900. .>902
/gene-"tail fiber gene 37"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                            /gene="tail fiber gene 36
241. .891
                                                                             /gene-"tail fiber gene 36
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/organism="coliphage T2"
/db_xref="taxon:10664"
1. .178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fiber protein; inverted repeat.
coliphage T2.
coliphage T2
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                                                                                                           /codon_start-1
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Best Local Similarity 93.8%;
Matches 167; Conservative
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X01755.1 GI:15189
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DEFINITION
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KEYWORDS
SOURCE
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ORIGIN
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TITLE
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COMMENT
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MEDLINE
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DETYKKVLIRHKEENYKEENYKENYKPVKGLGLPDEPGEFDIWTDDGWKE
DETYKKVLIRHKELIKKEFOVLNNHIEA"
2 others
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1 (bases 1 to 902)
Riedel, I., Drexler, V. and Eschbach, M.L.
The nucleotide sequences of the tail fiber gene 36 of bacterlophage
T2 and of genes 36 of the T-even type Escherichia coll phages K3
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229, .232
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                                                                                                                                                                                                                                                                                                                                                                                                                        no RNA stage; Tailed phages; Myoviridae;
                                                                                                                                                                                                                                                                                                                           61 IGGTATICGTGTTAATTATATCTGCGAATCCGCTTCACCTCCGGATATAATGGTACTICC 120
                                                                                                                                                                                                                                                                                                  1 AAGCTTTTCTGAAGTATCAAGAAATGGCGGCATTTCGAAACCTGCTGAATTTGGCGTCAA 60
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                                                                                                                                                                                              Score 176; DB 26; Length 4418;
Pred. No. 4.71e-119;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                              1; Indels
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Nucleic Acids Res. 13 (2), 605-616 (1985)
85215500
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1. .178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYOX2F36 902 bp DNA
Bacteriophage Ox2 tall fiber gene 36.
X01753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="tail fiber gene 35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <i. .178
/gene="tail fiber gene 35"
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X01753.1 GI:15122
fiber protein; inverted repeat.
Bacteriophage Ox2.
Bacteriophage Ox2.
Viruses; dSDNA viruses, no RNA st
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/rpt_type-INVERTED
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/note="repeat A'"
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                                                                                                                                                                                              Query Match 15.7%;
Best Local Similarity 99.4%;
Matches 177; Conservative
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Bacterlophage K3
Viruses: dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
1 (bases I to 944)
Riede,I., Drexler,K. and Eschbach,M.L.
The nucleotide sequences of the tail fiber gene 36 of bacteriophage
I.2 and of genes 36 of the T-even type Escherichia coli phages K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="Ca15893.1"
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Qatdndfvskanggtksqgfokevffregvkisatfsggsdlkglysengdgarrka
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Anlirkdyvdgainnvtanansrvlrsgdtmtgnltapnffsgnpasopshvprfdqi
Vikdsvqdfgyr
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                                         24-JUL-1995
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/gene="tail fiber gene 36 (aa 1-230)"
241. .933
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85215500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .944
/organism="Bacteriophage K3"
/db_xref="taxon:10674"
1. .178
944 bp DNA
Bacteriophage K3 tall fiber gene 36.
X01754
911108
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/gene="tail fiber gene 35"
/codon_start=2
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/db_xref="G1:4379273"
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/gene="tail fiber gene 37"
942. .>944
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/note="put. transcri
184. .190
/note="repeat A"
/rpt_type=INVERTED
195. .201
/note="repeat A"
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/transl_table=11
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                                                                                                                                             GI:15108
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fiber protein; inv
Bacterlophage K3.
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/translation="SPSEVSRNGSISKPAEFGVNGIRVNYVCESASPPDIMVLPTQAS
SKTGKVFGQEFREV"
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Pred. No. 1.17e-98;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                /note="put. transcription terminator"
184. .190
/note="imp. repeat A"
/rpt_type=INVERTED
195. .201
/rote="imp. repeat A'"
/rpt_type=INVERTED
210. .222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tail fiber gene 36 (aa 1-219)"
241. .900
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/citation=[1]
//replace="t"
909. .911
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909. .>911
                                                    /gene≕"tail fiber gene 35*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tail fiber gene 36
/codon_start=1
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/gene="tail fiber gene 37"
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241. .900
                                                                                                   /transl_table=11
/protein_id="CAA25896.1"
/db_xref="PID:915190"
/db_xref="GI:15190"
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                                                                                   /codon_start=2
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229. .232
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Best Local Similarity 92.7%;
Matches 165; Conservative
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Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
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P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            648 agttggcaatctcgcaatttcgtcattagttccaccaactgccgacatgaattgctcaac 589
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Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Trachaata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 4546 to 4553)
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                                                                                                                                                                                                                                                                            3.9%; Score 44; DB 25; Length 721
Similarity 3.5%; Pred. No. 2.46e-12;
7; Conservative 114; Mismatches 77; Indels
                                                                                                    1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23.5EP-1997;
Location/Qualifiers
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/db_xref="taxon:7227"
join(872. 1000,2310. .2426,6476. .(/gene="CP1"
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Genetics 144 (4), 1601-1610 (1996)
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Drosophila melanogaster
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                                               Score 152; DB 26; Length 94
Pred. No. 1.17e-98;
0; Mismatches 13; Indels
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Dorner,F., Schelfilinger,F. and Falkner,F.Gunter.
Recombinant fow,pox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367..
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ACCESSION 166494
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                                               Match 13.6%;
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nes 165; Conservative
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In Unpublished
Stay.Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.
Stay.Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.
Direct Submission
NL Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Blology Al2, Sydney University, NSW 2006, Australia Location/Qualifiers

Location/Qualifiers
Jice Jordanism="Drosophila melanogaster"
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//db.xref="taxon:7227"
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BERFRKLFRENKHKTAKHNORFAEGKVSFKLAVNKYADLLHBFROLMGFNYTLHK
QLRAADESFRGYTFFSPAHYTLPKSVDMRTKGAVTAVROGHGGSCWAFSSTGALEGG
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BEOCHAMOLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENOCGIAS
ASSYPLV*
                                                                                                                 AF012089 10772 bp DNA INV 05-AUG-1997 Consophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
                                                                                                                                                                                                                                                                                                             fruit fly.

Drosophila melanogaster

Bukaryotes, mitochondrial eukaryotes; Metazoa; Arthropoda;

Bukaryotes, mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 4553)

Gray, Y. H., Tanaka, W.M. and Sved, J.A.

Gray, Y. H., Tanaka, W.M. and Sved, J.A.

Pellement-induced recombination in Drosophila melanogaster: hybrid element insertion

Genetics 144 (4), 1601-1610 (1996)
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Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
Structure of the cysteine proteinase (CPI) gene of Drosophila
melanogaster and associated mutational effects
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4546. :4553
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cltation=[1]
6476. :6690
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6691. :6750
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872. .1000
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EERFREK IFURBKH KTAKHNORFAEGKVSFKLAVNKYADLLHHEFGLANGFNYTLHK
QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDQGHGGSCWAFSSYGALEGY
HFRKSGVLVSLSEQNLVDCSYKYGNNGCNGGLADNAFRYIKDNGGIDTEKSYFYEAID
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BPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENOCGIAS
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EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLEFFETWSGTLADPKLILPHP
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YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
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Pred. No. 1.32e-07;
68; Mismatches 42; Indels
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6751. .7707
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Best Local Similarity 17.0%;
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/db_xref="taxon:5944"
/transposon="tas"
/hote="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
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1 (base 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use control fungal disease
Patent: US 55089810-A 5 29-OCT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Score 34; DB 21; Length 354;
Pred. No. 1.13e-05;
49; Mismatches 51; Indels
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Pred. No. 2.01e-04;
63; Mismatches 70; Indels
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/organism="Oxytricha fallax"
/strain="9D1"
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Sequence 5 from patent US 5569830.
128278
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Best Local Similarity 26.5%;
Matches 36; Conservative
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I28278.1 GI:1819054
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Best Local Similarity 17.2%;
Matches 28; Conservative
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645 tggcaatctcgcaatt 630
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                                                                                                                                                    /product="phenylalanyl trna synthetase"
/product="phenylalanyl trna synthetase"
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/db_xref="plog330522"
/db_xref="plog330522"
/db_xref="gl:2305222"
/db_xref="gl:2305222"
/dranslation="MLITEVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
TDGWTWYTPKILSYYGANKHQTDHPHS.IIFRRIVEYRGARKNGRBPLEYYYDGNN
PVYTVQONFDNLLIPADHYSRQKSGYZYINQQHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFRNPGLELFEETWSGTLLADRAILLPHP
SSWTKPNSPATRAVKLMEHEMKHVLVGLTROLFGPRIKYRNVTPTPFTQSSWTELI
YFKDWMLEVLGGGINRHEILORSGVHQSIGTAFGQULEVDRAFTANNUFPDIPDIRLFWSNDS
GFLSGFSEKDLHNLDRXYRFSHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
GFLSGFSEKDLHNLDRXYRFSHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
DWVEQISLVDKFKHPKTGKSSVCFRIVYRHMERLTQARSVDSFNVQ
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Witherspoon, D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OFU89259 354 bp DNA INV 14-MAR-1997 Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxytricha fallax.

Eukaryotea: mitochondrial eukaryotes; Alveolata; Ciliophora; hypotrichs: Stichotrichida; Oxytricha.

I (bases I to 354)

Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G. A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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3 (bases 1 to 354)
Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 21; Length 10772;
Pred. No. 1.32e-07;
70; Mismatches 50; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                               158 others
                                                                                      /product="phenylalanyl tRNA synthetase"
join(8110. .9300,9370. .>9532)
/note="potential orf"
                                                                     .>9532)
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                                                                   join(<8110. .9300,9370.
               6751. .7707
/gene="CP1"
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Local Similarity 19.2%;
les 29; Conservative
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   OFU89262 370 bp DNA INV 14-MAR-1997
Oxytricha fallax 57kD zinc finger/protein kinase gene, partial cds.
U89262
                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
94134747
2 (bases 1 to 370)
Witherspoon D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBE1 family of transposable elements in the ciliates Oxytricha fallax and O.
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(Unpublished

(Dases 1 to 370)

Doak, T.G., Williams, K., Witherspoon, D.J. and Herrick, G.

Direct Submission

Submitted (11-EB-1977) Oncological Science, University of Utah,
School of Med. Rm5c334, USA, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CRAGRGARYMTYYDWARGYBGYWGWGCYTKAAYAAGCWAGHGARTYAGAGTAYGTDARGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 ARAAAGANWTAGARRTTGARRAKHAWGAMRHTSARYTGAAGYTDCTMAACAAAAGAAAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998
                                                                                                                                                                                       Doak T.G., Doerder, F.P., Jahn, C.L. and Herrick, G. A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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hypotrichs; Stichotrichida; Oxytricha.
1 (bases 1 to 370)
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/transl_table=6
/transl_table=6
/product=57kD_sinc_finger/protein_kinase"
/dp_xref="PID:91881682"
/db_xref="PID:1881682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 21; Length 370;
Pred. No. 4.81e-05;
39; Mismatches 52; Indels
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/organism="Oxytricha fallax"
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Sequence 22 from patent US 5795961.
AR024229
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/db_xref="taxon:5944"
/transposon="TBE1"
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Best Local Similarity 33.1%;
Matches 45; Conservative
                                                                             GI:1881681
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645 tggcaatctcgcaatt 630
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AR024229.1
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Medical Center Dr. ROCKVIIIE, MD 20830, USA, EMBII:

bjloftus@tigr.org

1 (bases 1 to 216021)

Adams.M.D. and Loftus.B.J.

Direct Submission

Submitted (24-JUL-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TISK (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAS are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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Homo sapiens Chromosome 16 BAC clone CIT9875K-A-952F10, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21601)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo Saplens Chromosome 16 BAC clone CIT987SK-A-952F10
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                                                      1 (bases 1 to 965)
Wallace,T.Paul, Harris,W.J., Carr,F.J., old,L.J., Welt,S. and
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                                                                                                                                                Ritamura K.
Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualifiers
1. 965
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Pred. No. 4.81e-05;
45; Mismatches 24
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170 c 226 g
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Adams, M.D. and Loftus, B.J.
Direct Submission
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AC004787.1 GI:3337381
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Best Local Similarity 22.8%;
Matches 21; Conservative
Unclassified.
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PCT-US99-13024-1.rge

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Submitted (24-JUL-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced 91:3241936.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge,
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2 (Dases I to 216021)
Adams.M.D. and Loftus.B.J.
Direct Submission
Submitted (02-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, Email:
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Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
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1 (bases 1 to 21601)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Unpublished
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                                                                            27765. 27872
/note="7766, STS1-CSRL-27g3-uA/cSRL-27g3-u2, Chr.
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175810 . 175945

//db.xref="dbSTS:G09935"

//db.xref="dbSTS:G09935"

199463 . 199572
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/db_xrs26. 73943
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Pred. No. 4.81e-05;
33; Mismatches 19; Indels
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Adams, M.D. and Loftus, B.J.
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AC004787.1 GI:3337381
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Best Local Similarity 26.8%;
Matches 19; Conservative
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952 cagaaaagctt 942
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http://gnomic.stanford.Edu/-chris/GENSCANW.html)searches of the complete sequence against a peptide database and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                                                    1. .216021

/docardsm="Homo sapiens"

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/map="#16021-22"

/clone="#4-952F10"

/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr. -, Homo
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175801. 175945
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73826. .73943
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Pred. No. 8.22e-04;
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51778 c 49172 g 53987 t
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Best Local Similarity 14.0%;
Matches 14; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 13.02 Seconds 807.364 Million cell updates/sec Wed Sep 1 16:00:35 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-372) from PCTUS9913024.pep (1 of 12) 2542 1 MEKEWAEFGGGYVQTPFLSE......LPTQASSKTGKVFGQEFREV 372 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 segs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 49.734; Variance 92.468; scale 0.538 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	0:00e+00	3.10e-35	7.12e-04	2.56e-02	1.21e-01	2.23e-01	2.23e-01	5.46e-01	5.46e-01	5.46e-01	3.01e-01	3.01e-01	3.01e-01	4.06e-01	1.75e+00	1.75e+00	2.32e+00	1.31e+00	1.75e+00	1.31e+00	1.31e+00	1.75e+00	3.08e+00
		Description	TAIL FIBER PROTEIN GP3	HYPOTHETICAL 7.3 KD PR	4-HYDROXY-2-OXOGLUTARA	DELTA-AMINOLEVULINIC A	NADH-UBIQUINONE OXIDOR	HYPOTHETICAL 74.4 KD P	NONSTRUCTURAL POLYPROT	MITOCHONDRIAL IMPORT R	NADP-SPECIFIC GLUTAMAT	DNA BINDING PROTEIN RF	NADH-UBIQUINONE OXIDOR	NADH-UBIQUINONE OXIDOR	AGGLUTININ RECEPTOR PR	NONSTRUCTURAL POLYPROT	GLUTAMATE DEHYDROGENAS	NUCLEOCAPSID PROTEIN (	HYPOTHETICAL 79.8 KD P	DNA MISMATCH REPAIR PR	GLUTAMYL AMINOPEPTIDAS	RETROVIRUS-RELATED POL	NON-STRUCTURAL POLYPRO	NONSTRUCTURAL POLYPROT	CAPM PROTEIN.
SUMMARIES	;	gi	VG35_BPT4	Y15A_BPT4	ALKH_BACSU	HEM2_HELPY	NQ03_PARDE	YA21_SYNY3	POLN_EEVVT	OM22_NEUCR	DHE4_SULSH	RFX2_HUMAN	NUAM_BOVIN	NUAM_HUMAN	SSP5_STRGN	POLN_EEVV3	DHE3_SULSO	NCAP_SYNV	YA76_SCHPO	MUTS_HAEIN	AMPE_MOUSE	POL2_MOUSE	POLN_HEVMY	POLN_EEVVP	CAPM_STAAU
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EMBL; J02509; G215885; -.
PIR; J0577; TLBP54.
FIBER PROTEIN.
SEQUENCE 295 Aa; 32282 MW; 2F9ACC4A CRC32; 8 **2** 2 2 2 2 2 3

Score 1893; DB 1; Length 295; Pred. No. 0.00e+00; Query Match Best Local Similarity 99.3%; a

PCT-US99-13024-2-01.rsp

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ACT_SITE
ACT_SITE
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                                 LPTSAAISKLSDYNLIPGDVLYLKAQLYADADLLALGTTNISIRFYNASNGYISSTQAEF 196
                                                                                                                                                                                                                           273
                                                                                                                                                                                                                                                               TGQAGSWELKEDYVVVPENAVGFTIYAQRTAQAGQGGMRNLSFSEVSRNGGISKPAEFGV 256
                                                                                                                                                                                                                                                                                 quence analysis of the Bacillus subtilis chromosome region between serA and kdg loci cloned in a yeast artificial chromosome.";
                                                                                                          IALEHVKLSNRKSTDDYQTILDVVFDSLEDVGATGFPRRTYESVEQFMSAVGGTNNEIAR 136
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
11-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
4-HYDROXY-2-OXOGLUTARATE ALDOLASE (EC 4.1.3.16) (2-KETO-4-HYDROXYGLUTARATE ALDOLASE) (KHG-ALDOLASE) / 2-DEHYDRO-3-DEOXYPHOSPHGLUCONATE ALDOLASE) (RHG-ALDOLASE) (PHOSPHO-2-DEHYDRO-3-DEOXYGLUCONATE ALDOLASE) (PHOSPHO-2-KETO-3-DEOXYGLUCONATE ALDOLASE)
(2-KETO-3-DEOXY-6-PHOSPHOGLUCONATE ALDOLASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEKFMAEIWTRICPNAILSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL 7.3 KD PROTEIN IN GP34-GP35 INTERGENIC REGION.
Y15A OR 34.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 300; DB 1; Length 65;
Pred. No. 3.10e-35;
3; Mismatches 7; Indels
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (NOV-1994) TO THE SWISS-PROT DATA BANK.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                                      NGIRVNYICESASPPDIMVLPTQASSKTGKVFGQEFREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2D7CE2D CRC32;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Y15A_BPT4 STANDARD; PRT; 65 AA. P39509; 01-FEB-1995 (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.1%;
Matches 46; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=168 / MARBURG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIOPHAGE T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRUSES; DSDNA
T4-LIKE PHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUTTER E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 3
ALKH_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                            11
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Matches
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                                                                                                      MEDLINE; 97394467.

MEDLINE; 97394467.

MEDLINE; 97394467.

MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., ELESCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSCHWANN R.D., RETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSCHWANN R.D., RETCHUM B.A., KIRNNESS E.F., PETERSON S., MCKENNEY K., PITZGERALD L.M., LEE N., MADANS H.D., HICKEY E.N., MCKENNEY K., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E., HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 TPSEIMEALTEGETTLKLEPSGVEGIPFMKNLAGPEPQVTFIPTGGIH-PSEVPDMLR-A 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OL-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
OL-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24) (PORPHOBILINOGEN SYNTHASE) (ALAD) (ALAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                   GLYOXYLATE.
-1- CATALYTIC ACTIVITY: 2-DEHYDRO-3-DEOXY-D-GLUCONATE 6-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
SCHIFF-BASE WITH KHG OR PYRUVATE
                         -1- CATALYTIC ACTIVITY: 4-HYDROXY-2-OXOGLUTARATE - PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 1; I
Pred. No. 7.12e-04;
27; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
14FCBED5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHIFF BASE; MULTIFUNCTIONAL ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00159; ALDOLASE_KDPG_KHG_1;
PROSITE; PS00160; ALDOLASE_KDPG_KHG_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
MICROBIOLOGY 142:2005-2016(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 AA; 20865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 4.9%;
Local Similarity 27.8%;
Les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L47838; G1146190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 299115; E1183656; -. SUBTILIST; BG11396; KDGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF01081; Aldolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 GISAFPSDSILS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 4
HEM2_HELPY
P56074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              XU X., MATSUNO-YAGI A., YAGI T.; "Structural features of the 66-kDa subunit of the energy-transducing NADH-ubiquinone oxidoreductase (NDH-1) of Paracoccus denitrificans."; ARCH. BIOCHEM. BIOPHYS. 296:40-48(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                           135 SVSNDKT-LEILNLQGLILAESGVDILAPSNM-MDGNVLS-LRKTLDNAGYTHTPIMS-Y 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEOBACTERIA; ALPHA SUBDIVISION; RHODOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE COMPLEX I 75 KD SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                ;
9
NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                   TIGR; HP0163; -
PROSITE; PS00169; D_ALA_DEHYDRATASE; 1.
PFAM; PF00490; ALAD; 1.
PORPHYRIN BIOSYNTHESIS; LYASE; ZINC.
DORPHYRIN BIOSYNTHESIS; LYASE; ZINC.
AMDOMAIN 115 132 ZINC-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3) (NADH
DEHYDROGENASE 1, CHAIN 3) (NDH-1, CHAIN 3).
                                                                                                                                                                                                                                                                                                                                                                                                               33; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 STKFASSYYGPFRDVANSAPSFGDRKSYQMDYANQKEALLESLED 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - COECTOR: ZINC.
- PATHWAY: SECOND STEP IN PORPHYRIN BIOSYNTHESIS.
- SUBUNIT: HOMOOCTAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              Match 4.4%; Score 113; DB 1; I
Local Similarity 25.7%; Pred. No. 2.56e-02;
                                                                                                                                                                                                                                                                                                                                  Y SIMILARITY.
9B60D720 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
STRAIN=ATCC 13548;
MEDLINE; 92296779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (REL. 25, CREATED)
01-FEB-1995 (REL. 31, LAST SEQ0
01-NOV-1995 (REL. 32, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                 323 AA; 36202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 657-672 FROM N.A. MEDLINE; 93136200.
                                                                                                                                                                                                                                      EMBL; AE000537; G2313250;
                                                                                                                                                                                                                                                                                                                                                                                                             27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARACOCCUS DENITRIFICANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQO3_PARDE
P29915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARACOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIA;
                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 VRFTTEVAGITQMGQTGRG-EDSEITSYLNQTLESNMQGNIIDLCPVGALV-SKPYAFTA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILIRE; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOGCHI T., MATSUNO A., MUBAKI A., NAKAZAKI N., NARUO K., OKUMURA S.
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100, 21.21e-01; Pred. No. 1.21e-01; Score Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (2FE-2S) (
IRON-SULFUR (4FE-4S) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (4FE-40DB761A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
HYPOTHETICAL 74.4 KD PROTEIN SLL1021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 108;
                                                                                                                                                                            EMBL; M84572; G150601; -.
PIR; S23948; S23948
PROSITE; PS00641; COMPLEX1_75K_1; 1.
PROSITE; PS00643; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 RPWELTKTESIDVMDALGSSIRI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 SN-DITSAAFVSFMNSLINN-RI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73028 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.2%;
Best Local Similarity 26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D90901; G1652020; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
1109
1118
1118
1157
1160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLL1021.
SYNECHOCYSTIS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YA21_SYNY3
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 89243175.
KINNEY R.M., JOHNSON B.J.B., WELCH J.B., TSUCHIYA K.R., TRENT D.W.;
KINNEY R.M., JOHNSON B.J.B., WELCH J.B., TSUCHIYA K.R., TRENT D.W.;
"The full-length nucleotide sequences of the virulent Trinidad donkey
strain of Venezuelan equine encephalitis virus and its attenuated
virocline derivative. Strain TC-83.";
VIROLOGY 170:19-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLREISI-DVVRAGNLAVRTQDYMRANMRVTFYVCITPNRNEILTAAARLS-KKGQISEA 183
                                                                                                                                                      310 GMRNLSFSEVSRNGGIS-KPAEFGVNGIRVN-YICESASPPDIMVLPTQASSKTGKVFGQ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION.
-i- PTH: SPECTIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-i- READTHROUGH OF THE TERMINATOR CODON UGA OCCURS BETWEEN THE CODONS FOR 1879-GLN AND 1880-ARG.
                                                                                                                                                                                                                                                                                        2.1. POLL 2
POLL 2
POLL 2
POLS 2
10-40G-1992 (REL. 23, CREATED)
01-40G-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-0GT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NONSTRUCTURAL POLYPROTEIN (CONTAINS: NONSTRUCTURAL PROTEINS NSP1 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               NN EQUINE ENCEPHALITIS VIRUS (STRAIN TRINIDAD DONKEY).
SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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PFAM; PF00978; RNA_dep_RNApol2; 2.
POLYPROTEIN; NONSTRUCTURAL PROTEIN; RNA-BINDING; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106; DB 1; Length 2492;
Pred. No. 2.23e-01;
26; Mismatches 39; Indels
                                                                 Length 673;
                                                                                                 26; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONSTRUCTURAL PROTEIN NSP1.
NONSTRUCTURAL PROTEIN NSP2.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $B4E2F03 CRC32;
                                                               Score 106; DB 1; ]
Pred. No. 2.23e-01;
              POTENTIAL.
2B642284 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDWLSDRPEATFRARLDLGIPGDVPKYDIIFVNVR 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 VSWLRTAGTSAFPSDSILS-RFDVS-YAAFYTSSK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
HYPOTHETICAL PROTEIN; TRANSMEMBRANE
                            673 AA; 74423 MW;
                                                             4.2%;
ilarity 20.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277902
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Local Similarity 24.2%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04332; G323709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535
1329
1879
2492
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                                                                                 Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               VENEZUELAN EQUINE
VIRUSES; SSRNA POS
ALPHAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536
1330
1880
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                                                                                                                                                                                                                                       EFRE 371
              TRANSMEM
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SEQUENCE
                                                                 Query Match
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                                                                                 Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   NSP4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cooperates with MoM19.";
EMBO J. 14:4204-4211(1995).
-!- FUNCTION: CENTRAL COMPONENT OF THE RECEPTOR COMPLEX RESPONSIBLE FOR THE RECGNITION AND TRANSLOCATION OF CYTOSOLICALLY SYNTHESIZED MITOCHONDRIAL PREPROPEINS. TOGETHER WITH TOWAG FUNCTIONS AS THE TRANSIT PEPTIDE RECEPTOR AT THE SURFACE OF THE MITOCHONDRION OUTER MEMBRANE AND FACILITATES THE MOVEMENT OF PREPROTEINS INTO
                                                                                      MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 (MITOCHONDRIAL 22 KD OUTER MEMBRANE PROTEIN) (MOM22 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 22 KD
                                                                                                                                                                                                                                                                                                                 "The mitochondrial receptor complex: a central role of MOM22 in mediating preprotein transfer from receptors to the general insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 EQFM-SAVGGTNDEIARLPTSAAISKLSDYNLIPGDVLYLKAOLYADADLLALGTTNISI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 HKYSTTTNFVKSTLS-FAGRA-AWAVSVSGLLIGVP-FAIAFAE-DONYAAMEQEARMRE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 EHFQOPQVGPEEDDEDFTDTDSEISVDSDYE--SQET-F-TDRLYALRDMVSPTTRGWFY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE TRANSLOCATION PORE.

-1- SUBURIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF A LEAST 8 DIFFERENT PROTEINS (TOM5, TOM6, TOM7, TOM20, TOM37, TOM40 AND TOM70).

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                              MEDLINE; 93351229.
KIEBLER M., KEIL P., SCHNEIDER H., VAN DER KLEI I.J., PFANNER N.,
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE; 96016192.
MAYER A., NARGANS F.E., NEUPERT W., LILL R.;
"MOM22 is a receptor for mitochondrial targeting sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN TRANSPORT; OUTER MEMBRANE; MITOCHONDRION;
                                                                                                                                                       NEUROSPORA CRASSA.
EUKRARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
SORDARIALES; SORDARIACEAE; NEUROSPORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; DB 1; I
Pred. No. 5.46e-01;
33; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASP/GLU-RICH (ACI
36E5251A CRC32;
                                                 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 (1
 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OUTER MEMBRANE.
                                 01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 30 A
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Best Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X71021; G311427; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
105
154
                                                                                                                                                                                                                                                                                                                                                                       CELL 74:483-492(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A40669; A40669
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                        TOM22 OR MOM22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEMBRANE.
OM22_NEUCR
Q07335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPORT
                                                                                                                                                                                                                                                                                                    NEUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION.
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PCT-US99-13024-2-01.rsp

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EMBL; J02877; G163414; -.
SEQUENCE FROM N.A. MEDLINE; 94119075.
                                                                                                                                                                                                         DNA-BINDING.
                                                                                                                                                                                      142765
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                                                                                                                                                                                                                                                                                                                                                  163 NR 164
                                                                                                                                                                                                                                                                                                                                                                                            NUAM_BOVIN
P15690;
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ъ,
                                                                                                                                                                                                                       *PCR-mediated cloning and Sequencing of the gene encoding glutamate dehydrogenase from the archaeon Sulfolobus shibatae: identification of putative amino-acid signatures for extremophilic adaptation.*; GENE 140:17-24(1994).

-!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)0 + NADP(+) = 2-OXOGLUTARATE + NH(3) + NADPH.

-:- SUBUNIT: HOMOHEXAMER.
-:- SUBUNIT: HOMOHEXAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 ELEDLSRKYVQLIHNYLGSDVDIPAPDINTNPQTMAWFL-DEYIKITGE-VDFAVFTGKP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Gaps
                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (EC 1.4.1.4) (NADP-GDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 103; DB 1; Length 390;
Pred. No. 5.46e-01;
25; Mismatches 26; Indels
                                                                                                                                                          SULFOLOBUS SHIBATAE.
ARCHAEA: CRENARCHAEOTA: SULFOLOBALES; SULFOLOBUS.
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 94171074.
BENACHENHOU-LAHFA N., LABEDAN B., FORTERRE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
36FC4083 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                        390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S7407; S37407.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
PFAM; PF00208; GLFV_dehydrog; 1.
HSSP: P80319; 1GTM.
                                                                        PRT;
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(REL. 33, LAST SEQI
(REL. 33, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 81 E
390 AA; 42091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 4.18;
Local Similarity 21.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X73990; G403324; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (REL. 33, LAS DNA BINDING PROTEIN RFX2.
                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPIENS (HUMAN).
       LG-SDVLTAGG 131
                            314 LSFSEVSRNGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 AQAGQGGMR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 SELGGIGVR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996
01-FEB-1996
01-FEB-1996
                                                                                                                                    (FRAGMENT).
                                                                     DHE4_SULSH
P39475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFX2_HUMAN
P48378;
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SEQUENCE
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       122
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"Mitochondrial NADH:ubiquinone reductase: complementary DNA sequence of the import precursor of the bovine 75 kDa subunit.";

BICCHEMISTRY 28:9452-9459(1989).

-I- FUNCTION: THIS IS THE LARGEST SUBUNIT OF COMPLEX I AND IT IS A COMPONENT OF THE IRON-SULEVIR (IP) FRAGMENT OF THE ENYME. IT MAY FORM PART OF THE ACTIVE SITE CREVICE WHERE NADH IS OXIDIZED.

-I- CATALITIC ACTIVITY: NADH + UBIQUINONE = NADH;) + UBIQUINOL.

-I- CATALITIC ACTIVITY: NADH + UBIQUINONE = NADH;) + UBIQUINOL.

-I- SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE MITOCHONDRIAL INNER MEMBRANE.

-I- SIMILARITY: BELONGS TO THE COMPLEX I 75 KD SUBUNIT FAMILY.
REITH W., UCLA C., BARRAS E., GAUD A., DURAND B., HERRERO-SANCHEZ C., KOBR M., MACH B.;
"REXI, a transactivator of hepatitis B virus enhancer I, belongs to a novel family of homodimeric and heterodimeric DNA-binding proteins.";
MOL. CELL. BIOL. 14:1230-1244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 VPSTLTQAIRNFAKSLEGWL-TNAMSDFPQQVIQTKVGVV-SAFAQTLRRYTSLNHLAQA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 IVAILTSGKVNFPPEVVSWLRTAGTSAFPSDSILSRFDVSYAAFYTSSKRAIALEHVKLS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (EC 1.6.5.3)
(EC 1.6.99.3) (COMPLEX I-75KD) (CI-75KD).
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ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 5.46e-01;
17; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 AA; 80003 MW; 45C7C6E9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (REL. 14, CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X76091; G452390; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSFAC; T01667; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 18; Conser
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EMBL; X61100; G38079; -.
                                                                                                                                    IRON-SULFUR; 4FE-4S.
                                                                                                                                                                                                                                                                                        182
226
727 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                 183 IRFASEIAGVDDLGTTGRGN-DMQVGTYIEKMFMSELSGNIIDICPVGALT-SKPYAFTA 240
                                                                                                             SUBUNIT
                                                                                                                                                                                                                                                                                                                                                  :|: ||| |:||| |:||: | 24 VRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTFSAGLHLRVFDP-STGALVDSKSYAFST 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHOW W. RAGAN I., ROBINSON B.H.;

Determination of the CDNA sequence for the human mitochondrial
15-kDa Fe-S protein of NaDH-coenzyme o reductase.*;

EUR. J. BIOCHEM. 201:347-550(1991).

-I-CHUCTION: THIS IS THE LARGEST SUBUNIT OF COMPLEX I AND IT IS A
COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF FIRE ENZYME: IT
MAY FORM PART OF THE ACTIVE SITE CREVICE WHERE NADH IS OXIDIZED.

-I-CAPALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

-I-COPACTOR: MAY BIND ONE 2FE-2S CLUSTER & ONE 4FE-4S CLUSTER.

-I-SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERRY SUBUNITS.

-I-SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (EC 1.6.5.3)
NDUFS1.
PROSITE: PS00641; COMPLEXI_75K_1; 1.
PROSITE: PS00642: COMPLEXI_75K_2; 1.
PROSITE: PS00643: COMPLEXI_75K_2; 1.
PROSITE: PS00643: COMPLEXI_75K_3; 1.
PFAM: PF00111; fer2; 1.
PFAM: PF00184; molybdopterin; 1.
OXIDOREDUCTASE; NAD: UBIQUINONE: MITOCHONDRION; TRANSIT PEPTIDE; IRON-SULFUR: 4FE-45.
                                                                                                                                                                                                                                                                                                               ۍ
ن
                                                                                                          REDUCTASE 75 KD S :-4S) (POTENTIAL).
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(POTENTIAL)
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                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                       Length 727;
                                                                                                                                                                                                                                                                                                            21; Mismatches 39; Indels
                                                                                                         NADH UBIQUINONE REDUCTE
IRON SULFUR (4FE-4S) (F
                                                                                                                                                                                                                                                                                       Score 105; DB 1; I Pred. No. 3.01e-01;
                                                                                                                                                                                                                                                                9CAF139C CRC32;
                                                                                               MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                  241 RPWETRKTESIDVMDAVGSNIVVSTRT-GEV 270
                                                                                                                                                                                                                                                                                                                                                                                               SN-DITSAAFVSFMNSLINNRIVALLISGKV 112
                                                                                                                                                                                                                                                                79442 MW;
                                                                                                                                                                                                                                                                                      Query Match 4.1%;
Best Local Similarity 28.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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53
64
64
75
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128
137
176
179
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226
227
AA:
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NUAM_HUMAN
P28331;
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MOL. MICROBIOL. 20:403-413(1996).

-I- FUNCTION: MAY BIND SIALIC ACID RESIDUES OF SALIVARY AGGLUTININ (SAG) IN A CALCIUM-DEPENDENT REACTION. THE INTERACTION OF SAG WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 IRFASEIAGVDDLGTTGRGN-DMQVGTYIEKMFMSELSGNIDICPVGALT-SKPYAFTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT
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MEDIARE; 90236997.
DEMOTH D.R., GOLUB E.E., MALANUD D.;
"Streptococcal-host interactions. Structural and functional analysis of a Streptococcus sanguis receptor for a human salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                          PROSITE; PS00641; COMPLEX1_75K_1; 1.
PROSITE; PS00642; COMPLEX1_75K_2; 1.
PROSITE; PS00643; COMPLEX1_75K_3; 1.
PRAM: PF00111; fer2; 1.
PFAM: PF00114; molybdopterin; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION; TRANSIT PEPTIDE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
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DEMUTH D.R., DUAN Y., BROOKS W., HOLMES A.R., MCNAB R., JENKINSON H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.01e-01;
21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 RPWETRKTESIDVMDAVGSNIVVSTRT-GEV 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105;
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les 26; Conservative
PIR; S16382; S16382.
PIR; S17854; S17854.
MIM; 157655; -.
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KINNEY R.M., TSUCHIYA K.R., SNEIDER J.M., TRENT D.W.;
"Genetic evidence that epizootic Venezuelan equine encephalitis (VEE)
viruses may have evolved from enzootic VEE subtype I-D virus.";
VIROLOGY 191:569-580(1992).

-1- FUNCTION: NSP2 MAY BE INVOLVED IN RNA BINDING DURING REPLICATION -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. -1- READTHROUGH OF THE TERMINATOR CODON UGA OCCURS BETWEEN THE CODONS FOR 1879-GLN AND 1880-ARG.

DURING REPLICATION.

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PIR; C44213; C44213. PFAM; PF00978; RNA_dep_RNApol2; 2. POLYPROTEIN; NONSTRUCTURAL PROTEIN; RNA-BINDING; ATP-BINDING;

EMBL; L00930; G323707; ALT_SEQ.

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OF DENTAL CARIES.

DOMAIN: THE PRZ REGION, BY SIMILARITY WITH THE PROLINE RICH
DOMAINS OF THE S.PYGGENES M6 PROTEIN AND STAPHYLOCOCCAL PROTEIN A,
MAY TRAVERSE THE CELL WALL PEPTIDOGIZCAN AND IS FOLLOWED BY
HYDROPHOBIC AA WHICH MAY FUNCTION TO ANCHOR THE PROTEIN TO THE
ITS RECEPTOR IN VARIOUS ORAL STREPTOCOCCI MODULATE BACTERIAL COLONIZATION OF ORAL TISSUE AND IS ASSOCIATED WITH REDUCED LEVELS
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
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6
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TO M PROTEIN OF S.PYOGENES.
4 X APPROXIMATE TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 1; Length 1500
Pred. No. 3.01e-01;
32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                    AGGLUTININ RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                   SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAA FAMILY.
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PROSITE; PSO0343; GRAM_POS_ANCHORING; 1.
SIGNAL; REPEAT; CALCIUM-BINDING; TRANSMEMBRANE.
SIGNAL
39 1500 AGGLUTININ RECEPTO
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931 950 POTER
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1500 AA; 164552 MW;
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les 25; Conservative
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P36327;
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1125 LRNYDPRINLVPVNRRLPHALVLHHNEHPQSDFSSFVSKL-KGRTVLVV-GEKLSVPGKT 1182

Gaps

25; Mismatches 40; Indels 7;

; DB 1; Length 2492; 4.06e-01;

Score 104; Pred.

A.18; Similarity 24.28; 23; Conservative

Best Local Similarity Matches 23; Conser

셤 ö g

Query Match

2492 AA;

NP_BIND SEQUENCE

NONSTRUCTURAL PROTEIN NSP1.

NONSTRUCTURAL PROTEIN NSP2.

NONSTRUCTURAL PROTEIN NSP3.

20 NONSTRUCTURAL PROTEIN NSP4.

21 ATP (POTENTIAL).

2777967 MW; A4AFC9B4 CRC32;

535 1329 1879 2492

536 1330 1880

CHAIN CHAIN

HELICASE

1183 VDWLSDRPEATFRARLDLGIPGDVPKYDIIFINVR 1217

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MERAS B., CONSALVI V., CHIARALUCE R., POLITI L., DE ROSA M., BOSSA F., SCANDURRA R., BARRA D., SCANDURRA R., BARRA D., "The protein sequence of glutamate dehydrogenase from Sulfolobus solfataricus, a thermoacidophilic archaebacterium. Is the presence of N-epsilon-methyllysine related to thermostability?"; EUR. J. BIOCHEM. 203:81-87(1992).
                                                                                                                                                                                                                                                                                                                                                                                                           2-OXOGLOTARATE + NH 3) + NAD(P)H.

1- SUBUNIT: HOMOHEXAMER.

1- PTH: METHITATION OF LYSINE RESIDUES MAYBE PLAYS A ROLE IN THE THERMAL STABILITY OF THIS ENZYME.

1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.

PIR: $30286, $20286.

PROSITE: PSO00074; GLFV_DEHYDROGENASE; 1.

PRAM: PF00208; GLEV_dehydrog; 1.

HSSP; P80319; 1GTM.

OXIDOREDUCTASE; NAD; ACETYLATION; METHYLATION.
                                                                                                                                                                                       SULFOLOBUS SOLFATARICUS.
ARCHAEA; CRENARCHAEOTA; SULFOLOBALES; SULFOLOBUS.
                                                                                                 01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
119 VSWLRTAGTSAFPSDSILS-RFDVS-YAAFYTSSK 151
                                                                      421 AA
                                                                    STANDARD;
                                                                                                                                                                                                                                                           STRAIN-ATCC 49255 / MT4;
                                                                  DHE3_SULSO
                                                                                                                                                                                                                                         SEQUENCE
                                                                                  P80053;
à
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VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN 3880). VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE; ALPHAVIRUS.

SEQUENCE FROM N.A. MEDLINE; 93079859.

01-JUN-1994 (REE. 29, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) NONSTRUCTURAL POLYPROTEIN (CONTAINS: NONSTRUCTURAL PROTEINS NSP1

01-JUN-1994 (REL. 29, CREATED)

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FT MOD_RES 254 METHYLATION.
FT MOD_RES 254 METHYLATION (MONO-).
FT MOD_RES 372 372 METHYLATION (MONO-).
FT MOD_RES 391 391 METHYLATION (MONO-).
FT MOD_RES 392 392 METHYLATION (MONO-).
FT MOD_RES 393 393 METHYLATION (MONO-).

ACT_SITE 108 108 BY SIMILARITY.
SQ SEQUENCE 421 AA; 46157 MW; 2BE7B538 CRC32;

OUERY MATCH

BEST LOCAL 3: 78, Pred No. 1.75e+00;
MATCHES 15; CONSETVATIVE 24; MISMATCHES 27; Indels 3; Gaps 3;
MATCHES 15; CONSETVATIVE 24; MISMATCHES 27; Indels 3; Gaps 3;

DD 122 ELEOLESRKYIQAIXKYLGSELDIPAPDVNTDSQTMAWFL-DEXIKITGK-VDFAVFTGKP 179
OY 245 DLLALGTTNISIRF-YNASNGYISSTQAEFTGQAGSWELKEDYVVVPENANGFTIYAQRT 303

DD 180 VELGGIGWR 312

SEARCH COMPLEGE: Wed SeP 1 16:00:59 1999
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 18.01 Seconds 827.821 Million cell updates/sec Wed Sep 1 16:02:42 1999; Tabular output not generated. Run on:

>PCT-US99-13024-2 (1-372) from PCTUS9913024.pep (1 of 12) 2542 1 MEKFWAEFGGGYVQTPFLSE......LPTQASSKTGKVFGQEFREV 372 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 48.649; Variance 104.828; scale 0.464 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	610-250	880-030	17e-03	45e-01	4.36e-01	72e-01	79e-01	79e-01	2.16e+00	.16e+00	16e+00	16e+00	28e+00	28e+00	28e+00	66e+00	2.81e+00	2.81e+00	3.64e+00	3.64e+00	7.82e+00	6.07e+00	6.07e+00
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SUMMARIES	DI	TLBP54	535028	H69647	C64540	н71968	A45456	S74795	MNWVTD	A40669	B71160	S37407	B55926	S17854	A33552	A35186	C44213	B32578	H71729	S52621	D71490	S66469	S20286	VHVNSY
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hypothetical protein 7.82e+00 hypothetical protein 7.82e+00 aminopepidase N homo 6.07e+00 glutamate receptor ch 6.07e+00 glutamate receptor ch 6.07e+00 glutamate receptor ch 6.07e+00 retrovinus-related re 4.70e+00 filamin, Mueller cell 7.82e+00 toxin-like outer memb 6.07e+00 hypothetical protein 1.29e+01 hypothetical protein 1.00e+01 p25(Shc) protein 1.00e+01 p25(Shc) protein 1.00e+01 p120speptide-binding 1.00e+01 scaffolding protein R 1.29e+01 bNA binding protein R 1.29e+01 delta-1-pyrroline-5-c 1.29e+01 proline/Pyrroline-5-c 1.29e+01 botulinum neurotoxin 1.29e+01	te - phage T4 evision 19-Apr-1996 #text_change 11 1991 11 fibre genes 36 and 37 of I the genes 36 and 37 of I the genes 36 and 37 of I the genes 36 and 37 of	the distal half-fiber contains two molecules each of gp36 the distal half-fiber contains two molecules each of gp36 (PIR.TLBP64) and gp37 (PIR.TLBP74), and one molecule of gp36 gp35 TION *superfamily phage T4 tail fiber protein gp35 structural protein; tail fiber protein gp35 structural protein; tail fiber #length 275 *molecular-weight 30237 *checksum 7602 tch
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33.9 9.9 3.9 9.9 9.9 9.9 9.9 9.9	p54 #: 1 fiber pi 1011-1982 5011-1982 9-May-199 9-May-19	tion 91.6-92.3 tion 91.6-92.3 the distal half-fibe (PIR:TLBP64) and 9p35 ON *superfamily phage T structural protein; #length 275 #molecu 244; Conservative 11; NSLTNNRIVALLTSGKVNEPPEVVS
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##note the authors translated the codon AAC for residue 155 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps 13;
                                                                                                                                                                                                                                                                                                                                                         #authors Peyret, J.L.; Bayan, N.; Joliff, G.; Gulik-Krzywicki, T.;
Mathieu, L.; Shechter, E.; Leblon, G.
#journal Mol. Microbiol. (1993) 9:97-109
#title Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum.
#cross-references MUID:94018618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain signal sequence #status predicted #label SIG\
#product protein PS2 #status predicted #label MAT\
              236
                                                                                   LPTSAAISKLSDYNLIPGDVLYLKAQLYADADLLALGTINISIRFYNASNGYISSTQAEF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESVAYALKVDQEAT-AAFEAYRNALRDAAI-SINPDGSIN-PDTSINLLIDAANAANRTD 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                         #type complete protein PS2 precursor - Corynebacterium glutamicum formal_name Corynebacterium glutamicum 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 R--AEIE-DYAHLYTQT--DIALETPQLAYAFQDLKALQAEVDADFEWLGEFGIDQ-EDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
#length 510 #molecular-weight 55425 #checksum 3744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128; DB 2; Length 510;
Pred. No. 1.88e-03;
55; Mismatches 100; Indels
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                                                                                                                                     NGIRVNYICESASPPDIMVLPTQASSKTGKVFGQEFREV 275
                                                                                                                                                       #type complete
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Best Local Similarity 23.3%;
Matches 52; Conservative
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolochin, A.; Borchert, S.; Borisier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.W.;
Chol, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Errari, E.; Foulger, D.; Fritz, C.; Fujita,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.
Guiseppi, G.; Guy, B.J.; Haga, K.; Hatch, C.; Robaysshi,
Y.; Koetter, P.; Komingstein, G.; Kroph, S.; Kumano, M.;
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M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Medigue, C.; Medino, B.; Park, S.; Hrando,
M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
Roche, B.; Rose, M.; Sadaie, Y.; Scato, T.; Scalon,
Schweisk, A.; Seror, S.J.; Serror, P.; Schich, S.;
Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Terpstra, P.; Tognoni, A.; Takagi, T.; Takahs, H.;
Terpstra, P.; Tognoni, A.; Takagi, T.; Takahs, H.;
Terpstra, P.; Vasarotti, A.; Yasumoto,
Winter, Yasa, K.; Yoshikawa, H.F.; Zumstein, E.;
Wandenbol, M.; Vannier, F.; Vassarotti, A.; Vasaumoto,
K.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.;
Wature (1997) 390:249-256
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27; Mismatches 21
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##cross-references GB:Z99115; GB:
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Local Similarity 27.8%;
les 20; Conservative
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                #authors Advance Advance Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
Button, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Uterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.

# fournal Nature (1997) 388:539-547
#title Helicobacter pylori.
#cross-references MulD:97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1.333 ##label TOM
##cross-references GB:AE000537; GB:AE000511; NID:g2313247; PID:g2313250;
TIGR:HP0163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

#journal Nature (1999) 397:176-180
#title Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
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delta-aminolevulinic acid dehydratase - Helicobacter pylori
(strain J99)
#formal_name Helicobacter pylori
strain J99
12.Feb-1999 #sequence_revision 12-Feb-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 STSNDTTSAAFVSFMNSLINNRIVAILTSGKVNFPPEVVSWLRTA-GTSAFPSDSILSRF 139
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*length 323 *molecular-weight 36202 *checksum 1005
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Pred. No. 4.36e-01;
26; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 DVSYAAFYTSSKRAIALEHVKLSNRKSTD-DYQTILDVVFDSLED 183
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Best Local Similarity 28.08;
Matches 23; Conservative
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Xu, X.; Matsuno-Yaqi, A.; Yaqi, T.
Blochemistry (1993) 32:968-981
DNA sequencing of the seven remaining structural genes of the
gene cluster encoding the energy-transducing NaDH-quinone
oxidoreductase of Paracoccus denitrificans.
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hypothetical protein s111021 - Synechocystis sp. (strain PCC
6803)
                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Xu, X.; Matsuno-Yagi, A.; Yagi, T.
#journal Arch. Blochem. Blophys. (1992) 296:40-48
#title Structural features of the 66-kDa subunit of the energy-transducing NADH-ubiquinone oxidoreductase (NDH-1) of Paracccus denitrificans.
#cross-references MUID:92296779
                          157 VDILAPSNM-MDGNVLS-LRKALDKAGYFHTPIMS-YSTKFASSYYGPFRDVANSPPSFG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 VRFTTEVAGITQMGQTGRG-EDSEITSYLNQTLESNMQGNIIDLCPVGALV-SKPYAFTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence extracted from NCBI backbone (NCBIN:123409,
NCBIP:123410)
*superfamily NADH dehydrogenase (ubiquinone) chain 11
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Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
                                                                                                                                                                                                                               A45456 *type complete
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO3
Paracoccus denitrilicans
*formal_name Paracoccus denitrificans
#formal_name paracoccus denitrificans
24-Feb-1994 *sequence_revision 12-Apr-1996 *text_change
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PCC 6803
25.Apr-1997 #sequence_revision 25-Apr-1997 #text_change
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#length 673 #molecular-weight 73159 #checksum 4307
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Pred. No. 5.72e-01;
26; Mismatches 30; Indels
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                                                                                                                         163 NRKSTD-DYQTILDVVFDSLED 183
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Best Local Similarity 26.5%;
Matches 22; Conservative
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##residues 1-6
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##residues 658
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#title The full-length nucleotide sequences of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and its attenuated vaccine derivative, strain TC-83.
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##COSS-references GB:J04332
##note readthrough of the terminator UGA between codons CAA for 1879-Gln and CGG for 1880-Arg occurs
IRTCATION #superfamily Semiiki Forest virus nonstructural protein
RDS nonstructural protein; polyprotein
                                                                                                                                                                                                                                                             ##cross-references EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017679; PID:g1652020
##note the nucleotide sequence was submitted to the EMBL Data Library, June 1996
##length 673 #molecular-weight 74423 #checksum 9140
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Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

#journal DNA Res. (1996) 3:109-136

#title Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

#cross-references MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinney, R.M.; Johnson, B.J.B.; Welch, J.B.; Tsuchiya, K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonstructural polyprotein - Venezuelan equine encephalitis virus (strain TRD) encephalitis nonstructural protein NS1; nonstructural protein NS2; nonstructural protein NS3; nonstructural protein NS4 #formal_name Venezuelan equine encephalitis virus 30.Jun-1992 #sequence_revision 30.Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 SLREISI-DVVRAGNLAVRTQDYMRANMRVTFYVCITPNRNEILTAAARLS-KKGQISEA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 GMRNLSFSEVSRNGGIS-KPAEFGVNGIRVN-YICESASPPDIMVLPTQASSKTGKVFGQ 367
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Pred. No. 9.79e-01;
26; Mismatches 39; Indels
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Pred. No. 9.79e-01;
26; Mismatches 21; Indels
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Best Local Similarity 20.3%;
Matches 13; Conservative
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Best Local Similarity 24.2%;
Matches 23; Conservative
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##molecule_type mRNA
##residues 1-154 ##label KIE
##cross-references GB:X71021; NID:g311426; PID:g311427
This protein resides in the mitochondrial outer membrane (MOM)
Where it serves as part of the receptor complex for mitochondrial preproteins.
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       # authors Kiebler, M.; Keil, P.; Schneider, H.; van der Klei, I.J.;
    Pfanner, N.; Neupert, W.
# journal Cell (1993) 74:483-492
#title The mitochondrial receptor complex: a central role of MOM22
# cross-references MUID:93351229
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mitochondrial receptor complex chain MOM22 - Neurospora
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14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
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                                                                                                                                                                                  1183 VDWLSDRPEATFRARLDLGIPGDVPKYDIIFVNVR 1217
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Best Local Similarity 28.2%;
Matches 37; Conservative
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DNA-binding proteins.
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##experimental_source strain OT3
##note this accession replaces an interim accession for a sequence replaced by GenBank
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Mol. Cell. Biol. (1994) 14:1230-124 RFX1, a transactivator of hepatitis B virus enhancer I, RefX1, a transactivator of hepatitis B virus enhancer I, belongs to a novel family of homodimeric and heterodimeric
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Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H. DNA Res. (1998) 5:55-76 Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91utamate dehydrogenase (NADP+) (EC 1.4.1.4) - Sulfolobus shibatae (fragment) fformal_name Sulfolobus shibatae (fragment) # Formal_name Sulfolobus shibatae (9.0Ec-1993 # sequence_revision 10-Nov-1995 #text_change 25.Mar-1998
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#length 277 #molecular-weight 30608 #checksum 4645
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                                                                                                                                                                                                                                                                                                                   Length 277;
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Pred. No. 2.16e+00;
25; Mismatches 26; Indels
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                                                                                                                               ##molecule_type DNA | ##label KAW | 1-277 ##label KAW
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                                                                                *cross-references MUID:98344137
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Best Local Similarity 28.6%;
Matches 16; Conservative
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Best Local Similarity 21.7%;
Matches 15; Conservative
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466 VPSTLTQAIRNFAKSLEGWL-INAMSDFPQQVIQTKVGVV-SAFAQTLRRYTSLNHLAQA 523
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#product NADH dehydrogenase (ubiquinone) 75K chain #status predicted #label MAT #checksum 8774 #molecular-weight 79573 #checksum 8774
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Eur. J. Blochem. (1991) 201:547-550
Determination of the cDNA sequence for the human
mitochondrial 75-kDa Fe-S protein of NADH-coenzyme Q
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NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 75K chain
precursor - human
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metalloprotein; mitochondrion; NAD; oxidoreductase
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                                                       #Fresidues 1.723 ##label REI
#Cross-references GB:X76091; NID:g452389; PID:g452390
Y #Longth 723 #molecular-weight 80003 #check
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30-Sep-1993 #sequence_revision 30-Sep-1993
26-Feb-1999
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17; Mismatches 25
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Pred. No. 1.28e+00;
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##cross-references GDB:132062; OMIM:157655
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                                                                                                                                                       Score 103;
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#accession S17854
Query Match 4.1%;
Best Local Similarity 29.0%;
Matches 18; Conservative
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Best Local Similarity 28.6%;
Matches 26; Conservative
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S17854
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CLASSIFICATION #superfami
                                                                                                                                                                                                                                                                                                                                      524 AR 525
                                                                                                                                                                                                                                                                                                                                                                                    163 NR 164
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##molecule_type mRNA
##residues 1-727 ##label RUN
##ross-references GB:002877; NID:9163413; PID:9163414
##note parts of this sequence, including the amino end of the
##note mature protein, were determined by protein sequencing
IFICATION #superfamily NADH dehydrogenase (ubiquinone) chain 11
iron-sulfur protein; membrane-associated complex;
metalloprotein; mitochondrion; NAD; oxidoreductase
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                                                                                     Runswick, M.J.; Gennis, R.B.; Fearnley, I.M.; Walker, J.E. Bochemistry (1989) 28:9452-9459
Mitochondrial NABH: ubiquinone reductase: complementary DNA sequence of the import precursor of the bovine 75-KDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Demuth, D.R.; Golub, E.E.; Malamud, D.
#journal J. Biol. Chem. (1990) 265:7120-7126
#title Streptcoccal-host interactions. Structural and functional analysis of a Streptcocccus sanguis receptor for a human salivary glycoprotein.
#cross-references MUID:90236997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 IRFASEIAGVDDLGTTGRGN-DMQVGTYIEKMFMSELSGNIIDICPVGALT-SKPYAFTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 NEAIKQRNETAKATYDAAVKKYEADLAAVKQANAINEADYQAKLAA-YQTELARVQKANA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain transit peptide (mitochondrion) #status
predicted #label TNP\
#product NADH dehydrogenase (ubiquinone) 75K chain
#status experimental #label MAT
#length 727 #molecular-weight 79442 #checksum 9285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Streptococcus sanguis
10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change
12-Apr-1995
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27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change
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#length 1473 #molecular-weight 162435 #checksum 9437
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Pred. No. 1.28e+00;
32; Mismatches 37; Indels 6;
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4.1%; Score 105; DB 2; Length 727;
Best Local Similarity 28.6%; Pred. No. 1.28e+00;
Matches 26; Conservative 21; Mismatches 39; Indels
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##cross-references GB:J05418
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#accession A33552
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Best Local Similarity 25.0%;
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Search completed: Wed Sep 1 16:03:23 1999 Job time: 41 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 15.64 Seconds 505.902 Million cell updates/sec Wed Sep 1 16:03:42 1999; Run on:

not generated Tabular output >PCT-US99-13024-2 (1-372) from PCTUS9913024.pep (1 of 12) 2542 1 MEKFMAEFGGGYVQTPFLSE.......LPTOASSI Description: Perfect Score: Sequence: Title:

........LPTQASSKTGKVFGQEFREV 372

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 3:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Variance 172.028; scale 0.199 Mean 34.285; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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£	R97371	R32658	W20625	W27126	W38306	W22755	R10444	R10445	R10446	R10568	R10441	R10567	R10442	R88003	W55665	W55735
DB	19	ဖ	22	25	56	23	7	~	~	7	~	7	~	11	53	30
å Query Match Length DB	65	510	330	2247	269	569	269	269	269	270	270	270	270	294	571	1213
Query Match	11.8	5.0	4.3	4.2	4.0	4.0	3.9	3.9	3.9	3.9	9. 9.	3.9	3.9	3.9	3.9	3.9
Score	300	128	109	107	101	101	66	66	66	66	66	66	66	66	66	66
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1 mekfmaeiwtricpnailsesnsvrykislagscplstagpsyvkfqdnpvgsqtf ||||||||| | MEKFWAEFGGGYVQTPFLSESNSVRYKISIAGSCPLSTAGPSYVKFQDNPVGSQTF LT 2 R32658 standard; Protein; 510 RESULT ID R3

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Gaps

Length 65;

Score 300; DB 19; Length 65 Pred. No. 8.92e-14; 3; Mismatches 7; Indels

Query Match 11.8%; Best Local Similarity 82.1%; Matches 46; Conservative

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WIT: 93-076515/09.

WPPSDB: 037239.

Threston expression and secretion system in corynebacteria -

Protein expression and secretion system in corynebacteria -

Transformed with cassette contg. signal sequence of protein PSI

Transformed with cassette contg. signal sequence of protein PSI

Transformed colymer and polypeptide prodn.

S Claim 1: Fig 12: 95pp: French.

C N-terminal signal peptide of PS2 is useful in recombinant protein

C C Transformant. Since PS2 is associated with the bacterial cell wall,

C transformant. Since PS2 is associated with the bacterial cell wall,

C and can be recovered (without lysis) by treatment with a surfactant.

Sequence 510 AA:
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                       PS2 protein from C.melassecola ATCC 17965.
NADPH dependent glutamate dehydrogenase; Corynebacterium glutamicum; csp2 gene; secretory peptide.
csp2 gene; melassecola ATCC 17965.
Key Location/Qualifiers
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14.701.1997 (first entry)
14. pylori cytoplasmic protein, 02ael1612orf26,
Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
Identification; binding compound; bacterium; life cycle; activator;
bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
diagnosis.
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Pred. No. 5.54e-01;
55; Mismatches 100; Indels 16;
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                                                                                                                  /label- signal
/note- for protein secretion"
26.30
/note- putative"
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Local Similarity 23.3%;
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              (first entry)
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07-JUN-1995; US-487032.
01-APR-1996; US-630405.
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30-JUL-1991; FR-009652.
02-AUG-1991; FR-009870.
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Renaud M;
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11-FEB-1998 (first entry)
Equine rhinovirus 1 (ERNV1) polyprotein amino acid sequence.
Equine rhinovirus 1; ERNV1; foot-and-mouth disease virus; vaccine; horse; diagnosis; antigenss; polyprotein; enzyme-linked immunosorbent assay; recombinant protein.
                                                                                                                                                                                                                                               The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (APCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and defermined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
Sequence 330 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vdilapsnm-mdgnvls-lrkaldkagyfhtpims-ystkfassyygpfrdvansppsfg 220
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Pred. No. 1.00e+01;
26; Mismatches 28; Indels 5; Gaps
                                                                               Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter. Claim 61; Page 1051-52; 1401pp; English. This sequence represents a H. pylori cytoplasmic protein involved in
Mellgaerd BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
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W27126 standard; Protein; 2247 AA.
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163 NRKSTD-DYQTILDVVFDSLED 183
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/label- vP4
288..517
/label- vP2
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/label- vp3
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/label- vPl
992..1007
/label- 2A
1008..1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.3%;
Local Similarity 28.0%;
les 23; Conservative
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1552..1553
1577..1578
1782..1783
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1144..1458
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Smith D,
                                                                                                                                                                                                                                 cofactor metabolism.
                          WPI; 97-052306/05.
N-PSDB; T67878.
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11-FEB-1998
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Matches
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Detergent compositions comprising Subtilisin variants - which exhibit improved stability and/or wash performance Claim 1: Page - 191pp; English.

Claim 1: Page - 191pp; English.

Claim 1: Page - 191pp; English.

The present subtilace BLG309 variant, which has improved storage stability and/or improved performance in detergents, has a residue to the hydrophobic domain substituted with a more hydrophobic residue. The hydrophobic domain comprises the residues Prol39, Prol31, Ile165, Tyr167, Tyr171 of BLS309 (in BASBPN numbering). Detergent compositions containing the mutant enzyme have improved storage stability, while retaining or improving their wash performance. This variant has a wash performance improving their factor of 3.3 compared to wild type BLS309.

Che wild type BLS309 sequence, Genbank A08332.

Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Table 19 Page -: 91pp; English.

The present subtilase BLS309 variant, which has improved storage stability and/or improved performance in detergents, has a residue in the vicinity a wild type hydrophobic domain substituted with a more hydrophobic residue. The hydrophobic domain comprises the residues Pro129, Pro131, Ile165, Tyr167, Tyr171 of BLS309 (in BASBPN numbering). Detergent compositions containing the mutant enzyme have improved storage stability, while retaining or improving their factor of 3.3 compared to wild type BLS309.

N.B. Sequence not given in the specification, but constructed using Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 isypafyanamavgatdq-n-nnrasfsqygagldivapgv-nvqst-ypgstyasln 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A subtilase variant with amino acid substitutions in or near hydrophobic domain - has improved storage stability and/or improved performance in detergents, whilst retaining or improving its wash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1997 (first entry)
subtilisin 309 (BLS309) mutant Arg170Phe (in BASBPN numbering).
Variant; mutant; subtiliase; enzyme; BASBPN; storage stability;
wash performance; detergent; hydrophobic domain; subtilisin 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 26; Length 26
Pred. No. 3.25e+01;
21; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Mismatches 14; Indels
(UNIL ) UNILEVER PLC.
Bauditz P, Markvardsen P, Sierkstra LN, Von Der Osten C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1995; DK-000119.
12-APR-1996; DK-000421.
(NOVO ) NOVO-NORDISK AS.
Bauditz P, Klugkist J, Markvardsen P, Sierkstra LN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "wild type Arg replaced by Phe"
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Pred. No. 3.25e+01;
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W22755 standard; protein; 269
W22755;
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Best Local Similarity 32.8%;
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Best Local Similarity 32.8%;
Matches 19; Conservative
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02-MAY-1996; DK0207
05-MAY-1995; DK-000!
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                                                 Klugkist J;
WPI; 96-506142/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus lentus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For a second sequence of equine rhinovirus 1 - and derived proteins or virus-like particles, useful in vaccines and as diagnostic agents

For virus-like particles, useful in vaccines and as diagnostic agents

For virus-like particles, useful in vaccines and as diagnostic agents

For virus-like particles, useful in vaccines and as diagnostic agents

For virus-like particles, useful in vaccines to the sequence of the sequence represents the amino acid sequence of the sequence shown that the conclet acid density and base comparison of ERNV1 differs from other runces. To this end, the nucleotide sequence encoding the collyprotein of ERNV1 was deduced. Analysis of this sequence engogests that ERNV1 proteins can be used to make vaccines to protect horses (and ERNV1 proteins can be used to make vaccines to protect horses (and ERNV1) of the ranimals of ERNV1 of sequence primars and probes can be used for diagnosis of ERNV1. Oligonucleotide primars and probes can be used for diagnosis of ERNV1. Oligonucleotide primars and can be used for diagnosis of ERNV1. Oligonucleotide primars of the blood, particularly in ensyme-linked immunosorbent assay. They can differentiate between infected animals will not). Fragments of the on-capsid proteins but vaccinated animals will not). Fragments of the DNA sequence represent individual genes of the virus and can be expressed in host systems to produce recombinant proteins. Virus like particles containing the individual ERNV1 proteins. can also be used as vectors for delivering therapeutic or other useful agents, including vaccinating epitopes from other pathogens or reproductive hormones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1041 tyspfykmakmlfklatlavaamrtkdpvvvvmliadf-gle-vfdtgfffsyfqeklgp 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 SYAAFYISSKRAIALEHVKLSNRKSTDDYQTILDVY-FDSLEDVGATGFPRGTY-ESVEQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Mismatches 32; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subillisin 309 (BLS309) mutant Argl70Phe (in BASBPN numbering). Variant; mutant; subtilase; enzyme; BASBPN; storage stability; wash performance; detergent; hydrophobic domain; subtilisin 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 25; Length 2247; Pred. No. 1.35e+01;
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Misc_difference 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W38306 standard; protein; 269 AA.
W38306;
                                                                                                                                                                                                                                                                                                                                               Crabb BS, Feng L, Studdert MJ;
WPI; 97-341692/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 4.2%;
Local Similarity 23.4%;
les 22; Conservative
                                              /label= 3A
|1553..1577
|/label= 3B
|1578..1782
|1578..1782
|1783..2246
|1783..2246
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18-DEC-1996; AUO815.
18-DEC-1995; AU-007201.
(UYME ) UNIV MELBOURNE.
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12-APR-1996; E01610.
05-MAY-1995; EP-201161.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                   The mutant enzyme is produced by mutating the gene of subtilisin 309 protease and expressing the mutated gene in suitable hosts. The enzyme exhibits improved wash performance in comparison with their wild type parent enzyme. The enzyme is well suited for use in detergent compositions. The wild type sequence is taken from the international Patent Application No. PCT/DK 88/00002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease Claim 9; Page 47; 57pp; English. Sol4) 71D + R170Y + G195E + K251E. The mutant enzyme is produced by mutating the gene of subtilisin 309 protease and expressing the mutated gene in sultable hosts. The enzyme exhibits improved wash performance in comparison with their wild type parent enzyme. The enzyme is well suited for use in detergent compositions. The wild type sequence is taken from the international Patent Application No. PCT/DX 88/00002.
159 isypafyanamavgatdq-n-nnrasfsqygaqldivapgv-nvqst-ypgstyasln 212
            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 isypayyanamavgatdq-n-nnrasfsqygaeldivapgv-nvqst-ypgstyasin 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 VSYAAFYTSSKRAIALEHVKLSNRKSTDDYQTILDVVFDSLEDVGATGFPRGTYESVE 198
                                                                                                                                                                                                                                                         Enzymatic detergent compsns. - contg. a mutant subtilisin
protease with an isoelectric PH lower or higher than the parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casteleijn E., Egmond MR, Haverkamp J, Marugg JD, Mooren AT; WPI; 91-009217/02.
Enzymatic detergent compsns. - contg. a mutant subtilisin protease with an isoelectric pH lower or higher than the parent
                                                                                                                                                                                                          (UNIX.) VONLEVER PLC.
Casteleijn E, gamond MR, Haverkamp J, Marugg JD, Mooren AT;
WPI; 91-009217/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 269;
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                                                                                          18-MAR-1991 (first entry)

$004 mutant of the subtilisin 309 enzyme.

Subtilisin 309 mutant; detergent; $004.

ED-405901-A.

02-JAN-1991.

26-JUN-1999; 306952.

26-JUN-1989; GB-014604.

07-JUL-1989; GB-01560.

26-JUN-1999; EP-306952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1991 (first entry)
S014 mutant of the subtilisin 309
Subtilisin 309 mutant; detergent;
Bacillus subtilis 309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R10445 standard; Protein; 269 AA.
                                                                       R10444 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                              Claim 9; Page 47; 57pp; English.
S004) R170Y + G195E.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 3.9%;
Best Local Similarity 31.0%;
Matches 18; Conservative
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26-JUN-1990; 306952.
26-JUN-1989; GB-014604.
07-JUL-1989; GB-015660.
26-JUN-1990; EP-306952.
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$020) H120D + R170Y + G195E + K235L + K231E.

The mutant enzyme is produced by mutating the gene of subtilisin 309 protease and expressing the mutated gene in suitable hosts. The enzyme exhibits improved wash performance in comparison with their wild type parent enzyme. The wild type is well suited for use in detergent compositions. The wild type sequence is taken from the linternational Patent Application No. PCT/DK 88/00002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 6; 10pp; English.

$20) G195E + R170Y + H120D + K235L + K251E.

The Wild-type sequence is obtained from the International Patent Application No. PCTOM 88/0002. The mutant protease is used in certain detergent compositions formulated as detergent powders contg. Phosphate or zeolite builder, aqueous detergent liquids, nonaqueous
                                                                                                                       159 isypayyanamavgatdq-n-nnrasfsqygaeldivapgv-nvqst-ypgstyasln 212 :||:|:|:::: | ::::| |::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detergent compsns. contg. enzyme - comprising mutated subtilisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic detergent compsns. - contg. a mutant subtilisin protease with an isoelectric pH lower or higher than the parent
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WPI; 91-009217/02.
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WPI; 91-009218/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 269;
                 Length 269;
                                                                    14; Indels
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                                          Pred. No. 4.33e+01;
22; Mismatches 14
                   Score 99; DB 2;
                                                                                                                                                                                                                                                                                                                                                               S020 mutant of the subtilisin 309 enzyme.
Subtilisin 309 mutant; detergent; S020.
Bacillus subtilis 309.
EP-405901.A.
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Subtilisin mutant; S20; detergent.
Subtilisin 309.
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R10568 standard; Protein; 270 AA.
                                                                                                                                                                                                                                                                                      R10446 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%;
Best Local Similarity 31.0%;
Matches 18; Conservative
Query Match
Best Local Similarity 31.0%;
watches 18; Conservative
                                                                                                                                                                                                                                                                                                                                           (first entry)
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26-JUN-1989; GB-014604.
07-JUL-1989; GB-015660.
26-JUN-1990; EP-306952.
(UNIL ) UNILEVER PLC.
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26-JUN-1990; EP-306953.
(UNIL ) UNILEVER PLC.
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26-JUN-1989; GB-014605.
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S19) G195E + R170Y + H120D + K235L.
The wild-type sequence is obtained from the International Patent Application No. PCT/DK 88/V0002. The mutant protease is used in Certain detergent compositions formulated as detergent powders contg.
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                            160 isypayyanamavgatdq.n.nnrasfsqygaeldlvapgv.nvqst.ypgstyasln 213
                                                                                                                                              160 isypayyanamavgatdq-n-nnrasfsqygaeldivapgv-nvqst-ypgstyasln 213 :||:|:|: | | :: :| | | |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also R10440-41, R10499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detergent compsns. contg. enzyme - comprising mutated subtilisin
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WPI; 91-009218/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casteleijn E, Femond MR, Haverkamp J, Marugg JD, Mooren AT; WPI; 91-009218/02.
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Pred. No. 4.33e+01;
22; Mismatches 14; Indels
                                                               Score 99; DB 2; Length 270;
Pred. No. 4.33e+01;
22; Mismatches 14; Indels
detergent liquids, or detergent bars. S 500, R10567-68, EP-405901 and W09100345. Sequence 270 AA;
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19-MAR-1991 (first entry)
Subtilisin of the subtilisin 309 enzyme.
Subtilisin 309
Subtilisin 309.
                                                                                                                                                                                                                                        S12 mutant of the subtilisin 309 e
Subtilisin mutant; S12; detergent.
Subtilisin 309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 10pp; English.
S12) G195E + R170Y + K251E.
                                                                                                                                                                                                                          standard; Protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 270 AA
                                                               Query Match 3.9%;
Best Local Similarity 31.0%;
Matches 18; Conservative
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Best Local Similarity 31.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                  EP-405902-A.
02-JAN-1991.
26-JUN-1990, 306953.
26-JUN-1989; GB-014605.
26-JUN-1989; EP-015660.
26-JUN-1989; EP-015660.
26-JUN-1989; EP-015660.
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26-JUN-1990; 306953.
26-JUN-1989; GB-014605.
07-JUL-1989; GB-015660.
26-JUN-1990; EP-306953.
(UNIL.) UNILEVER PLC.
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R10441
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$024) *36D + H120D + R170Y + G195E + K235L + K251E.

The mutant enzyme is produced by mutating the gene of subtilisin 309 protease and expressing the mutated gene in suitable hosts. The enzyme exhibits improved wash performance in comparison with their wild type parent enzyme. The enzyme is well suited for use in detergent compositions. The wild type sequence is taken from the linternational Patent Application No. PCT/DK 88/00002.

See also R10442-56, EP-405902 and W09100345.
                                                                                                                      Gaps
                                                                                                                                                phosphate or zeolite builder, aqueous detergent liquids, nonaqueous detergent liquids, or detergent bars. See also R10440-41, R10499-5500, R10567-68, EP-405901 and W09100345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 isypayyanamavgatdq-n-nnrasfsqygaeldivapgv-nvqst-ypgstyasln 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams L, Liu C, Lufburrow PA, Thomas MD;
WPI; 96-054415/06.
New delta-endotoxins from Bacillus thuringiensis strains - used in insecticidal compsns. against lepidopteran and coleopteran pests claim 2; Page 33-34; 53pp; English.
R88002 and R88003 represent delta-endotoxins obtained from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta-endotoxin; insecticide; Bacillus thuringiensis; B.t.; MKHHK; lepidoptera; coleoptera; pest control; biopesticide.
Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic detergent compsns. - contg. a mutant subtilisin protease with an isoelectric pH lower or higher than the parent
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                                                                                Score 99; DB 2; Length 270;
Pred. No. 4.33e+01;
22; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 2; Length 270;
Pred. No. 4.33e+01;
22; Mismatches 14; Indels
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22-JDN-1994; US-264100.
10-NOV-1994; US-337358.
(NOVO ) NOVO-NORDISK ENTOTECH INC.
Adams L, Liu C, LuIburrow PA, Thomas MD;
                                                                                                                                                                                                                                                                                   18-MAR-1991 (first entry)
SOL4 mutant of the subtilisin 309 enzyme.
Subtilisin 309 mutant; detergent; SO24.
Bacillus subtilis 309.
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R10442 standard; protein; 270
R10442;
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R88003;
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Best Local Similarity 31.0%;
Matches 18; Conservative
                                                                                   / Match 3.9%; Local Similarity 31.0%;
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                                                                                                                    18; Conservative
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07-JUL-1989; GB-015660.
26-JUN-1990; EP-306952.
(UNIL.) UNILEVER PLC.
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26-JUN-1990; 306952.
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                                                                                 Query Match
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relicobacter protein and sequences and encoded polypeptide(s) - useful in vaccines to prevent H. pylori infection and for diagnosis of H. pylori secreted protein.

This is the sequence of a Helicobacter pylori secreted protein.

This is the sequence of a Helicobacter pylori secreted protein.

This is the sequence of a Helicobacter pylori secreted protein.

This is the sequence of a Helicobacter pylori secreted protein.

The protein may be used in a vaccine to prevent or treat H. pylori in sequences or infection of H. pylori in a sample and the diagnosis of H. pylori infection of H. pylori in a sample and the diagnosis of H. pylori infection of A. pylori in a santisens sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori sequences of H. pylori (APCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed to rompute evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ore proteins analysed for significant homology to other known or exported.
thuringiensis (B.t.). This sequence represents the MKHHK delta-endotoxin, and has a molecular weight of 33 kDa. Delta-endotoxins have molecular weights ranging from 27-140 kDa, and kill insect larvae upon ingestion. These sequences can be used in insecticidal compositions, which can be used to control lepidopteran and coleopteran pests. These compositions can optionally contain spores from a biologically pure B.t. strain. The compositions also contain at two other delta-endotoxins, each having a molecular weight of 130 kDa. The delta-endotoxins increase the spectrum of available biopesticides, Sequence 294 AA:
                                                                                                                                                                                                                                                                                                                                                                                      119 tqsltvsskfsfnfpvagaennisfsvgfeqnlsttetkteststlmrippqpvsvrprt 178
                                                                                                                                                                                                                                                                                                                                                                                                                    membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                              Gaps
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H. pylori ORF hp2el0911_4882027_c2_87 secreted protein.
H. pylori oxe hp2el0911_4882027_c2_87 secreted protein.
Exploration: vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
Helicobacter pylori.
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Pred. No. 4.33e+01;
28; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 571 AA.
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Best Local Similarity 26.0%;
Matches 25; Conservative
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06-DEC-1996; US-76318.

29-MAR-1996; US-76318.

22-MAR-1996; US-758731.

25-OCT-1996; US-758905.

28-OCT-1996; US-738859.

(ASTR.) ASTRA AB.

AIM RA, SMITH D.
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N-PSDB; V25074.
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190 Infsnnngfnsgsfeigakntifn-nan-fnnstsfnfnnssatts--fvgdftnansnl 245
                                                                            44 VKF-QDNPVGSQTFSAGLHLRVFDPSTGALVDSKSYAFSTSNDTTSAAFVS-FMNSLTNN 101
                                                                                                                          246 qiagnavfgnstngsqntanfnntgsvniagnatfdnv-vfnsptntsvkgkvtlnnitl 304
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Pred. No. 4.33e+01;
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Matches 30; Conservative
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:01:19 1999; MasPar time 25.10 Seconds 808.836 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-372) from PCTUS9913024.pep (1 of 12) 2542 1 MEKFMAEFGOGYVQTPFLSE.......LPTQASSKTGKVFGQEFREV 372 Title: Description: Perfect Score:

PAM 150 Gap 11 Scoring table:

Sequence:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 47.705; Variance 93.090; scale 0.512 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	1.12e-52	1.70e-51	9.94e-50	3.35e-04	7.82e-02	4.22e-02	4.22e-02	4.22e-02	1.44e-01	2.63e-01	3.55e-01	2.63e-01	3.55e-01	3.55e-01	3.55e-01	8.59e-01	8.59e-01	4.78e-01	1.53e+00	1.53e+00
	Description	TAIL FIBER GENE 35 (FR	TAIL FIBER GENE 35 (FR	FIBER	ROTEIN PRECURS	T24A6.11 PROTEIN.	POLYPROTEIN.	POLYPROTEIN.	NONSTRUCTURAL POLYPROT	GLUTAMATE RECEPTOR DEL	SBSB GENE.	REVERSE TRANSCRIPTASE	POLYPROTEIN.	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	PUTATIVE NONSTRUCTURAL	277AA LONG HYPOTHETICA	PUTATIVE TRANSCRIPTION	SCAFFOLDING PROTEIN PR	AMIDOPHOSPHORIBOSYLTRA	H17B01.4 PROTEIN.
SUMMARIES	ID	038400	038425	038393	004985	061942	066775	066774	826880	043424	045664	906800	039818	090163	066594	066592	058196	088073	045996	039000	044825
	DB	σ	σ	σ	7	ß	7,	14	14	4	7	7	14	14	14	14	~	7	7	10	ß
	% Query Match Length DB	28	28	28	510	373	2227	2248	2497	1001	920	1300	2247	2493	2493	2493	277	325	1546	548	997
	% Ouery Match	15.6	15.4	15.0	5.0	4.4	4.4	4.4	4.4	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4 . 1	4.0	4.0
	Score	397	391	382	128	111	113	113	113	109	107	106	107	106	106	106	103	103	105	101	101
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101 4.0 1004 2 101 4.0 1577 2 98 3.9 3.10 3.11 2 98 3.9 3.11 5 98 3.9 3.11 5 100 3.9 572 2 100 3.9 663 1 100 3.9 1007 11 99 3.9 1007 11 99 3.9 1007 11 99 3.9 1281 11 99 3.9 1281 11 99 3.9 1281 11 99 3.9 1281 11 99 3.9 2567 2 100 1 3.9 1007 11 99 3.9 1281 11 99 3.9 1281 11 99 3.9 2567 3 97 3.8 413 2 97 3.8 413 2 97 3.8 583 4	NUCLEAS SFERASE N PROTE M-DIOXYG M-DIOXYG M-DIOXYG M-DIOXYG SEDON SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOSON, SPOS
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## ALIGNMENTS

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DINGMENTO	PRT; 58 AA.	TREMBLREL. 01, CREATED) (TREMBLREL. 01, LAST SEQUENCE UPDATE) (TREMBLREL. 08, LAST ANNOTATION UPDATE) SNE 35 (FRAGMENT).	DATABLES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDAE; 14-LIKE PHAGES.	CH M.L.; the tail fiber gene 36 of bacteriophage even type Escherichia coli phages K3 and	6(1985). 29127C56 CRC32;	Score 397; DB 9; Length 58; Pred. No. 1.12e-52; 1; Mismatches 0; Indels 0; Gaps	SFSEVSRNGGISKPAEFGYNGIRVNYVCESASPPDIMVLPTQASSKTGKVFGQEFREV 58 	1 2 038425 038425 038425 03.00000000000000000000000000000000000
đ	RESULT 1 ID Q38400 PRELIMINARY;	01-NOV-1996 01-NOV-1996 01-NOV-1996 TAIL FIBER GI		RP SEQUENCE FROM N.A. RX MEDLINE; 85.15500. RA RIEDE I. DREXLER K., ESCHBACH M.L.; RT "The nucleotide sequences of the tail RT 12 and of genes 36 of the T-even type	NUCLEIC ACIDS RES. 13:605-616 EMBL, X01753; E7867; NON_TER 1 1 SEQUENCE 58 AA; 6206 MW;	Query Match Best Local Similarity 98.3%; Matches 57; Conservative	Db 1 SFSEVSRNGGISKPAEFGVNGIRV	Sal

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SEQUENCE
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MEDLINE: 85215500.
RIEDE I., DREXLER K., ESCHBACH M.L.;
"The nucleotide sequences of the tail fiber gene 36 of bacteriophage T2 and of genes 36 of the T-even type Escherichia coli phages K3 and 0x2.";
                        bacteriophage
phages K3 and
                                                                                                                                                                                                                    Gaps
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MEDLINE; 94018618.
MEDLINE; 94018618.
Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum.";
MOL. MICROBIOL. 9:97-109(1993).
EMBL; X69103: G40489; -.
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                                                                                                                                                                           Length 58
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RIEDE I., DREXLER K., ESCHBACH M.L.;
"The nucleotide sequences of the tail fiber gene 36 of 12 and of genes 36 of the T-even type Escherichia coll
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                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TAIL FIBER GENE 35 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                       Score 391; DB 9; 1
Pred. No. 1.70e-51;
2; Mismatches 0;
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146DDF70 CRC32;
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                                                                                                                                     E15E16A4 CRC32;
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                                                            NUCLEIC ACIDS RES. 13:605-616(1985).
EMBL, X01755; G15190; .
NON_TER 1 1 SEQUENCE 58 AA; 6236 MW: F15F16N
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EMBL; X01754; E7855; -.
NON_TER 1 1
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94.8%;
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510 AA;
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Q04985
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Matches
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Score 128; DB 2; Length 510;
Pred. No. 3.35e-04;
55; Mismatches 100; Indels 16; Gaps 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94150718.
MEDLINE; 94150718.
MEDLINE; 94150718.
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J., COLLSON A.,
CRAKTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STABEN R., SULGTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN R., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.)
"2.2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                             134 ESVAYALKVDQEAT-AAFEAYRNALRDAAI-SINPDGSIN-PDTSINLLIDAANAANRTD 190
                                                                                                                                                                     157 SPEV-TRVSSTST-VFQSSAYDMSDADWRFFTMYTTIEFLLNLDFWEKLEHSDKMVLLQN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 FSAKATLLFNSLRTVRGNNDRLTTPGGHEIVPDLMSTLFNVSLSFIRQIRSRVVSKLIEL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                    191 R--AEIE-DYAHLYTQT--DIALETPQLAYAFQDLKALQAEVDADFEWLGEFGIDQ-EDG
                                                                                                                                                                                                                                                                                                                                                                                 245 NY--VQRYHLPAVEALKAEVDARVAAIEPLRADSIAKNLEAQKSDVLVRQLFLERATAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels 10;
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STRAIN-BRISTOL N2;
WAIERSTON R.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 DILRVVEAIFSTSARYVELYENVENVNVENKTLRQHYSALIPN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAICH A., GATTUNG S., LE T.T.;
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GTINISIRFYNASNGYISSTQAEFTGQAGSWELKEDY-VVVPE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07, CREATED)
07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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4.4%; Score 111; DB 5; 1
Best Local Similarity 24.0%; Pred. No. 7.82e-02;
Matches 36; Conservative 44; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF068713; G3168946; -.
SEQUENCE 373 AA; 43176 MW; B6D589CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Mismatches
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Query Match 5.0%;
Best Local Similarity 23.3%;
Matches 52; Conservative
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01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATURE 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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Query Match
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Q88978
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170 YQTILDVVFDSLEDV-GATG-FP-RGTYESVEQFMSAVGGTNDEIARLPTSAAISKLSDY 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PERV;
MEDLINE; 96332508.
WUTZ G., AUER H., NOWOTNY N., SKERN T., KUECHLER E.;
WUTZ G., AUER H., NOWOTNY N., SKERN T., KUECHLER E.;
Tequine rhinovirus serotypes 1 and 2: relationship to each other and to aphthoviruses and cardioviruses.";
J. GEN. VIROL. 77:1719-1730(1996).
EMBL; X96870; E236020;
PERM; PF00073; rhv; 2.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00680; RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUINE RHINOVIRUS TYPE 1.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE;
APHTHOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE; 96332508.
WUTZ G., AUER H., NOWOTNY N., SKERN T., KUECHLER E.;
"Equine rhinovirus serotypes 1 and 2: relationship to each other and to aphthoviruses and cardioviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 113; DB 14; Length 2227; Pred. No. 4.22e-02; 33; Mismatches 31; Indels 7.
                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RNA POLYMERASE)
A4B1C493 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VPG).
(PROTEINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 YMKTIPGKISELVTDAATAAAQIPK-GVYSFVSS 1112
                                                                                                                                                                                                                      PRT; 2227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| :: | | :: :|:|| | :: ::::: 200 FMSAVGGTNDE-IARLPTSAA-ISKLSDYNLIPG 231
                                                                                        275 EITDEEFLLVTVILFCDPAISGLSSHAISI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VP4.
VP2.
VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 38.
33 38.
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
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08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 24.5%;
Matches 23; Conservative
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                       TYPE
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                                                                                                                                                                                                                                                                                                                                                       POLYPROTEIN.
EQUINE RHINOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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1440
1535
1559
1764
                                                                                                                                                                                                                                                                                                                                                                                                              VIRUSES; SSR
APHTHOVIRUS.
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SEQUENCE
                                                                                                                                                                                       LT 6
Q66775
Q66775;
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Q66774
Q66774
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                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDE, SECTION. SMITH J.F.; OBERSTE W.D., SMITH J.F.; COMPLETE SEQUENCE Of Venezuelan equine encephalitis virus subtype IE reveals conserved and hypervariable domains within the C terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
NONSTRUCTURAL POLYPROTEIN.
VENEZUELAN EQUINE ENCEPHALITIS VIRUS.
VENEZUELAN POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.
                                                                                                                                                                                                                                                                                                                                             Length 2248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2497;
                                                                                                                                                                                                                                                                                                                                        Score 113; DB 14; Length 22
Pred. No. 4.22e-02;
33; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 14; Length 24
Pred. No. 4.22e-02;
23; Mismatches 27; Indels
                                                                                                   LEADER (PROTEINASE).
                                                                                                                                                                                                                                                                                        2248 3D (RNA POLYMERASE)
, 249446 MW; F6416AD3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2497 AA; 278720 MW; C746FA71 CRC32;
                                                                                                                                                                                                                                                         (VPG).
(PROTEINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 YMKTIPGKISELVTDAATAAAQIPK-GVYSFVSS 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 FMSAVGGTNDE-IARLPTSAA-ISKLSDYNLIPG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2497 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 AA.
          EMBL; X96870; E235486;
PFAM; PF00073; rhv; 2.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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VIROLOGY 219:314-320(1996).
EMBL: U34999; G1144528; -.
PFAM: PF00978; RNA_dep_RNApol2; 2.
J. GEN. VIROL. 77:1719-1730(1996)
                                                                                                                                                    VP3.
VP1.
22A.
22C.
33A.
                                                                                                                                                                                                                                                                                                                                          / Match 4.4%;
Local Similarity 24.5%;
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-68U201 (SUBIYPE IE);
MEDLINE; 96204604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.4%;
Best Local Similarity 25.7%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1183 VDWLSETPDSTFRA 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                  1009
11145
1460
1555
1579
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1580 178
1785 224
2248 AA;
                                                                                                                                290
520
746
994
1010
1146
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SEQUENCE
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ID 043424
AC 043424;
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4
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                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                               HU W., ZUO J., DE JAGER P.L., HEINTZ N.;
"The human glutamate receptor delta 2 gene (GRID2) maps to chromosome 4922.";
                                                                                                                                                                                                                                                                                                                                      193 T-YESVEQFMSAVGGINDEIARLPISAAISKLSDYNLI-PGDVL-YLKAQLY-ADADLLA 248
                                                                                                                                                                                                                                                                                                                    644 VISSYTANLAAFLTITRIESSIQSLQDLSKQTEIP-YGTVLDSAVYEHVRMKGLNPFERD 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 INTFKVTVTEVPVQVQNQGFTLVDNLSNAPQNTVAFNK-AEKVTSMFAGETKTVAMYDTK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PV72;
MEDLINE: 97197531.
KUEN B., KOCH A., ASENBAUER E., SARA M., LUBITZ W.;
Molecular characterization of the Bacillus stearothermophilus PV72
S-layer gene sbsB induced by oxidative stress.";
J. BACTERIOL. 179:1664-1670(1997).
EMBL: X98095; E245076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                              703 SMYSQMWRMINRSNGSENNVLESQAGIQKVKYGNYAFVWDAAVLEYV-A-IYDPDCSFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                         42; Mismatches 53; Indels 10;
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 NGDPETKPVDFKDATVRSLNPIIATAAINGSELLVTANAGQSGKASFEVTFKD 487
                                                                                                                                                                                                                                                            Score 109; DB 4; Length 1007; Pred. No. 1.44e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 2; Length 920;
Pred. No. 2.63e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Mismatches 56; Indels
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-MOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLUTAMATE RECEPPOR DELTA-2 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                 GENOMICS 47:143-145(1998).
EMBL; AF009014; G2853315; -.
SEQUENCE 1007 AA; 113430 MW; BB46EE51 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920
97916 MW; 1253823C CRC32;
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045664:
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.28;
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Best Local Similarity 21.6%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 20.4%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      761 IGNT-VADRGYGIA 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | : : | : : 249 LGTTNISIRFYNAS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00395; SLH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 9
920 AA;
                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 98126449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 NGMKKQAGVAILISDKIDFQPKVIKKDK-EGHFILIKGKILQE-ELSILNIYAPNKRAAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; PICORNAVIRIDAE.
                                                                                                                                                                        MEDLINE; 96414308.
TAKARARA T., OHSUMI T., KUROMITSU J., SHIBATA K., SASAKI N., OKAZAKI Y., SHIBATA K., SASAKI N., OKAZAKI Y., SHIBATA H., SATO S., YOSHIKI A., KUSAKABE M., WIRAMANISU M., URKI M., OKUDA K., HAYASHIZAKI Y.;
"Dysfunction of the Orleans reeler gene arising from exon skipping due to transposition of a full-length copy of an active L1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 96165505.
LI F., BROWNING G.F., STUDDERT M.J., CRABB B.S.;
Eguine rilnovirus 1 is more closely related to foot-and-mouth disease virus than to other picornaviruses.";
PROC. NATL. ACAD. SCI. U.S.A. 93:990-995(1996).
EMBL; L43052; G2231134; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.2%; Score 106; DB 11; Length 13 sest Local Similarity 27.1%; Pred. No. 3.55e-01; Atches 23; Conservative 22; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                           Into the skipped exon.;
HUM. MOL. GENET. 5:989-993(1996).
EMBL. D84931; D1021252;
PFAM: PF01260; AP_endonulease1; 1.
PRAM: PFCTED DNA POLYMERASE.
NON_TER.
SEQUENCE 1300 AA; 152068 MW; 3656A0F1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 14; I
Pred. No. 2.63e-01;
33; Mismatches 32;
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               PRT; 1300 AA
O08906 PRELIMINARY; PRT; O08906; O1-101-1997 (TREMBLREL: 04, LAST SEQ 01-NOV-1998 (TREMBLREL: 08, LAST ANN REVERSE TRANSCRIPTASE (FRAGMENT).
                                                                                                                                  SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 FTKETLVKLKAHIAPHTIIVGDFNT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00073; rhv; 1.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PEAM; PF00910; RNA_hellcase; 1.
POLYPROTEIN.
SEQUENCE 2247 AA; 249301 MW; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-NOV-1998 (TREMBLREL. 08,
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les 22; Conservative
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SEQUENCE FROM N.A.
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039818;
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Matches
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1125 LRNYDPRINLVPVNRRLPHALVLHHNEHPQSDFSSFVSKL-KGRTVLVV-GEKLSVPGKM 1182
                                                                                        STRAIN-TC-83;
MEDLINE; 89343175.
KINNEY R.M., JOHNSON B.J., WELCH J.B., TSUCHIYA K.R., TRENT D.W.;
KINNEY R.M., JOHNSON B.J., WELCH J.B., TSUCHIYA K.R., TRENT D.W.;
The full-length nucleotide sequences of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and its attenuated vaccine derivative, strain TC-83.";
VIROLOGY 170:19-30(1889).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINNEY R.M., JOHNSON B.J., BROWN V.L., TRENT D.W.;
"Nucleotide sequence of the 26 S mRNA of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and deduced sequence of the encoded structural proteins.";
VIROLOGY 152:400-413(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINNEY R.M., JOHNSON B.J., WELCH J.B., TSUCHIXA K.R., TRENT D.W.; "The full-length nucleotide sequences of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and its attenuated vaccine derivative, strain TC-83."; VIROLOGY 170:19-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOHNSON B.J., KINNEY R.M., KOST C.L., TRENT D.W.;
"Molecular determinants of alphavirus neurovirulence: nucleotide and deduced protein sequence changes during attenuation of Venezuelan equine encephalitis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENEZUELAN EQUINE ENCEPHALITIS VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE;
 deduced protein sequence changes during attenuation of Venezuelan equine encephalitis virus."; J. GEN. VIROL. 67:1951-1960(1986).
                                                                                                                                                                                                                                                                                                                                                                                        Length 2493;
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01-AUG-1998 (TREMBLREL, 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
PUTATIVE NONSTRUCTURAL POLYPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                     MW; E16755C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 14;
Pred. No. 3.55e-01;
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                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
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PFAM; PF00978; RNA_dep_RNApol2; 2.
                                                                                                                                                                                                                                                                           1 535
536 1329
1330 1886
1887 2493
2493 AA; 277927 M
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STRAIN-TRINIDAD DONKEY;
MEDLINE; 86263392.
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STRAIN-TRINIDAD DONKEY;
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STRAIN-TRINIDAD DONKEY;
MEDLINE; 89243175.
                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           POLYPROTEIN.
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Q66592
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                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
STRAIN-71-180, 600035-71-180/4;
MEDLINE; 89243175.
KINNEY R.M., JOHNSON B.J., WELCH J.B., TSUCHIYA K.R., TRENT D.W.;
The full-length nucleotide sequences of the virulent Trinidad donkey strain of Venezuelan equine encephalitis virus and its attenuated vaccine derivative. strain TC-83.";
VIROLOGY 170:19-30(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-TC-83; MEDLINE; 86306669.
JOHNSON B.J., KINNEY R.M., KOST C.L., TRENT D.W.; "Molecular determinants of alphavirus neurovirulence: nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                           01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NONSTRUCTURAL POLYPROTEIN.
VENEZUBLAN EQUINE ENCEPHALITIS VIRUS.
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE: TOGAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VENEZUELAN EQUINE ENCEPHALITIS VIRUS.
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOGAVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINNEY R.M., TSUCHIYA K.R., SNEIDER J.M., TRENT D.W.; "Molecular evidence for the origin of the widespread Venezuelan equine encephalitis epizootic of 1969 to 1972."; J. GEN. VIROL. 73:0-0(0).
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Pred. No. 3.55e-01;
26; Mismatches 39; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NONSTRUCTURAL PROTEIN NSP1.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-71-180, 600035-71-180/4;
KINNEY R.M., TRENT D.W.;
SUBMITTED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AFK09003; G3249014; -.
POLYPROTEIN.
                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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200 FMSAVGGTNDE-IARLPTSAA-ISKLSDYNLIPG 231
                                                                                        2493
                                                                                                                            CREATED)
                                                                                      PRT;
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STRAIN-71-180, 600035-71-180/4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 4.2%;
Local Similarity 24.2%;
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONSTRUCTURAL POLYPROTEIN
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066594 PRELIMINARY;

066594, 066594,

01-NOV-1996 (TREMBLREL. 0

01-NOV-1998 (TREMBLREL. 0

01-NOV-1998 (TREMBLREL. 0
                                                                                        PRELIMINARY;
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                                                                                                                         01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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536 132
1330 188
1887 249
2493 AA;
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                                                                                                                                                                                                                                      ALPHAVIRUS
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090163
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RP SEQUENCE FROM N.A.

RC STRAIN-TRINIDAD DONKEY;

RA KINNEY R.

KINNEY R.

BL SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.

BL SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.

DR EMBL; LO1442; G3201595; -.

DR PFAM; PF00978; RNA_dep_RNApol2; 2.

KW POLYPROTEIN 1 535 NONSTRUCTURAL PROTEIN NSP1.

FT CHAIN 1330 1886 NONSTRUCTURAL PROTEIN NSP3.

FT CHAIN 1330 1887 24.93

NONSTRUCTURAL PROTEIN NSP3.

FT CHAIN 1887 24.93

NONSTRUCTURAL PROTEIN NSP3.

SQUENCE 2493 AA; 277915 MW; A6B7B200 CRC32;

OUMERY MALCH

4.2%; SCOTE 106; DB 14; Length 2493;

Best Local Similarity 24.2%; Pred. NO. 3.55e-01;

MATCHES 23; CONSERVATIVE ALS; Pred. NO. 3.55e-01;

MATCHES 23; CONSERVATIVE ALS; Pred. NO. 3.55e-01;

MATCHES 23; CONSERVATIVE ALS; PICH NO. 3.55e-01;

MATCHES 23; CONSERVATIVE ALVENTED ALTES ARVSENNSLINNRIVALLTS GRVNFPPEV 118

DD 1125 LRNYDPRINLY PHALVLHHNEH POSPESSFYSKL-KGRTVLYV-GEKLS VPGKM 118;

CY 62 LRVFDPSTGAL-VDSK-SYAFSTS-NDTTSAAFVSFNNSLINNRIVALLTS GRVNFPPEV 118

DD 1183 VDWLSDRPEATFRARLDLG IDED VPKYDIIFVNYR 1217

QY 119 VSWLRTAGTSAFPSDSILS-RFDVS-YAAFYTSSK 151

SEATCH COMPLETED: 64 SECS.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.33 Seconds 117.961 Million cell updates/sec Wed Sep 1 16:06:41 1999;

not generated. Pabular output

>PCT-US99-13024-2 (1-24) from PCTUS9913024.pep (2 of 12) I MEKFWAEFGGGYVQTPFLSESNSV 24

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

Database:

a-geneseq35

Mean 21.293; Variance 79.022; scale 0.269 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Ouery Match Length DB	DB	ID	Description	Pred. No
-	74	42.0	65	19	R97371	Phage T4 ORFX gene or	8 970+00
~	65	36.9	591	37	W72912		5 69 e+01
m	65	36.9	621	53	W55645	_	5.696+01
7	65	36.9	637	30	W55739	ORF	5.696+01
'n	65	36.9	645	37	W73030	er D	5.69e+01
φ	65	36.9	652	37	W73029		5.69e+01
7	9	36.4	358	35	W44826		6 960+01
00	64	36.4	358	23	W23324	Pseudomonas fluoresce	6.96e+01
σ	63	35.8	364	33	W62047	Streptococcus pneumon	8 50e+01
10	63	35.8	389	~	P70668	D-alanine racemase.	8 508+01
11	63	35.8	409	σ	R48060	Sequence of protease	8 500+01
12	63	35.8	461	30	W39928	Human CDP-diacylglyce	8 500+01
13	63	35.8	740	33	W62045	Streptococcus pheumon	8.50+01
14	62	35.2	146	53	W55354		1.046+02
15	62	35.2	269	53	W55518	ORF	1.046+02
16	62	35.2	479	58	W55555	ORF	1 040+02

### ALIGNMENTS

New proteins derived from T4 phage tail fibre proteins - that can self assemble into nano-structure(s), useful as filters etc, also corresponding DNA corresponding DNA protein (R97371) of unspecified function is the product of open reading frame X of the tail fibre protein gene region (see also T29053) of phage T4. This gene region also includes open reading frames for tail fibre proteins (see also R97370 and R97372-74). Tail fibre proteins (see also R97370 and R97372-74). Tail fibre proteins (active or modified) can be produced in large quantities in microbial cells and used as building blocks of strong, stable nanostructures. 07-JAN-1997 (first entry)
Phage T4 ORFX gene product. Kgp34.
Phage T4: tail fibre protein; nanotechnology; nano-structure; filter; molecular sieve.
MO9611947-Al. T 1 R97371 standard; Protein; 65 AA. 13-CCT-1995, U13023, 13-CCT-1994, US-322760, (GOLD/) GOLDBERG E B. GOLDERG EB, WPI; 96-221942/22. N-PSDB; T29053. RESULT NAME OF THE PROPERTY OF THE PR

Score 74; DB 19; Length 65; Pred. No. 8.97e+00; 3; Mismatches 7; Indels Query Match
Best Local Similarity 58.3%;
Matches 14; Conservative

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Gaps

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1 mekfmaeiwtricpnailsesnsv 24 

엄 à RESULT 2 ID W72912 standard; Protein; 591 AA.

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polypeptide(s) useful in vaccines to treat or prevent H. pylori polypeptide(s) useful in vaccines to treat or prevent H. pylori claims 14,80; Pages 850-851; 1145pp; English.

This is a H. pylori call envelope outer membrane protein having a C-terminal tyrosine cluster motif. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or linhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of
                                                                                                                                                                                                                                                                                                                   New isolated mycobacteria polypeptides and nucleic acids - used for developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis claim 1: Page 188-190; 163pp: English.

The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments derived from M.tuberculosis, can be used in particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, sequence 591 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1998 (first entry)
4-JUN-1998 (first entry)
H. pylori ORF 06ep10615_961562_f2_41 cell envelope OMP.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
identification; binding compound; bacteria; life cycle; activator;
inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                              Mycobacterium tuberculosis antigen RDI-ORF2.
Mycobacterium tuberculosis; antigen; vaccine; immunological;
                                                                                                                                                                                                                          (STAT.) STATENS SERUM INST.
Andersen P. Florio W. Nielsen R. Oettinger T. Rasmussen PB,
Rosenkrands I. Weldingh K;
WPI; 98-542705746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 37; Length 591;
Pred. No. 5.69e+01;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522 mdkfvgaafgsg-aptmfls 540
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1 MEKFM-AEFGOGYVQTPFLS 19
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55.0%;
                                                                    immunogen; infection.
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                      01-APR-1998; DK0132.
05-JAN-1998; US-070488.
02-APR-1997; DK-000376.
18-APR-1997; US-044624.
10-NOV-1997; DK-001277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997; U05223.
06-DEC-1996; US-76318.
02-ARR-1996; US-625811.
02-APR-1996; US-7589731.
25-OCT-1996; US-738959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori.
WO9737044-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 11; Conserv
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                                                                                                                                                                                                                                                                                                      N-PSDB; V63936
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27-MAR-1997; U
06-DEC-1996; U
             21-JAN-1999
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W55645;
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Matches
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H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylorispecific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interest, particular regions can be isolated from n. pyror, wy the amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                              Gaps
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H. pylori ORF O6epl0615_961562_fl_15 cell envelope OMP.

H. pylori ORF O6epl0615_961562_fl_15 cell envelope OMP.

H. pylori ORF O6epl0615_961562_fl_15 cell envelope OMP.

Identification, binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; cell envelope outer membrane protein; OMP; tyrosine cluster motif.

M09737044_A1.
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                  DB 29; Length 621;
                                                                                                                                                                                               // Match 36.9%; Score 65; DB 29; Length 621
Local Similarity 22.2%; Pred. No. 5.69e+01;
hes 4; Conservative 10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and encoded
                                                                                                                                                                                                                                                                                                                                        standard; Protein; 637 AA.
                                                                                                                                                                                                                                                     475 dynhgyikssffnsssdi 492
                                                                                                                                                                                                                                                                        7 EFGQGYVQTPFLSESNSV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1997; U05223.

27-MAR-1996; US-761318.

29-MAR-1996; US-75811.

02-APR-1996; US-75811.

25-CCT-1996; US-756905.

28-CCT-1996; US-736859.

(ASTR.) ASTRA AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-503122/46.
N-PSDB; V25148.
                                                                                                                                                                        621 AA;
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W55739;
W55739;
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                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter and gastroducdenal diseases

Laim 9: Page 123-125: 184pp: English.

This is the amino acid sequence of a 76 kDa Helicobacter pylority polypeptide designated GHPO 185. It was deduced from an isolated polypeptide designated GHPO 185. It was deduced from an isolated genomic DNA sequence (see V07919). The invention provides a family of 76 kDa Helicobacter polypeptides (see W73012-312), as well as a 12 kDa polypeptide (see W73014) and a 50 kDa polypeptide (see W73015), and methods for producing the unprocessed or mature polypeptides in host cells. The polypeptides on methods in host cells. The polypeptides on methods and products of the invention allow treatment and prevention of gastroducdenal diseases associated with Hb infections, including acute, chronic, and atrophic gastritis, and not diagnostic methods are also provided.

Sequence 645 AA;
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             Gaps
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                                                                                                         W73030;
02-FEB-1999 (first entry)
Helicobacter pylori 76 kDa polypeptide GHPO 185.
GHPO 185; infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEE-1999 (first entry)
Helicobacter pylori 76 kDa polypeptide GHPO 190.
GHPO 190; infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 37; Length 645;
 Pred. No. 5.69e+01;
10; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
(INMR) MERIEUX ORAYAX PASTEUR MERIEUX SERUMS ET VACCINS.
Al-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;
WPI; 98-568251/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.9%; Score 65; DB 37
22.2%; Pred. No. 5.69e+
vative 10; Mismatches
                                                                                                                                                                                                /label= Sig_peptide
20..645
/label= Mat_protein
                                                                                                                                                                             Location/Qualifiers
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/label= Sig_peptide
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/label= Mat_protein
                                                                                      J. 5
W73030 standard; Protein; 645 AA.
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                                491 dynhgyikssffnsssdi 508
Best Local Similarity 22.2%;
Matches 4; Conservative
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                                                      7 EFGOGYVQTPFLSESNSV 24
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31-MAR-1998, U06421.
01-APR-1997, US-834666.
01-APR-1997, US-831310.
                                                                                                                                                       therapy.
Helicobacter pylori
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A Narabis viscou.

Thimmaric gene imparting resistance to two or more herbicides - such as hydroxyphenylpyruvate dioxygenase inhibitors, also related vectors and transformed plants

Y vectors and transformed plants

Disclosure; Fig 1: 4Ppp: French.

The invention relates to the generation of transgenic plants resistant to preferably at least 2 herbicides by introducing a chimaeric gene comprises at least 2 gene subunits where one sequence encodes hydroxyphenylpyruvate dioxygenase (HPPD), an enzyme that promotes to learnee to herbicides such as isoxaflutole or sulcotrione. This sequence was used to derive the degenerate primers sequence (V19280). This in turn was used to derive the degenerate primers (V19270-V19274) for the isolation of the HPPD gene from P. fluorescens strain A32 (V19269). The plants, e.g. tobacco, cotton, rape, soya,
                                                                                                                                                                                             N-Garawi A, Kleanthous H, Lissolo L, Miller C, Tomb J;
NP1: 98-568351/48

N-PSDB; V07918.

New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter products for the amino acid sequence of a 76 kDa Helicobacter pylori polypeptide designated GHPO 190. It was deduced from an isolated genomic DNA sequence (see V07918). The invention provides a family of 76 kDa Helicobacter polypeptides (see W73022-32), as well as a 3 kDa polypeptide (see W73034) and a 50 kDa polypeptide (see W73035), and also polynucleotides (see V72001, V07912-21 and V07963-64) encoding them, expression cassettes, and methods for producing the unprocessed or mature polypeptides in host cells. The polypeptides can be used in vaccination methods to prevent or treat Hb infection in a mammal. Methods and products of the invention allow treatment in the prevention of gastroduodenal diseases associated with Hb
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Transgenic plant; resistance; herbicide; chimaeric gene; tolerance; PCR; hydroxyphenylpyruvate dioxygenase; isoxaflutole; sulcotrione; primer; amplification; tobacco; cotton; rape; soya; sugar beet; cereal; ioxynil; nitrilase; dihalohydroxybenzonitrile; bromoxinyl; nematode; insecticide; glyphosate oxidoreductase; Bacillus thuringiensis; fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections, including acute, chronic, and atrophic gastritis, peptic ulcer diseases, e.g. gastric and duodenal ulcers. Dete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 37; Length 652;
Pred. No. 5.69e+01;
10; Mismatches 4; Indels
                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
(INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptic ulcer diseases, e.g. gastric and duodenal ulcers and diagnostic methods are also provided. GHPO 190 was demonstrated to be a protective antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-1997; F01256.
16-JUL-1996; FR-009137.
(RHON ) RHONE-POULENC AGROCHIMIE.
Ballett K, Pelissier B, Sailland A;
WPI; 98-110608/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W44826 standard; Protein; 358 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::||:::|:::|
7 EFGQGYVQTPFLSESNSV 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens
                                          01-APR-1997; US-834666.
01-APR-1997; US-831310.
31-MAR-1998; U06421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V19280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9802562-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Thu Sep

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14-JAN-1987
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sugar beet, cereals, may also contain a gene encoding e.g. a nitrilase for resistance to dihalohydroxybenzonitriles such as bromoxinyl or ioxynil, alyphosate oxidoreductase for resistance to glyphosate. A third gene encoding a Bacillus thuringiensis insecticidal protein or proteins imparting resistance to fungi or nematodes, may also be introduced into
                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New sequences encoding hydroxy-phenyl pyruvate di:oxygenase - pref. from Pseudomonas fluorescens, useful for generating transgenic plants resistant to isoxazole or tri:ketone herbicides
Example 1: Fig 3: 26pp; French.

Example 1: Fig 3: 26pp; French.

C dioxygenase (HPPD) gene sequence from Pseudomonas sp. PJ874 and were used to amplify fragments of the HPPD gene of P.fluorescens

C A32. The present sequence was deduced from the insert of one positive clone and it has 92% identity to the known PJ874 HPPD protein. The coding sequence can be used to generate transgenic plants which are resistant to the isoxazole or di- or tri-ketone family of herbicides, especially 4-[4-CF3-2-(methylsulphonyl) benzoyl]-5-cycloppropyl isoxazole or sulcotrione.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae spo/rel distal terminal portion.
Streptococcus pneumoniae: spo/rel: spoT/relA family; screening;
antibacterial; otitis media; conjunctivitis; pneumonia; bacteraemia;
                                                                                                                                Gaps
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                                                                                                                                                                                                                                                        05-SEP-1997 (first entry)
Pseudomonas fluorescens hydroxy-phenyl pyruvate dioxygenase.
PPPD: isoxazole; diketone; triketone; herbicide; resistance;
4-{4-CF3-2-(methylsulphonyl)benzoyl]-5-cyclopropyl isoxazole;
sulcotrione; transgenic plant; marine bacterium.
                                                                                                  Score 64; DB 35; Length 358; Pred. No. 6.96e+01; 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 6.96e+01;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1996.

03-JUN-1996; FR0831.

02-JUN-1995; FR-006800.

10-MAY-1995; FR-013570.

17-MAY-1996; FR-005944.

(RHON ) RHONE POULENC AGROCHIMIE.

MALINGE M. PALLELT K, ROLland A, Sailland A;

WPI; 97-034380/03.
                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by TTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 36.4%; Score 64; Local Similarity 33.3%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                   W23324 standard; Protein; 358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W62047 standard; Protein; 364 AA.
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                                                                                                                                                       227 ieeflmgfngegighvafltd 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 ieeflmqfngegighvafltd 247
                                                                                                                                                                     1 MEKFMAEF-GOGYVOTPFLSE 20
                                                                                                   Ouery Match 36.4%;
Best Local Similarity 33.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                            Pseudomonas fluorescens A32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W62047;
01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae. EP-849362-A2.
                                                                            358 AA;
                                                                                                                                                                                                                                                                                                                                                      misc_difference 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T49369
                                                                                                                                                                                                                                                                                                                                                                                WO9638567-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitis.
                                                              the plant.
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                             Matches
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The present sequence is the distal terminal portion of a spo/rel protein (spor/relA family) from Streptococcus pneumoniae. The protein is of the spor/relA family) from Streptococcus pneumoniae. The protein is of the spor/relA family, which, in Escherichia coli, is involved in the stringent response to nutrient limitation and regulate the accumulation of (p)ppdpp which is involved in the regulation of gene expression and other cellular processes. Spo/rel proteins have a homology to e.g. S. equisimilis rel protein. Spo/rel proteins can be used: (a) in the treatment of an individual in need of spo/rel protein, by administering to the protein to the patient; (B) in the treatment of an individual in need of spo/rel protein, by administering an antagonist which inhbits the activity of the protein; and (C) for inducing an immunological response by inoculating the mammal with spo/rel protein, or a fragment or variant of it, adequate to produce antibody and/or T cell immune response to protect the animal from disease. Conditions which may be treated include otitis media, conjunctivitis, pneumonia, bacteriamia meningits, sinustis, pleural empyema, endocarditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Protein may be produced in a transformed cell-line defficient in b-alanine production. The cell will then express the required sequence and a second sequence operably linked to the D-alanine racemase. Other sequences which may be used in the same way include those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteraemia, meningitis, sinusitis, pleural empyema, endocarditis and especially meningitis and compositions may be used as antibacterials. Sequence 364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                        New Streptococcus spoT/relA polypeptide(s) - useful in treatment of otitis media, conjunctivitis, pneumonia, bacteremia and especially meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stable maintenance of heterologous DNA in host cell - using host cells deficient in ability to synthesise cell wall transformed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
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Sequence 389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 33; Length 364;
Pred. No. 8.50e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-alanine racemase.
L-glutamate racemase; D-alanyl-D-alanine ligase.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 2; Lo
Pred. No. 8.50e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 31-32; 40pp; English.
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24-JUN-1998.
23-CCT-1997; 308473.
24-CCT-1996; US-029049.
(SMIX ) SMITHKLINE BEECHAM CORP.
Gentry DR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P70668 standard; protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 emlmagfgengyvankfm 136
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EKFMAEFGQ-GYVQTPFL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1986; 014702.
18-JUN-1985; US-746437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENENCOR INC. Ferrari E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 mdqfmveldqey 324
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Best Local Similarity
Matches 8; Conser
                                                                                                                                                                WPI; 98-324673/29.
N-PSDB; V37948.
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N-PSDB; N70668.
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PCT-US99-13024-2-02.rag

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                                                                                                                                                                                                                                                            New Kluyveromyces yeast with modified protease gene - esp. used for high yield prodn. of recombinant protein, also DNA encoding yeast protease and derived peptide(s)
Disclosure: Page 31-33; 49pp; English.

The protease gene is to be modified in order to render it (partially) incapable of producing the natural protein; or result in a nonfunctional protease or in a protease with modified proteolytic activity. The modifications can be introduced in vitro or in situ by standard genetic engineering technqiues or by exposure to mutagenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises human CDP-diacylglycerol synthase (hCDS), or CTP:phosphatidate cytidylyltransferase, an enzyme that converts phosphatidic acid to CDP-diacyl-glycerol, a precursor of phosphatidylinostiol, phosphatidylglycerol and cardioliphn. Its amino acid sequence was deduced from an isolated cDNA clone (see V09944). It shows homology to Drosophila CDS (see W3929), yeast CDS and E. coli CDS. hCDS polypeptides can be obtained by chemical synthesis or by recombinant expression. A claimed method for screening drug candidate componds having activity as antinifammatory agents, for increasing haematopoiesis, and preventing reoxygenation injury following cytoreductive therapy involves contacting a CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Nucleic acid encoding human CDP-diacyl-glycerol synthase and related proteins - used to identify compounds that are antiinflammatory, increase haematopoiesis or prevent re-oxygenation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1998 (first entry)
Muman CPP-diacyldlycerol synthase.
CDP-diacyldlycerol synthase; hCDS; human;
CTP-phosphatidate cytidylyltransferase; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 9; Length 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.50e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoiesis; reoxygenation injury; therapy.
                                              20-JUL-1994 (first entry)
Sequence of protease A encoded by gene PRA1.
Protease; yeast; proteolysis.
Protease; yeast; proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "encoded by GGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .f. 12
k39928 standard; Protein; 461 AA.
                                                                                                                                                                                             SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ekylnsfqraypqesfskdnvdv 76
              R48060 standard; Protein; 409
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25.JUN-1997; U11294.
28.JUN-1996; US-672814.
(CELL-) CELL THERAPEUTICS INC.
                                                                                                                                                                                         (RHON ) RHONE POULENC RORER S
Fleer R, Fournier A, Yeh P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:: | ::| | :: |
EKFMAEFGQGYVQTPFLSESNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 35.8%;
Local Similarity 30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                        23-JUN-1993; F00623.
25-JUN-1992; FR-007785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference 412
                                                                                                                                                                                                                            WPI; 94-026215/03.
N-PSDB; Q55348.
                                                                                                                                                                                                                                                                                                                                                                                                                                              409 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9800550-A1.
                                                                                                                                         06-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                   R48060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              injury
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RESULT
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The present sequence represents a spo/rel protein (spoT/relA family) from Streptococcus pneumoniae. The protein is of the spoT/relA family, which, an Esteptococcus pneumoniae. The protein is of the spoT/relA family, which, an Esteptococcus pneumoniae. The protein is of the spoT/relA family, which, and spot in Esteptical coli, is involved in the stringent response to nutrient limitation and regulation of gene expression and other cellular processes.

Spo/rel proteins have a homology to e.g. S. equisimilis rel protein. Spo/rel proteins can be used: (a) in the treatment of an individual in need of spo/rel protein, by administering to the protein to the patient; (b) in the treatment of an individual having need to inhibit spo/rel corporating an antagonist which inhibits the activity of the protein; and (c) for inducing an immunological response by concert the mammal with spo/rel protein, or a fragment or variant conflucted the mammal from disease. Conditions which may be treated include otilis media, conjunctivitis, pneumonia, becteraemia, meningitis, shown in the include otilismus and sepecially meningitis and compositions may be used as antibacterials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae spo/rel protein sequence.
Streptococcus pneumoniae; spo/rel; spof/relA family; screening;
antibacterial; otitis media; conjunctivitis; pneumonia; bacteraemia;
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus spor/relA polypeptide(s) - useful in treatment of otitis media, conjunctivitis, pneumonia, bacteremia and especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
polypeptide with a drug candidate (preferably a pool of compounds from combinatorial library expression), and measuring CDS activity with and without different concentrations of the drug candidate. Modulator compounds can be used e.g. as inhibitors of the inflammatory cascade following hypoxia and reoxygenation, as in cases of sepsis, trauma or adult respiratory distress syndrome. CDS is also used to raise specific antibodies for therapeutic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                         Length 461;
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Pred. No. 8.50e+01;
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                                                                                                                                                                                                       Score 63; DB 30; I
Pred. No. 8.50e+01;
7; Mismatches 4;
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H. pylori ORF 01cp11710orf5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .r 14
W55354;
17-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         W62045 standard; Protein; 740 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP. Gentry DR;
                                                                                                                                                                                                                                                                                      fmatlvhgyi-tsfirgpnp 423
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FMAEFGQGYVQTPFLSESNS 23
                                                                                                                                                                                                       Query Match
Best Local Similarity 40.0%;
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01-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-029049
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                                                                                                                                                               461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                              diagnostic use
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Matches
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Polypeptide(s) - useful in vaccines and encoused

polypeptide(s) - useful in vaccines to treat or prevent H. pylori

infection and for diagnosis of H. pylori infection

PS Claim 14; Page 576-577; 1145pp; English.

This sequence is a H. pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori

infection or to identify H. pylori polypeptide binding compounds,

conseful as potential H. pylori life cycle activators or inhibitors. The

CNA and probes derived from it may be used for the identification of

H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic

CNA and probes derived from it may be used for the identification of

H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic

CNA and probes complementary to the DNA act as antisense sequences and

CA and distribution of H. pylori-specific antigens. The genomic sequence

CA and distribution of H. pylori-specific antigens. The genomic sequence of

CA pylori (ATC 55679) was determined from overlapping contigs generated

CA pylori (ATC 55679) was determined from voralapping contigs generated

CA pylori (ATC 55679) was determined from voralapping contigs generated

CA pylori (ATC 55679) was determined from voralapping contigs generated

CA pylori (ATC 55679) was determined from voralapping contige by mechanically shearing the bacterial DNA. The sequences were analysed

CA of ORF of at least 180 nucleotides, and the predicted from various ORF

CA of ORF of a least 180 nucleotides and determined the sequences of

CA of ORF of a maino acid sequences predicted from various ore

CA of or ore proteins. Having identified and determined the sequences of

CA or ore proteins. Having identified and determined from various ore

CA or ore proteins. Having identified and determined from the sequences of
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cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification: binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis. W09737044-A1.
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h. pylori ORP Orepi1916_5913592_f3_18 cell envelope OMP.
Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis. Helicobacter pylori.
W09737044-A1.
27-MAR-1997; U05223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and encoded
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W55518 standard; Protein; 269 AA.
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                                                                                                                                                                                                                                                                                       27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-7589731.
25-CCT-1996; US-738859.
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29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-0CT-1996; US-738059.
28-0CT-1996; US-738059.
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Alm RA, Smith D;
WPI; 97-503122/46.
N-PSDB; V24764.
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N-PSDB; V24927.
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Alm RA, Smith D;
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PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection

C Tains 14,80; page 721-722; 1145pp; English.

C This sequence is a H. pylori cell envelope outer membrane protein which is stated to have a terminal Phe residue.

CC The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, consetul as potential H. pylori life cycle activators or inhibitors. The protein can be used from it may be used for the identification of for H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies and distribution of H. pylori's pecific antigens, The genomic sequence of M. pylori (ATCC 55679) was determined from overlapping contigs generated for ORF of at least 180 nucleotides, and the predicted coding regions of defined by computer evaluation. To identify 1kkely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest particular regions can be isolated from H. pylori by PCR can amplification for recombinant polypeptide production, e.g. in E. coli
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Pred. No. 1.04e+02;
4; Mlsmatches 7; Indels
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larity 45.0%;
Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm wed Sep 1 16:06:10 1999; MasPar time 4.18 Seconds 229.968 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-24) from PCTUS9913024.pep (2 of 12) 176 1 MEKFWAEFGGGYVQTPFLSESNSV 24 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 30.660; Variance 51.855; scale 0.591 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	1.618-01	7 076-01	4.22e+00	4.22e+00	4.22e+00	5.97e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.18e+01	1.66e+01	1.66e+01
	Description	hypothetical protein		DNA ligase (ATP) (EC	4	DNA-directed RNA poly	hypothetical 25K prot		probable membrane pro	gene 33 protein - pha	hypothetical protein	4-hydroxyphenylpyruva	hypothetical protein	probable membrane pro	hypothetical protein	DNA-directed RNA poly	malD protein - Strept	id	outer membrane protei	outer membrane protei	probable outer membra	probable outer membra	hypothetical protein	
SUMMARIES	ΩI	F71000	T02323	S41974	QQBE34	A25884	JQ0061	S35168	E64757	GWBPT4	B71121	S21209	164032	H64775	H70470	S65068	S32571	E70802	B64610	E64610	B71904	E71904	164029	D70428
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đ	Query Match	43.8	41.5	38.6	38.6	38.6	38.1	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	36.9	36.9	36.9	36.9	36.9	36.9	36.4	36.4
	Score	77	73	89	99	89	. 67	99	99	99	99	99	99	99	99	99	65	65	65	65	65	65	64	64
	Result No.	1	7	m	4	5	Q	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23

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phosphoglycerate kina 1.6 hypothetical protein 2.3 maltodextrin phosphor 1.6 hypothetical protein 2.3 phosphoglycerate kina 2.3 phosphoglycerate kin	BH1302	MMARY #length 860 #molecular-weight 95454 #checksum 371  Query Match Best Local Similarity 29.4%; Score 77; DB 2; Length 860; Best Local Similarity 29.4%; Pred. No. 1.61e-01; Matches 5; Conservative 9; Mismatches 3; Indels 0;   MSKELTDFSNAFIRVAF 17	<pre>Uy I MEAFMADEGGGIVQIPF 1/ RESULT 2 T02323 #type complete TITLE hypothetical protein F13P17.19 - Arabidopsis thaliana</pre>
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S41971
Skinner, M.A.; Moore, J.B.; Binns, M.M.; Boursnell, M.E. submitted to the EMBL Data Library, February 1994
Deletion of fowlpox virus homologues of vaccinia virus genes between the 3b-hydroxysteroid dehydrogenase (A44L) and DNA
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                                                                                                                                                                                                                                                                                                                                       Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S41974 *type complete
DNA ligase (ATP) (EC 6.5.1.1) - fowlpox virus
#formal_name fowlpox virus
06.Jan-1995 *sequence_revision 06.Jan-1995 *text_change
24.Sep-1998
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BBLF4 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Mar-1999
                                                                                                                                    submitted to the EMBL Data Library, July 1998
Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.
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                                                                                                                                                                                                                                                                ##residues 1-2301 ##label ROU
##cross-references EMBL:AC004481; NID:g3337347; PID:g3337366
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#length 564 #molecular-weight 64472 #checksum
                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 7.07e-01;
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Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
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DNA sequence and expression of the B95-8 Epstein-Barr virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Sweetser, D.; Nonet, M.; Young, R.A.
#submission submitted to the EMBL Data Library, July 1987
#description Prokaryotic and eukaryotic RNA polymerases have homologous
core subunits.
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#journal J. Biol. Chem. (1990) 265:16498-16503
#title Mapping the active site of yeast RNA polymerase B (II).
#cross-references MUID:90375520
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Proc. Natl. Acad. Sci. U.S.A. (1987) 84:1192-1196
Prokaryotic and eukaryotic RNA polymerases have homologous
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DNA-directed RNA polymerase (EC 2.7.7.6) II 140K chain -
yeast (Saccharomyces cerevisiae)
DNA-directed RNA polymerase B chain B150; protein 03533;
protein YOR151c
#formal_name Saccharomyces cerevisiae
16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
21-Aug-1988
A25884; S36860; A37894; S67039
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                                                                                      MOI. Biol. Med. (1983) 1:21-45
Sequence analysis of the 17,166 bp EcoRI fragment C of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation; protein coding region
*superfamily varicella-zoster virus gene 55 protein
*length 809 *molecular-weight 89853 *checksum 6134
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##residues 1-809 ##label BAN
##cross-references EMBL:V01555; NID:959074; PID:91334885
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##residues 1-1002, RRRY',1007-1224 ##label SW2
##cross-references EMBL:M15693; NID:9172210; PID:9172211
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Pred. No. 4.22e+00;
3; Mismatches 8; Indels
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##residues 961-990 ##label RIV
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##residues 1-1224 ##label_SWE
##cross-references_EMBL:M15693
SNCE S36860
                   F43043; A03776; S33026
                                                                                                                                         virus.
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cross-references MUID:85035713
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Best Local Similarity 42.18;
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##molecule_type mRNA
#fresidues 1-56 ##label MEI
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                                                                             ##residues 1.1224 ##label BOR
##cross-references FMBL:275059; NID:91420378; PID:e252039; PID:91420379;
##experimental_source_strain S288C
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##residues
1-236 ##label_NUT
##cross_references GB:X14736; NID:960529; PID:960533
##note this protein probably corresponds to the capsid protein
NT Maize chlorotic mottle virus causes a severe disease in maize
NT called corn lethal necrosis.

RY #Length 236 #molecular_weight 25149 #checksum 3718
                                                                                                                                                                                                                                            *superfamily DNA-directed RNA polymerase 132K polypeptide DNA binding; nucleotidyltransferase; nucleus; transcription;
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#journal Plant Mol. Biol. (1993) 22:379-383
#title Isolation of cytochrome P-450 cDNA clones from the higher plant Catharanthus roseus by a PCR strategy.
#cross-references MUID:93283641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Nutter, R.C.; Scheets, K.; Panganiban, L.C.; Lommel, S.A.
#journal Nucleic Acids Res. (1989) 17:3163-3177
#title The complete nucleotide sequence of the maize chlorotic mottle virus genome.
#cross-references MUID:89263725
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hypothetical 25k protein - maize chlorotic mottle virus
#formal_name maize chlorotic mottle virus
host Zea mays (maize)
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
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13-Jan-1995 #sequence_revision 09-May-1997 #text_change
17-Mar-1999
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#length 1224 #molecular-weight 138750 #checksum 8452
O.; Tarassov, I.A.; Winsor, B.
submitted to the Protein Sequence Database, July 1996
S67039
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Pred. No. 4.22e+00;
5; Mismatches 8;
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Best Local Similarity 40.9%;
Matches 9; Conservative
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                   chromoprotein; electron transfer; heme; iron; monooxygenase;
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nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-70 ##label BLAT
##cross-references GB:AE000137; GB:U00096; NID:g2367108; PID:g1786500;
UMGP:b0309
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#formal_name Escherichia coli
12.5ep-1997 #sequence_revision 17.5ep-1997 #text_change
24.0ct-1998
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gene 33 protein - phage T4
#formal_name phage T4
host Escherichia coli
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
05-Sep-1997
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th 70 #molecular-weight 7854 #checksum 6854
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#journal Nucleic Acids Res. (1989) 17:6729
#title Organization of the bacteriophage T4 genome between map positions 150.745 and 145.824.
#cross-references MUID:89386003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal Science (1997) 277:1452
#title The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
#accession E64757
##CITOSS references EMBL.X69775; NID:g395301; PID:g395302 CLASSIFICATION #superfamily unassigned cytochrome P450; cytochrome homology
                                                                                                                                                                 #binding_site heme iron (Cys) (axial ligand)
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DS transmembrane protein
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#length 56 #checksum 2986
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Similarity 53.3%;
8; Conservative
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Similarity 29.4%;
5; Conservative
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##experimental_source strain OT3
##note this accession replaces an interim accession for a sequence replaced by GenBank
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
DNA Res. (1998) 5:55-76
Complete sequence and gene organization of the genome of a
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Barros-Soederling, J.; Persson, B.; Joernvall, H.
Eur. J. Blochem. (1992) 205:459-466
Characterization of 4-hydroxyphenylpyruvate dioxygenase.
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hypothetical protein PH0737 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14.hug-1998 #sequence_revision 14.hug-1998 #text_change
14.Aug-1998
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#formal_name Pseudomonas sp.
19 Mar-1997 #sequence_revision 19-Mar-1997 #text_change
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#superfamily phage T4 gene 33 protein
#length 112 #molecular-weight 12830 #checksum 9958
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Pred. No. 8.42e+00;
4; Mismatches 7; Indels
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                                                ##residues 1-112 ##label HAH
##cross-references EMBL:X15818; NID:q15210; PID:q15213
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8.42e+00;
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Pred. No. 8.42e+
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                                                                                                                                                                                                                                                                 1-336 ##label KAW
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Best Local Similarity 38.9%;
Matches 7; Conservative
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Best Local Similarity 46.2%;
Matches 12; Conservative
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Fletschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandom, R.C.; File, L.D.; Fritchman, J.L.; Coophagen, N.S.M.; Gnehm, C.L.; Krichman, J.L.; Coophagen, N.S.M.; Gnehm, C.L.; McDonald, L.B.; Scance (1995) 269:406-512
Whole-genome random sequencing and assembly of Haemophilus
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
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hypothetical protein Hils00 - Haemophilus influenzae (strain
Rd KW20)
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##molecule_type DNA
##residues 1-508 ##label TIGR
##cross-references GB:U32826; GB:L42023; NID:g1574322; PID:g1574341;
##cross-references GB:U32826; GB:L42023; NID:g1574322; PID:g1574341;
##cross-references GB:U32826; GB:U42023; NID:g1574322; PID:g1574341;
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#formal_name Escherichia coll
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
                                                                                                                                                                                                                                                                                    Gaps
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18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
30-Jun-1998
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#title The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
                                                                                                           ##molecule_type protein
##residues 1-357 ##label RUE

XY #length 357 #molecular-weight 40060 #checksum 6289
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Score 66; DB 2; Length 357;
Pred. No. 8.42e+00;
7; Mismatches 5; Indels
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Pred. No. 8.42e+00;
4; Mismatches 5; Indels
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                                                                                 preliminary
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8; Conservative
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Best Local Similarity 43.8%;
Matches 7; Conservative
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Plant Mol. Biol. (1996) 30:337-342
Sequence analysis of the second largest subunit of tomato RNA
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                   nucleic acid sequence not shown; translation not shown
                                                       ##cross-references GB:AE000152; GB:U00096; NID:g1786660; PID:g1786662; UWGP:b0457
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DNA-directed RNA polymerase (EC 2.7.7.6) II second largest
chain - tomato
#formal_mame Lycopersicon esculentum #common_name tomato
28-0cr-1996 #sequence_revision 13-Mar-1997 #text_change
21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
#authors Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
                                                                                                                                                                                                                                           #domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TM2
#length 518 #molecular-weight 58932 #checksum 2466
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hypothetical protein aq_1989 - Aquifex aeolicus
#formal_name Aquifex aeolicus
08-may-1998 *sequence_revision 08-May-1998 #text_change
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#length 853 #molecular-weight 99499 #checksum 642
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                                                                                                                        ##experimental_source strain K-12, substrain MG1655
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Best Local Similarity 35.0%; Pred. No. 8.42e+00;
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Warrilow, D.; Symons, R.H.
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                                  ##molecule_type DNA
##residues 1-5
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                     ##molecule_type mRNA
##residues 1-1191 ##label WAR
##cross-references EMBL:028403; NID:g1049068
                                                                                                                                                                                                                                                                                                    DB 2; Length 1191;
                                                                                                                                                                                                                                                                                               Query Match 37.5%; Score 66; DB 2; Length 1191
Best Local Similarity 35.0%; Pred. No. 8.42e+00;
Matches 7; Conservative 8; Mismatches 5; Indels
                                                                    nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Wed Sep 1 16:06:24 1999. Job time: 14 secs.
polymerase II.
#cross-references MUID:96178872
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 1 16:05:00 1999; MasPar time 2.92 Seconds 232.136 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-24) from PCTUS9913024.pep (2 of 12) 176 1 MEKFWAEFGGGYVQTPFLSESNSV 24 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.468; Variance 47.304; scale 0.665

# SUMMARIES

	Pred. No.	1.458-01	7.11e-01	1.54e+00	1.54e+00	1.54e+00	2.25e+00	3.28e+00	3.28e+00	3.28e+00	3.28e+00	3.28e+00	4.76e+00	6.88e+00	6.88e+00	6.88e+00	6.88e+00	6.88e+00	6.88e+00	6.88e+00	6.88e+00	9.89e+00	9.89e+00	9.89e+00
	Description	HYPOTHETICAL 7.3 KD PR	MEIOTIC RECOMBINATION	DNA LIGASE (EC 6.5.1.1	PROBABLE HELICASE.	DNA-DIRECTED RNA POLYM	COAT PROTEIN (CAPSID P	RNA POLYMERASE-ASSOCIA	4 - HYDROXYPHENYLPYRUVAT	HYPOTHETICAL PROTEIN H	HYPOTHETICAL 58.9 KD P	CYTOCHROME P450 72A1 (	MALTODEXTRIN TRANSPORT	HYPOTHETICAL PROTEIN H	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	HYPOTHETICAL 74.8 KD P	ANTHRANILATE SYNTHASE	DNA-DIRECTED RNA POLYM	CAPSULE POLYSACCHARIDE	ALANINE RACEMASE (EC 5	PHOSPHOGLYCERATE KINAS
SUMMARIES	D	X15A_BPT4	RE11_SCHPO	DNLI_FOWPM	HELI_EBV	RPB2_YEAST	COAT_MCMV	VG33_BPT4	HPPD_PSESP	YFOO_HAEIN	YLAB_ECOLI	CP72_CATRO	MALD_STRPN	YOCB_HAEIN	PGKE_TRYBB	PGKC_TRYBB	PGKA_TRYBB	PGKD_TRYBB	YNE7_YEAST	TRPG_SCHPO	RPB2_ARATH	KSS5_ECOLI	ALR_BACSU	PGKB_CRIFA
	DB	; -	-	٦	-	٦		-	Н	-	-	-	н	-	-	-	Н	-	Н	Н	Н		П	1
	Length DB	65	923	564	809	1224	236	112	357	508	518	524	277	239	420	440	505	208	929	759	1188	389	389	417
аP	Query Match	42.0	39.8	38.6	38.6	38.6	38.1	37.5	37.5	37.5	37.5	37.5	36.9	36.4	36.4	36.4	36.4	36.4	36.4	36.4	36.4	35.8	35.8	35.8
	Score	74	70	89	68	99	29	99	99	99	99	99	65	64	64	64	64	64	64	64	64	63	63	63
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и согни ихо нивирия в	PRT; 65 AA ED) SEQUENCE UPDAT: IN GP34-GP35 IN IN GP34-GP35 IN RNA STAGE; TAILE SWISS-PROT DATA C2D7CE2D CRC32 SCOTE 74; DB 1 Pred. No. 1.45e 3; Mismatches 3; Mismatches SV 24	PRT; 923 AA. HATED) T SEQUENCE UPDATE) T ANNOTATION UPDATE TEIN REC11. (FISSION YEAST). OTA; ARCHIASCONYCET SCHIZOSACCHAROMYCET SCHIZOSACCHAROMYCET recombination in Sci
6655 6675 6675 6675 6675 6675 6675 6675	ARD; CREAT, LAST, LAST, PROTEIN PROTEIN TO THE 334 MW; 58.3%; S8.3%; ative AILSESN	RE11_SCHPO STANDARD; PR 092380; 092380; 01-NOV-1997 (REL. 35, LAST SEQUE 01-NOV-1997 (REL. 35, LAST SEQUE 01-NOV-1997 (REL. 35, LAST SEQUE O1-NOV-1997 (REL. 35, LAST SEQUE RECITIC RECOMBINATION PROTEIN RECITIC RECOMBINATION PROTEIN RECITIC SCHIZOSACCHAROMYCES POMBE (FISSI SCHIZOSACCHAROMYCES POMBE (FISSI SCHIZOSACCHAROMYCETALES; SCHIZOS SCHIZOSACCHAROMYCES SCHIZOS
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40000000000000000000000000000000000000	RESULT 15 P15 AC P15 DT O11-1 DT O11-1 DT O11-1 DE HIPP GN VIRK OC VIRK OC VIRK OC T4-1 RR SEQ RR SEQ OUETY BEST LAMATCHE	RESULT TO REIL TO POT OT O

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00697; DNA_LIGASE_A1; 1.
PROSITE; PS00333; DNA_LIGASE_A2; FALSE_NEG.
PRAM; PF01068; DNA_LIGAGE,
DNA_REPAIR; DNA_LIGAGE,
DNA_REPAIR; DNA_REPLICATION; DNA_RECOMBINATION; CELL DIVISION; LIGASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKINNER M.A., MOORE J.B., BINNS M.M., SMITH G.L., BOURSNELL M.E.; "Deletion of fowlpox virus homologues of vaccinia virus genes between the 3 beta-hydroxysteroid dehydrogenase (A44L) and DNA ligase (A50R) genes.";
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).
VIRUSES: DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; CHORDOPOXVIRINAE;
AVIPOXVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDRATION UPDATE)
DIA LIGASE (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THIS PROTEIN SEALS, DURING DNA REPLICATION, DNA RECOMBINATION AND DNA REPAIR, NICKS IN DOUBLE-STRANDED DNA. IT IS NOT ESSENTIAL FOR VIRAL REPLICATION AND RECOMBINATION. CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) + (DEOXYRIBONUCLEOTIDE)(N) - AMP + PYROPHOSPHATE + (DEOXYRIBONUCLEOTIDE)(N+M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                    Score 70; DB 1; Length 923;
Pred. No. 7.11e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 564;
                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 AMP (BY SIMILARITY).
64472 MW; 861BEDB9 CRC32;
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Pred. No. 1.54e+00;
8; Mismatches 6;
                                                                                                                                                                                                                                                                  923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIROL. 75:2495-2498(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 MYKYVINIGDVAYVIGSFLKKSKSV 103
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                                                                                                                                                                                                                                                                                                                       39.88;
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 42.1%;
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Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                              EMBL; U70737; G1619901; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 AA;
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Q67480;
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                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEN.
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                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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AREALIES 942.00.00

RA BAER R., BANKIER A.T., BIGGIN W.D., DEININGER P.L., FARRELL P.J.,

RA GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,

RA TUFFNELL P.S., BARRELL B.G.;

TONA sequence and expression of the B95-8 Epstein-Barr virus genome.";

RI TONA sequence and expression of the B95-8 Epstein-Barr virus genome.";

REPLICATION: THIS PROTEIN MAY BE AN HELICASE AND IS REQUIRED FOR

SINILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 ULS,

C. SINILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 ULS,

EHV-1 57, EBV BBLF4, HCWV ULIO5, AND VZV 55.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPB2_YEAST STANDARD; PRT; 1224 AA.
P08518; Q12738;
01-A0G-1988 (REL. 08, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (EC 2.7.7.6) (B150)
(RNA POLYMERASE II SUBUNIT 2).
RPB2 OR RPO22 OR RPB150 OR YOR151C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 87147239.
SWEETSER D., NONET M., YOUNG R.A.;
"Prokaryotic and eukaryotic RNA polymerases have homologous core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.6%; Score 68; DB 1; Length 809; Best Local Similarity 42.1%; Pred. No. 1.54e+00; Matches 8; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                       EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
GAMMAHERPESVIRINAE; LYMPHOCRYPTOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
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PIR; S33026; S33026.

DNA REPLICATION; ATP-BINDING; HELICASE; EARLY PROTEIN.

72 79 ATP (BY SIMILARITY).

SEQUENCE 809 AA; 89853 MW; F70F2487 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288C / FY1678;
AYADI A., BORDONNE R., CAMASSES A., MADANIA A., POCH
TARASSOV I.A., WINSOR B., MARTIN R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'ROC. NATL. ACAD. SCI. U.S.A. 84:1192-1196(1987)
                                                21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-EC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PROBABLE HELICASE.
809 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 METFSPEFDPELSEPPFLP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKFMAEFGOGYVQTPFLS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V01555; G59126; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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RESULT 8
ID HPPD_PSESP
                                                                                                                                                                                                                                                                                      LT 7
VG33_BPT4
P13338;
                                                                                                                                SEQUENCE
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                     RNA(N).
SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
THIS SUBUNIT IS THE SECOND LARGEST COMPONENT OF RNA POLYMERASE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: COAT PROTEINS FROM CÁRMOVIRUSES (CARMY, MNSW, TCV), DIANTHOVIRUSES (RCNMV), SOBEMOVIRUSES (MCMV, SBMV), TOMBUSVIRUSES (AMCW, CNV, CYRSV, AND TBSV), AND TNV ARE RELATED IN THEIR S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUTTER R.C., SCHEETS K., PANGANIBAN L.C., LOMMEL S.A.,
                                                                                                                          THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-ANG-1991 (REL. 19, LAST ANNOTATION UPDATE)
01-ANG-1991 (REL. 19, LAST ANNOTATION UPDATE)
MAIZE CHLOROTEIN (CAPSID PROTIEIN).
WRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; MACHLOMOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                        CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                  SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                DNA-DIRECTED RNA POLYMERASE; TRANSCRIPTION; ZINC; ZINC-FINGER; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 1; Length 1224; Pred. No. 1.54e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1163 1185 C4-TYPE (POTENTIAL).
1003 1006 AEGI -> RRRY (IN REF. 1).
1224 AA; 138751 MW; DAZED93A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome.";
NUCLEIC ACIDS RES. 17:3163-3177(1989).
                                                                                                                                                                                                                                                                                                                                                                         PIR; A25884; A25884.
SGD; L0001676; RPB2.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 KYEISFGKIYVTKPMVNESDGV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: || || | ::||::|
KFMAEFGQGYVQTPFLSESNSV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 38.6%;
Local Similarity 40.9%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                              EMBL; M15693; G172211; -.
EMBL; U55020; G1293711; -.
EMBL; Z75059; E252039; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                         AND TRNA GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 89263725.
                                           SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COAT_MCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P11642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Organization of the bacteriophage T4 genome between map positions 150.745 and 145.824."; NUCLEIC ACIDS RES. 17:6729-6729(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. BACTERIOL, 176:1164-1171(1994).
-I- FUNCTION: BINDS TO E.COLI RNA POLYMERASE AND IS REQUIRED FOR TRANSCRIPTION OF LATE GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIOPHAGE 14.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; MYOVIRIDAE;
14-LIKE PHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WINKELMAN J.W., KASSAVETIS G.A., GEIDUSCHEK E.P.,
"Molecular genetic analysis of a prokaryotic transcriptional
coactivator: functional domains of the bacteriophage T4 gene 33
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
m
                                                                                                                             51 R DOMAIN, INTERACTION WITH RNA.
217 S DOMAIN, VIRION SHELL.
236 P DOMAIN, PROJECTING.
25149 MW: 647462A9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 1; Length 112; Pred. No. 3.28e+00;
                                                                                                                                                                                                                                                          Length 236
                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                          Score 67; DB 1; L
Pred. No. 2.25e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AA; 12830 MW; 5B4A3D25 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
RNA POLYMERASE-ASSOCIATED PROTEIN GP33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 AA.
                                                                                                                                                                                                                                                                                                            4; Mismatches
EMBL; X14736; G60533; -.
PIR; JQ0061; JQ0061.
PROSITE: PS00555; ICOSAH_VIR_COAT_S; 1.
PRAM: PF00729; V1ral_coat; 1.
COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 IEKMVEEFGMSYLEATTAFLEE-NSI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HERFMAEFGGGYVQ--TPFLSESNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQC
01-FEB-1995 (REL. 31, LAST ANNC
                                                                                                                                                                                                                                                                                                                                                               111 ETFTADTTSGYISMAFLSD 129
                                                                                                                                                                                                                                                                                                                                                                                                               2 EKFMAEFGGGYVQTPFLSE 20
                                                                                                                                                                                                                                                          Query Match 38.1%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.5%;
Best Local Similarity 46.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X15818; G15213; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                             51
217
236
                                                                                                                             1
52 2
218 2
236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAHN S., RUEGER W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89386003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BK536;
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508 AA; 57190 MW; 98DDC6AA CRC32;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
4-HYDROXYPHENYLPYRUVATE DIOXYCENASE (EC 1.13.11.27) (4HPPD) (HPD).
PSEUDOMONAS SP. (STRAIN P.J. 874).
                                                                                                                                                                                                                                                                                                                                        MEDLINE: 92241278.
MEDLINE: 922412778.
MEDLINE: 92241671278.
MEDLINE: 922416712.
MEDLINE: 922412712.
MEDLINE: 922
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 1; Le
Pred. No. 3.28e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AA; 40060 MW; AACF4F88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SNOTATION UPDATE)
HYPOTHETICAL PROTEIN HII500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: IRON.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE 4HPPD FAMILY.
PIR: S21209; S21209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OXIDOREDUCTASE; DIOXYGENASE; IRON.
DOMAIN 167 196 TYR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 IEEFLMQFNGEGIQHVAFLSD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 37.5%;
Local Similarity 38.1%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32826; G1574341; -
                                                                                                                                                                                                                                                             SACTERIA; PROTEOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    influenzae Rd.
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P44224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
CYTOCHROME P450 72A1 (EC 1.14.14.1) (CYPLXXII) (PROBABLE GERANIOL-10-
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

ROBERTS D., ALLEN E., ARAUJO R., APARICIO A., CHUNG E., DAVIS K.,
RODCAN M., FEDERSPIEL N., HYMAN R., KALMAN S., KOPP C., KURDI O.,
LEW H., LIN D., NAMATH A., OEFNER P., SCHRAMM S., DAVIS R.W.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-- SIMILARITY: BELONGS TO THE YECE/YHDA/YHJK/YJCC FAMILY.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 9742611.
BLATTER F.R., FLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                              ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANDTAILON UPDATE)
HYPOTHETICAL 58.9 KD PROTEIN IN TESB-HHA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66; DB 1; Length 518;
Pred. No. 3.28e+00;
6; Mismatches 7; Indels
Score 66; DB 1; Length 508;
Pred. No. 3.28e+00;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
80D18559 CRC32;
                                                                                                                                                                  518 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECOGENE; EG14237; YLAB.
PFAM; PF00563; DUF2; 1.
HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                  PRT;
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58932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000152; G1786662; -.
EMBL; U82664; G1773140; -.
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31.6%;
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Query Match 37.5%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                411 MPKYKALYESGYIQIP 426
                                                                                               1 MEKFMAEFGOGYVOTP 16
                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                              ESCHERICHIA.
                                                                                                                                                 LT 10
YLAB_ECOLI
P77473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 11
CP72_CATRO
Q05047;
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SEQUENCE
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
STREPTOCOCCUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L08611; G153725; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                MEDLINE; 93240534.
PUYET A., ESPINOSA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
159
217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
241
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                  SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
01-NOV-1997
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                           VETTER H.-P., MANGOLD U., SCHROEDER G., MARNER F.-J.,
WERCK-REICHHART D., SCHROEDER J.;
"Molecular analysis and heterologous expression of an inducible
cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
PLANT PHYSIOL. 100:998-1007(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                 CYP72AI OR CYP72 OR P450CR3.
CYP72AI OR CYP72 OR PERTAINKLE) (MADAGASCAR PERIMINKLE).
CATHARANTHUS ROSEUS (ROSY PERTAINKLE) (MADAGASCAR PERIMINKLE).
EURARVOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
EUPHYLLOPHYTES: SPERWATOPHYTA; MAGNOLIOPHYTA;
ASTERIDAE: GENTIANANAE: GENTIANALES: APOCYNACEAE; CATHARANTHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                      "ISOLATION of Cytochrome P-450 CDNA clones from the higher plant Catharanthus roseus by a PCR strategy.";
PLANT MOL. BIOL. 22:379-3811993).
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. MAY BE A GERANIOL-10-HYDROXYLASE.
-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) - ROH + OXIDIZED FLAVOPROTEIN + H(2)0.
-!- PATHWAY: INDOLE ALKALOID SYNTHESIS.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00067; p450; 1.
OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
MALTODEXTRIN TRANSPORT SYSTEM PERMEASE PROTEIN MALD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                    SOUER E., VERPOORTE R., HOGE J.H.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FC0286BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1775; G395302; -.
PS00086; CYTOCHROME_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 469-524 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60557 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L10081; G167484; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
HYDROXYLASE) (GE10H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 AA;
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Best Local Similarity
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 93283641
                                                                                                                                                                                         STRAIN-LINE CP3A;
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470
190
194
1223
312
318
403
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MEIJER A.H.,
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Q04699;
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     STRAINED / KW20.
MEDINE; 95350630.
PLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCATNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
WITZERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
Structure of the maltodextrin-uptake locus of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 4.76e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8510E35C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REL. 32, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
PFAM; PF00528; BPD_transp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPORT; SUGAR TRANSPORT; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN HI1435
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DDFA3B80 CRC32;

420 AA; 45087 MW;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                                                                                            -i- SIMILARITY: BELONGS TO THE RLU FAMILY OF PSEUDOURIDINE SYNTHASES. STRONG. TO E.COLI YOCB.
-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS INTRODUCED IN POSITION 160 TO EXTEND THIS ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: CYTOPLASMIC.
-:- IN T. BRUCEL, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
-:- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88286728.
LE BLANCQ S.M., SWINKELS B.W., GIBSON W.C., BORST P.;
"Evidence for gene conversion between the phosphoglycerate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-REB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE_KINASE, CYTOSOLIC (B) (EC 2.7.2.3) (ALLELE 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes of Trypanosoma brucei.";
J. Mol. BIOL. 200:439-447(1988).
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP + 3-PHOSPHO-D-GLYCERATE - ADP + 1-PATHWAX: SECOND SIEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- PATHWAX: SCOOLD SIEP IN THE SECOND PHASE OF GLYCOLYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 1; Length 239;
Pred. No. 6.88e+00;
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94C9014D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 AA.
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PROSITE: PSO0111; PCLYCERATE_KINASE; 1.
PFAM: PF00162; PGK; 1.
HSSP; P07378; 13PK;
                                                                              UNPUBLISHED OBSERVATIONS (SEP-1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                 EMBL; U32822; G1574274; ALT_FRAME.
TIGR; H11435; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 AA; 27773 MW;
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01129; PSI_RLU; 1. PFAM; PF00849; YABO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 IANLMCEQFEQKYVQKSYLA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEKFM-AEFGOGYVOTPFLS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7: Conservative 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPANOSOMA BRUCEI BRUCEI.
SCIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X05890; G10494; -.
                                       CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGKE_TRYBB
P08893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 86136022.
OSINGA K.A., SWITKELS B.W., GIBSON W.C., BORST P., VEENEMAN G.H.,
VAN BOOM J.H., MICHELS P.A., OPPERDOES F.R.;
"Topogenesis of microbody enzymes: a sequence comparison of the genes
for the glycosomal (microbody) and cytosolic phosphoglycerate kinases
of Trypanosoma brucei.";
EMBO J. 4:3811-3817(1995).
                                                                                                                                                                                                                                                                                                                            EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BERNSTEIN B.E., MICHELS P.A.M., HOL W.G.J.;
"Synergistic effects of substrate-induced conformational changes in phosphoglycerate kinase activation.";
NATURE 385:275-278(1997).
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: GLYCOSOMAL.
-1- IN T. BRUCEL, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE
ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
-1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98308020.
BERNSTEIN B.E., WILLIAMS D.M., BRESSI J.C., KUHN P., GELB M.H.,
BLACKBURN G.M., HOL W.G.;
"A bisubstrate analog induces unexpected conformational changes
phosphoglycerate kinase from Trypanosoma brucei.";
J. MoL. BIOL. 279:11137-1148 (1998).
-1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP +
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
-1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-1- SUBUNIT: MONOMER.
                  Length 420;
                                red. No. 6.88e+00;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                 01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHOGIVERATE KIMASE, GLYCOSOMAL (C) (EC 2.7.2.3).
TRYPANOSOMA BRUCEI BRUCEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 5-419
                                                                                                                                                                                                     440 AA
                 Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ALLELES 2 AND 4).
                                                                                                                                                                                                     PRT;
                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. MOL. BIOL. 200:439-447(1988).
                 36.4%;
Query Match
Best Local Similarity 35.33,
6; Conservative
                                                                                         151 MAKILASYGDVYISDAF 167
                                                                                                                         1 MEKFMAEFGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X03370; G10498; -.
EMBL; X05889; G10491; -.
EMBL; X05890; G10495; -.
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B25119; KIUTGG
S02235; TVUTGB
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SEQUENCE FROM N.A.
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P07378:
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DR PDB; 13PK; 24-DEC-97.

DR PDB; 16PK; 25-NOV-98.

DR PRB; 16PK; 25-NOV-98.

DR PRAM; PFOOJIE; PGLYCERATE_KINASE; 1.

DR PFAM; PFOOJIE; PGLYCERATE_KINASE; 1.

KW TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; GLYCOSOME;

FT ASTRUCTURE.

TO SEQUENCE 440 AA; 47118 MW; 4A1F7393 CRC32;

QUEFY MACCH

BEST LOCAL Similarity 35.3%; Pred. No. 6.88e+00;

MATCHAS 6; Conservative 6; Mismatches 5; Indels 0; Gaps

DD 151 MAKILASYGDVYISDAF 167

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QY 1 MEKFMAEFGGGYVQTPF 17

Search completed; Wed Sep 1 16:05:11 1999

Job time: 11 secs.
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· 一个,我们也是一个,我们也有一个,我们的人,我们的人,我们们的人,我们们的人,我们的人,我们的人,我们的人,我们		<b>在在在在我们的现在分词在我们的现在分词的现在分词的现在分词的现在分词的现在分词的现在分词的现在分词的现在分词</b>
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:05:29 1999; MasPar time 5.87 Seconds 223.019 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-24) from PCTUS9913024.pep (2 of 12) 176 1 MEKFWAEFGGGYVQTPFLSESNSV 24

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 29.931; Variance 49.849; scale 0.600 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	1.28e-01	2.75e-01	4.03e-01	5.87e-01	2.58e+00	3.70e+00	3.70e+00	3.70e+00	3.70e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	7.55e+00	1.07e+01	1.07e+01
		Description	860AA LONG HYPOTHETICA	MANNOSE-1-PHOSPHATE GU	HYPOTHETICAL 19.4 KD P	F13P17.19 PROTEIN.	KIAA0287 (PEG3) (FRAGM	LECITHINASE.	LECITHINASE.	PATERNALLY EXPRESSED P	ZINC FINGER PROTEIN.	FROM BASES 311709 TO 3	PYRROLIDONE CARBOXYL P	REGION 1 GENE PRODUCT	COSMID ZK1248.	336AA LONG HYPOTHETICA	CYTOCHROME P450 (EC 1.	HYPOTHETICAL 99.5 KD P	RNA POLYMERASE II SUBU	ZK1067.2 PROTEIN.	RIBA PROTEIN.	PERIPLASMIC ALPHA-AMYL
SUMMARIES		ΙD	059003	074624	060074	080784	P78418	056631	087325	061138	054978	P75688	087765	047402	023414	058468	042701	962290	042877	Q23388	024752	060102
		DB	П	٣	٣	10	4	~	7	1	11	7	7	7	'n	-	10	7	10	ß	~	7
		Match Length DB	860	364	178	2301	1132	418	470	1378	1571	70	215	296	334	336	516	853	1191	2219	423	526
đ	Query	Match	43.8	42.6	42.0	41.5	39.2	38.6	38.6	38.6	•	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	36.9	36.9
		Score	77	75	74	73	69	68	99	68	68	99	99	99	99	99	99	99	99	99	65	65
	Result	No.	1	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20

1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 1.52e+01 2.14e+01 2.14e+01 2.14e+01 2.14e+01 2.14e+01 2.14e+01 3.01e+01 3.01e+01 4.2e+01		occus.	SAI Y., JKU Y., OGUCHI A., SHIZUYA H.,	Gaps 0;	
HYPOTHETICAL 64.6 KD P BHYPOTHETICAL 32.9 KD P SMILAR TO FAMILY 1 OF MAJOR OUTER MEMBRANE P PHOSPHOGLYCERATE KINAS PHOSPHOGLYCERATE KINAS PHOSPHOGLYCERATE KINAS PHOSPHOGLYCERATE KINAS CYTOCHROWE P450 (EC 1. HYPOTHETICAL 65.2 KD P CELLODEXTRIN PHOSPHORY DNA FOR EARLY RECION 1 175A LONG HYPOTHETICA HYPOTHETICAL 30.9 KD P ACYLTRANSFERASE. PE-FAMILY PROTEIN. CKROMOSOME XV READING ORF16. HYPOTHETICAL 115.5 KD DNA FOR SEROTYPE B CAP STABLE PROTEASE PRECUR FUCULOSE 1-PHOSPHATE A MEMBRANE SPANNING PROT BUTULINUM NEUROTOXIN T NEUROTOXIN COMPLEX M N NPH-II, HELICASE.	860 AA.	NCE ATI	HAIKAWA Y., HINO Y H., HOSOYAWA A., NAW T. TAKANIYA M., OHF AKI J., KUSHIDA N., HI K., MASUCHI Y., Of the Genome of a coccus horikoshii Of	DB 1; 1.28e- itches	'; 364 AA. ED) SEQUENCE UPDATE) ANNOTATION UPDATE) FERRASE (EC 2.7.7.13),
2 069736 2 067454 5 067454 8 0377445 9 0377445 0 042700 2 033086 2 024780 2 024780 2 066991 2 066991 3 06991 3 06991 3 04234 3 04234 2 058887 2 045844 4 057457 4 057457 4 057457 6 057457 7 057457 8 045844 6 057457 7 057457 8 045844 8 057457 8 045844 9 057457 9 057457 9 057457 9 057457	ALIGNMENTS PRT; 8	D) EQU NNO	M., HORIKAWA H., BABA S., KOSUGIJ A R., NAKAZAWA H KUDOH Y., YAWAZ, BB T.F., HORIKOS; ene Organization ebacterium, Pyron ; ""	d.	PRT CREAT LAST LAST LTRANS
36.9 36.4 36.4 36.4 36.4 36.4 36.4 36.4 36.4 420 36.4 420 36.4 420 36.4 420 36.4 420 370 370 370 370 370 370 370 37	PRELIMINARY;	059003; 01-AGG-1998 (TREMBLREL. 01-AGG-1998 (TREMBLREL. 01-JAN-1999 (TREMBLREL. 860AA LONG HYPOTHETICAL PHI302. PYRCOCCUS HORIKOSHII. ARCHAEA; EURYARCHAEDOTA;	SEQUENCE FROM N.A. STRAIN-OT3; MEDLINE; 98344137. KAWARABAYASI Y., SAWADA M., HOR YAMAMOTO S., SEKINE M., BABA S. SAKAI M., OGURA K., OTUKA R., N FUNAHASHI T., TANAKA T., KUDOH AOKI K., NAKAWURA Y., ROBB T.F. KIKUCHI H.; RAKAWURA Y., ROBB T.F. "Complete Sequence and Gene Org Hyper-thermophilic Archaebacter DNA RES. 5:55-76(1998). SEMBL; APDO00065, D1031349; SEOURNCE 860 AA: 95455 MM:	43.8 cal Similarity 29.4 5; Conservativ MSKFLTDFSNAFIRVAF 1       ::: : ::: :  MEKFMAEFGGGVVQTPF 1	PRELIMINARY; (TREMBLREL. (TREMBLREL. (TREMBLREL. OSPHATE GUAN.
4444 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	LT 1 059003	059003; 01-AUG-1998 01-AUG-1998 01-JAN-1999 800A LONG 1 PH1302. PYROCOCCUS 1 ARCHAEA; EUJ	[1] SEQUENCE FRO SEGUENCE FRO SERIN-OT3; MEDLINE; 983 KAWARABAYASI KAWARABAYASI KAWARABAYASI SARAI M., OG FUNAHASHI T. FUN	Query Match Best Local Sim: Matches 5; 1 MSKFLTI	2 74624 74624; 1-NOV-1998 1-NOV-1998 1-NOV-1998 ANNOSE-1-P PGI.
	ľΛ		80 9 2 2 4 4 4 4 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Que Bes Mat Db Db	RESULT ID O AC O DT O DT O DT O CN M

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EUKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                            STRAIN-RUT C-30;
MEDLINE; 98309839.
RRUSZEWSKA J.S., SALOHEIMO M., PENTTILA M., PALAMARCZYK G.;
RRUSZEWSKA J.S., SALOHEIMO EN., PENTTILA M., PALAMARCZYK G.;
"ISOJation of a Trichoderma reesei cDNA encoding GTP:
alfa-d-mannose-1-phosphate guanyltransferase involved in early steps
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
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STRAIN-972H-:
STRAIN-972H-:
CHURCHER M. WOOD V., RAJANDREAM M.A., BARRELL B.G., BADCOCK K.,
CHURCHER C.M.:
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AL025600; E1287787; -.
HYPOTHPTICAL PROFIEN.
SEQUENCE 178 AA: 19432 MW; F002D830 CRG32;
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
HYPOCREALES; HYPOCREACEAE; HYPOCREA.
                                                                                                                                                                    Score 75; DB 3; Length 364;
Pred. No. 2.75e-01;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 3; Length 178;
Pred. No. 4.03e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
HYPOTHETICAL 19.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                 SPBC13G1.12.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA: ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                   of protein glycosylation.";

CURR. GENET. 33.445-450(1998).

EMBL: U89991. 63323397; -.

SEQUENCE. 364 AA: 40284 MW; 9504573B CRC32;
                                                                                                                                                                                                                                                                                    178 AA
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                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                               1 MEKFMAEFGOGY-VOTPFLSESNSV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 MDKFEAQFDDVNVQTGYMNKA 113
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08,
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Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                    42.6%;
Local Similarity 40.0%;
les 10; Conservative
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01-NOV-1998 (TREMBLREL. 08
01-NOV-1998 (TREMBLREL. 08
01-NOV-1998 (TREMBLREL. 08
F13P17.19 PROTEIN.
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                   SEQUENCE FROM N.A.
                                                                                                                                                                      Query Match
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060074
060074;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAAO287 (PEG3) (FRAGENT).
KIAAO287 OR PEG3.
HOMO SAPIENS (HUMAN).
EUKRYCOR, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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"Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC004481; G3337366; -- SEQUENCE 2301 AA: 253398 WW: FB931E6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO
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                                                                                                                Length 2301;
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Pred. No. 2.58e+00;
6; Mismatches 2; Indels
                                                                                                              Score 73; DB 10; Length 230
Pred. No. 5.87e-01;
3; Mismatches 5; Indels
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STRAIN-E7946 EL TOR;
FIORE A.E., KAPER J.B.;
SUBMITED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U50074; G1236642; -.
PFAM; PF00657; Lipase_GDSL; 1.
SEQUENCE 418 AA; 47600 MW; 408D6983 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
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LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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KIM J., ASHWORTH L., BRANSCOMB E., STUBBS L.;
GENOME RES. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                              PRT; 1132 AA
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EMBL; U90336; G1899244; --
PFAM; PF00096; zf-C2H2; 7.
ZINC-FINGER; METAL-BINDING; DNA-BINDING.
NON II
SEQUENCE 1132 AA; 127715 MW; FED2439;
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P78418;
01-MAY-1997 (TREMBLREL. 03, CI
01-NOV-1998 (TREMBLREL. 08, LA
01-NOV-1998 (TREMBLREL. 08, LA
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01,
08,
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                Query Match 41.5%;
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                                                                                                                                          977 NFLGRFGAGYVSDTFL 992
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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7 EFGQGYVQTPFLSES 21
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PRELIMINARY;
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Best Local Similarity
Matches 8; Conser
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O54978;
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EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                               VIBRIO MIMICUS.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
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Z STRINGS 129; TISSUE-LIMB BUD;

MEDLINE; 96400442.

A RELAIX F., WENG X., MARAZZI G., YANG E., COPELAND N., JENKINS N.,

A SPENCE S.E., SASSOON D.;

T neuronal lineages.";

I DEV, BIOL. 177:383.396(1996).

R EMBL; U48804; G1197857;

R MGD; MGI.104748; PEGJ.

R PROSITE; PSO0028; ZINC_FINGER_CZH2; 11.

R PROSITE; PS00028; ZINC_FINGER_CZH2; 11.

R PROSITE; METAL-BINDING; DNA-BINDING.

SEQUENCE 1378 AA; 156916 MW; 756F3644 CRC32;
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                                                                                                                                                                                                          KONG I.S.;
"Cloning and identification of a phospholipase gene from Vibrio mimicus.";
BIOCHINS.";
EMBL. AF03162; G3746409; -.
PROSITE; PS01098; LIPASE_GDSL_SER; 1.
SEQUENCE 470 AA; 53194 MW; LEFLE5A5 CRC32;
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Pred. No. 3.70e+00;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                            38.6%; Score 68; DB 2; Length 470; 33.3%; Pred. No. 3.70e+00; ative 9; Mismatches 5; Indels
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061138 PRELIMINARY; PRT; 1378 AA.
061138; 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PATERNALLY EXPRESSED PROTEIN 3 (ZN-FINGER PROTEIN PM1).
                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                       229 FLGHFSNGFVWTEYLAQGLNV 249
           177 FLGHFSNGFVWTEYLAQGLNV 197
                       4 FMAEFGOGYVQTPFLSESNSV 24
                                                                                                                                                                                                                                                                                                                                                            4 FMAEFGOGYVOTPFLSESNSV 24
                                                                                            08,
08,
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Matches 7; Conservative
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Similarity 40.0%;
6; Conservative
                                                             ULT 7 PRELIMINARY; 087325 087325; 01-00-1998 (TREMBLREL. 01 01-NOV-1998 (TREMBLREL. 01 01-NOV-1998 (TREMBLREL. 0)
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7 EFGQGYVQTPFLSES 21
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                                                                                                                                                                                                  MEDLINE; 98440110
                                                                                                                            LECITHINASE
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                                                                                                                                                          MUS MUSCULUS (MOUSE).
EURARYOTA, METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                               KUROIWA Y., KANEKO-ISHINO T., KAGITANI F., KOHDA T., LI L.L., TADA M., SUZUKI R., YOKOYAMA M., SHIROISHI T., WAKANA S., BARTON S.C., ISHINO F., SURANI M.A.; "Peg3 imprinted gene on proximal chromosome 7 encodes for a zinc finger protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K-12;
MEDLINE; 97426617.
MEDLINE; 97426617.
BLATTHER F.R., PLUNKETI III G., BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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P7568
P7568
P7568
P7568
P7568
01-F2B-1997 (TREMBLREL. 02, CREATED)
01-F2B-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FROM BASES 311709 TO 323910
ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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Pred. No. 3.70e+00;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
EMBL; AECO0137; G1786500; -
SEQUENCE 70 AA: 7854 MW; B754D938 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 2; Length /u;
Pred. No. 7.55e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SURANI A.M.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BROSITE; PSO0028; ZINC_FINGER_C2H2; 11.
ZINC-FINGER; METAL-BINDING; DNA-BINDING.
SEQUENCE 1571 AA; 178824 MW; 6F2820E6 CRC32;
                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )137; G1786500; -.
70 AA; 7854 MW; B754D938 CRC32;
PRT; 1571 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AA.
                                                CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                  NAT. GENET. 12:186-190(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.5%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1295 EYGPSYTHASFLTEP 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                           01-JUN-1998 (TREMBLREL. 01-JUN-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| :| ::||:|:
7 EFGQGYVQTPFLSES 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 QVYVQTSYLSQQSSI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 QGYVQTPFLSESNSV 24
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ID 087765
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CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-OT3;
MEDLINE; 98344137.
                                                                                 SEQUENCE FROM N.A.
                                                                                                 STRAIN-BRISTOL N2 MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATERSTON R.;
SUBMITTED (JU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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058468
058468;
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    ID DATA BERNA BERN
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                                                                                                                                                          LACTOCOCCUS LACTIS SUBSP. CREMORIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
LACTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                         J. BACTERIOL. 180:4834-4842(1998).
-!- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O - ACYLAMINO
                                                                                                                                                                                                                                                                            DAVERAN-MINGOT M.L., CAMPO N., RITZENTHALER P., LE BOURGEOIS P.; "A natural large chromosomal inversion in Lactococcus lactis is mediated by homologous recombination between two insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
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                  01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
101-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PYRROLIDONE CARBOXYL PEPTIDASE (EC 3.4.19.1)
PARROLIDONE CAPETIDASE) (ACYLAMINOACYL-PEPTIDASE) (ACYLAMINOACYL-PEPTIDASE)
(N-ACYLPEPTIDE HYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEENBERGEN S.M., WRONA T.J., VIMR E.R.;
"Functional analysis of the sialyltransferase complexes Escherichia coli K1 and K92.";
J. BACTERIOL. 174:1099-1108(1992).
EMBL: M76370; G146950; -.
NON_TER 1 1 1 SEQUENCE 296 AA; 35733 MW; E10BA47B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
REGION 1 GENE PRODUCT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 2; LA Pred. No. 7.55e+00;
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Pred. No. 7.55e+00;
9; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA; 23519 MW; 004FCDDF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RFLA-FEEGYLRPQFITVEEDGV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KFMAEFGQGYVQTPFLS-ESNSV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 DKMFPDIKAGFMHIPFLPE 171
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01,
08,
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Local Similarity 31.6%;
les 6; Conservative
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Local Similarity 34.8%;
les 8; Conservative
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EMBL; AJ223960; E1323722;
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Q23414;
Q13414;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
Q1-NOV-1998 (TREMBLREL. 0
COSMID ZK1248.
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 98406035.
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047402
047402;
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MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
BIGHTNING J., LLOYD C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULGSTON J.,
THIERRY-MIEG J., THOMAS K., VADUGHAN R., WOHLDMAN P.,
WATSON A., WEINSTOK L., WILKINSON-SPROAT J., WOHLDMAN P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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YAMAMOTOS., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
SARAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHABHI T., TANKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI P.
AOKI K., NAKAWURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA I
KIKUCHI H., "Complete Sequence and Gene Organization of the Genome of a
Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3.";
DNA RES. 5:55-76 (1998).
ENBL: APO00003; D1030771; -.
SEQUENCE 336 AA; 37579 MM; 62430DEB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 7.55e+00;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U29244; G862494; -.
SEQUENCE 334 Aa; 38293 MW; 9ACC97C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LATREILLE P.;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
336AA LONG HYPOTHETICAL PROTEIN
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1 MEKFMAEFGOGYVOT-PFLSESN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 IKKFKEAWGNDYHQTLTFLKDSD 77
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Local Similarity 39.1%;
les 9; Conservative
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Search completed: Wed Sep 1 16:05:53 1999 Job time : 24 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:09:02 1999; MasPar time 3.86 Seconds 93.552 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-17) from PCTUS9913024.pep (3 of 12) 138 1 MEKFMAEFGGGYVQTPF 17 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq35 Database:

Mean 20.181; Variance 71.670; scale 0.282 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

4.48e+01	8.42e+01	1.04e+02	1.04e+02	1.04e+02	1.04e+02	1.04e+02	1.28e+02	1.28e+02	1.28e+02	1.28e+02	1.28e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02
D-alanine racemase.	S. pneumoniae protein	Leader peptide sequen	Streptococcus pneumon	Glycerol dehydrogenas	Sequence of protease	Streptococcus pneumon	Human oxalyl-CoA deca	Oxalyl-CoA decarboxyl	Sequence of N-termina	Apolipoprotein B-100.	A. mediterranei rifam	Phage T4 ORFX gene pr	Carnitine dehydrogena	HSV-2 strain SB5 Cont	SB5
P70668	W80717	W78736	W62047	W69360	R48060	W62045	W22882	R75085	P70647	W41262	W52846	R97371	R36268	W72197	W72105
7	36	35	33	35	σ	33	23	14	7	28	30	19	œ	36	36
389	130	38	364	380	409	740	578	578	2721	4536	5069	65	321	623	1196
45.7	43.5	42.8	42.8	42.8	42.8	42.8	42.0	42.0	42.0	42.0	42.0	41.3	41.3	41.3	41.3
63	9	59	29	59	59	56	58	28	28	28	28	57	57	57	22
-	7	3	4	2	9	7	∞	σ	10	11	12	13	14	12	16
	2 P70668 D-alanine racemase. 4	2 P70668 D-alanine racemase, 436 W80717 S. pneumoniae protein 8	2 P70668 D-alanine racemase. 4 36 W80717 S. pneumoniae protein 8 35 W78736 Leader peptide sequen 1	2 P70668 D-alanine racemase. 4 M80717 S. pneumoniae protein 8 33 W78736 Leader peptide sequen 13 W62047 Streptococcus pneumon 1	2 P70668 D-alanine racemase. 36 W80717 S. pneumoniae protein 8 35 W78736 Leader peptide sequen 13 37 W62047 Streptococcus pneumon 135 W69360 Glycerol dehydrogenas 1	2 P70668 D-alanine racemase. 36 W80717 S. pneumoniae protein 8 35 W78736 Leader peptide sequen 1 33 W62047 Streptococcus pneumon 1 35 W6950 Glycerol dehydrogenas 1 9 R48060 Sequence of protease 1	45.7 389 2 P70668 D-alanine racemase. 4 3.5 130 36 M80717 S. pneumoniae protein 8 4 2.8 38 W704736 Leader peptides sequen 1 4 2.8 380 35 W62047 Streptococcus pneumon 1 4 2.8 380 35 W65360 Glycerol dehydrogenas 1 4 2.8 4 0.9 9 R48060 Sequence of protease 1 4 2.8 4 0.3 W62045 Streptococcus pneumon 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 38 W78736 Leader peptide sequen 1 42.8 380 35 W62047 Streptococcus pneumon 1 42.8 380 35 W69360 Glycerol dehydrogenas 1 42.8 409 9 R48060 Sequence of protease 1 42.9 740 33 W62045 Streptococcus pneumon 1 42.0 778 23 W22882 Human oxalyi-CoA deca 1	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 35 W78736 Leader peptide sequen 142.8 36 33 W62047 Streptococcus pneumon 42.8 409 9 R48060 Sequence of protease 142.8 740 33 W62045 Streptococcus pneumon 142.8 740 33 W62045 Human oxalyl-CoA decarboxyl 42.0 578 14 R75085 Oxalyl-CoA decarboxyl 14	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 W80717 S. pneumoniae protein 8 42.8 38 W80247 Streptococcus pneumon 1 42.8 409 9 R46960 Sequence of protease 1 42.8 40 3 W62045 Streptococcus pneumon 1 42.0 578 14 R75085 Oxalyl-CoA deca 1 42.0 578 14 R75085 Oxalyl-CoA deca 1 42.0 578 14 R75085 Oxalyl-CoA deca 1 42.0 578 12 P70647 Sequence of N-termina	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 W8735 Leader peptide sequen 1 42.8 380 35 W62047 Streptococcus pneumon 1 42.8 40.9 9 R48060 Sequence of protease 1 42.8 40.9 9 R48060 Sequence of protease 1 42.0 578 23 W22882 Human oxalyl-CoA decaloxyl 1 42.0 578 14 R75085 Oxalyl-CoA decaloxyl 1 42.0 4236 28 W41262 Apolipoprotein B-100.	45.7 389 2 P70668 D-alanine racemase. 42.8 38 W80717 S. pneumoniae protein 8 42.8 38 W80717 S. pneumoniae protein 8 42.8 380 35 W78736 Leader peptide sequen 1 42.8 380 35 W65047 Streptococcus pneumon 1 42.8 740 9 R48060 Sequence of protease 1 42.0 578 23 W22882 Human oxalyl-CoA deca 1 42.0 578 14 R75085 Sequence of N-termina 1 42.0 2721 2 P70647 Sequence of N-termina 1 42.0 578 W41262 Apolioporotein B-100 1 42.0 5059 30 W422846 A. mediterranei Irjam 1	389 2 P70668 D-alanine racemase.  130 36 W80717 S. pneumoniae protein 8 38 35 W78736 Leader peptide sequen 1 380 35 W62047 Streptococcus pneumon 1 380 35 W62045 Streptococcus pneumon 1 409 9 R48060 Sequence of protease 1 578 23 W22882 Human oxalyl-CoA deca 1 578 14 R75085 Oxalyl-CoA deca 1 2721 2 P70647 Sequence of N-termina 1 4536 28 W41262 Apolioprotein B-100. 1 565 19 R97371 Phage T4 ORFX qene pr	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 38 W78336 Leader peptide sequen 142.8 380 35 W62047 Streptococcus pneumon 142.8 409 9 R48060 Sequence of protease 142.8 400 31 W62045 Streptococcus pneumon 142.0 578 23 W22882 Human oxalyl-CoA decarboxyl 142.0 578 14 R75085 Oxalyl-CoA decarboxyl 142.0 578 14 R75085 Sequence of N-termina 142.0 569 30 W52846 A. mediterranei rifam 141.3 51 8 R836268 Carnitine dehydrogene 141.3 51 8 R836268 Carnitine dehydrogene	45.7 389 2 P70668 D-alanine racemase. 43.5 130 36 W80717 S. pneumoniae protein 8 42.8 38 35 W78736 Leader peptide sequen 142.8 380 35 W62047 Streptococcus pneumon 142.8 740 9 R48060 Sequence of protease 142.0 778 23 W22882 Human oxalyl-CoA decarboxyl 142.0 578 14 R75085 Oxalyl-CoA decarboxyl 142.0 578 14 R75085 Sequence of W-termina 142.0 578 14 R75085 Apoliopprotein B-100. 42.0 5069 30 W52846 A. mediterranel rifam 141.3 55 19 R97371 Phage T4 ORRY gene pr 141.3 523 36 W72197 HSV-2 strain SB5 Cont

Full length heat-resi 1.57e+02 DNA polymerase from s 1.57e+02 DNA polymerase. contg 1.57e+02 HID OMP PI P2 hybrid 1.92e+02 Human CDP-diacylglyc 1.92e+02 Human CDP-diacylglyc 1.92e+02 Acetyl-esterase II N- 2.36e+02 Streptococcus pneumon 2.36e+02 H. Pylori cytoplasmic 2.36e+02 DS88 Squence encoded by 0.2.36e+02 DS70 Bacillus subtilis ino 2.89e+02 Human gpspecific co 2.89e+02 Human gpspecific co 2.89e+02 Human gpspecific co 2.89e+02 Human gpspecific co 2.89e+02 Utamin D3-binding pr 2.89e+02 Nitamin D3-binding pr 2.89e+02 MITL glycosidase 29G 2.89e+02 Sequence encoded by v 2.89e+02 DNA-ligase III. S99e+02 DNA polymerase of a 2.89e+02 DNA polymerase of a 2.89e+02	ALIGNMENTS  1; 389 AA.  1y)  alanyl-D-alanine ligase.  terologous DNA in host cell - using host  ty to synthesise cell wall transformed to  English.  In a transformed cell-line defficient in  te cell will then express the required sequence erably linked to the D-alanine racemase.  y be used in the same way include those emase or D-alanyl-D-alanine ligase.  \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$	130 AA. ) unknown function.
17 57 41.3 1670 28 W41.1 18 57 41.3 1670 18 R951 20 57 41.3 1670 18 R951 20 57 41.3 1670 18 R972 21 56 40.6 43 8 R420 22 56 40.6 40.6 43 8 R420 22 55 39.9 218 39 W895 22 839.9 218 39 W895 23 839.9 218 39 W895 23 839.9 218 39 W895 23 839.9 622 8 R388 23 W673 23 24 839.1 448 8 R420 23 24 839.1 458 4 R222 8 R361 24 839.1 458 4 R222 8 R361 24 839.1 458 1 R534 44 54 39.1 1312 10 R534 45 54 39.1 1312 37 W709 27 W709	RESULT  ID P70668 standard; protein; 389 AA. AC P70668; DT 11-MAR-1991 (first entry) DE D-alanine racemase. KW L-glutamate racemase. CS Bacillus subtilis. PP 14-JAN-1987. PP 14-JAN-1987. PP 17-JUN-1986; 014702. PP 18-JUN-1986; 014702. PR WPI; 87-000482/02. DR WPI; 87-000482/02. DR WPSDB; N70668. PT Ferrari E: DR WPI; 87-000482/02. DR WPSDB; N70668. PT Cells deficient in ability to synthesi PT regain ability PC C Protein may be produced in a transform CC Protein may be produced in a transform CC Protein may be produced in a transform CC C and a second sequence operably linked CC other sequences which may be used in the coding L-glutamate racemase or D-ala SQ Sequence 389 AA;  OUBEY MATCH SIMILARILY 50.0%; Pred. No. Marches 6; Conservative 2; Misma Db 313 mdgfmveldqey 324	RESULT 2 ID W80717 standard; Protein; 130 AC W80717; DT 24-DEC-1998 (first entry) DE S. pneumoniae protein of unkno

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PCT-US99-13024-2-03.rag

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This sequence represents a Streptococcus pneumoniae protein of unknown the invention provides DNA sequences (V6201 to V6304) from the Streptococcus pneumoniae genome and corresponding protein sequences (W80605 to W80728). The protein sequences are classified as hypothetical (cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The pair fragment of any one or more of these DNA sequences. The DNA chip can be used may not any or the proteins of the protein of the proteins of the protein of the protein of the protein of the protein of the companies of these by pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively signed to the above proteins or peptide fragments can be used to treat S. pneumoniae cells.
Streptococcus pneumoniae protein; recombinant; gene expression; DNA chlp; virulence; antibody; infection; detection; treatment; hypothetical; cell wall biosynthetic, external target; minimal gene set protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and transformed yeast Claim 14; Page 10; 41pp; English.

A DNA construct has been developed encoding a polypeptide and has the formula given below, components in parentheses may be omitted:

SP-LP-(PS)-(9)-(PS)-gene (1); where SP = sequence encoding a signal peptide; LP = sequence encoding synthetic leader peptide without any wilnked glycosylation; PS = sequence encoding a protease processing site; S = sequence encoding a spacer peptide; gene = sequence encoding a polypeptide. Also described are: (1) an expression cassette (EC) comprising (1), fused to a 5'-promoter and 3'-terminator; (2) a yeast expression vector containing (1); (3) a yeast cell containing the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA construct containing synthetic leader sequence with no N-linked glycosylation - for high yield and efficient expression and secretion of proteins, e.g. insulin, in yeast, also related vectors
                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Leader peptide sequence TA75.50.
YAP3 signal peptide; synthetic leader peptide; construct; yeast; insulin; insulin-like growth factor; glucagon.
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Pred. No. 8.42e+01;
....matches 2; Indels
                                                                                                                                                                                           SR,
                                                                                                                                                           ELIL ) LILLY & CO ELI.
Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas
Mills BJ, Norris FH, Peery RB, Rockey PK, Rosteck PR,
Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ,
WPI; 98-348529/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balschmidt P, Havelund S, Kjeldsen TB, Pettersson AF;
WPI; 98-427963/36
                                                                                                                                                                                                                                                                                                                                                             genes
Claim 3; Pages 306-307; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W78736 standard; peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%;
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                                                            Streptococcus pneumoniae.
WO9826072-Al.
                                                                                                    18-JUN-1998.
09-DEC-1997; U22578.
13-DEC-1996; US-036281.
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24-JAN-1997; DK-000097.
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Best Local Similarity
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g
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Claim 11; Page 31-32; 40pp; English.

Claim 11; Page 31-32; 40pp; English.

The present sequence is the distal terminal portion of a spo/rel

C the present sequence is the distal terminal portion of a spo/rel

C for the spoT/relA family, which, in Escherichia coli, is involved in the spoT/relA family, which, in Escherichia coli, is involved in the spoT/relA family, which, in Escherichia coli, is involved in the coli is involved in the regulation of gene expression and other cellular processes. Spo/rel proteins have a homology to e.g.

S. equisimilis rel protein. Spo/rel proteins can be used: (a) in the treatment of an individual in need of spo/rel protein, by administering to the protein to the patient; (B) in the treatment of an individual lawing need to inhibit spo/rel protein, by administering an antagonist which inhibits the activity of the protein; and (c) for inducing an indunological response by inoculating the mammal with spo/rel protein, or a fragment or variant of it, adequate to produce antibody and/or in the response to protect the animal from disease. Conditions
as in (2); (4) DNA encoding a synthetic preproleader sequence that lacks the consensus N-linked glycosylation site NAT/S (x = ny codable anino acid other than P); and (5) the preproleader sequence. Expression vectors of (2) are used to produce (both express and secrete) polypeptides in yeast, e.g. insulin. insulin-like growth factor, glucagon or its fragments. The synthetic preproleader sequences are used to direct secretion of proteins from yeast cells. These LP provide high yield and more efficient recovery and/or purification of secreted proteins expressed in eukaryotic cells. The present sequence represents a specifically claimed leader peptide sequence of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae spo/rel distal terminal portion.
Streptococcus pneumoniae; spo/rel; spoT/relA family; screening;
antibacterial; otitis media; conjunctivitis; pneumonia; bacteraemia;
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus spoT/relA polypeptide(s) - useful in treatment of otitis media, conjunctivitis, pneumonia, bacteremia and especially
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                                                                                                                                                                                                                                                                 Score 59; DB 35; Length 38;
Pred. No. 1.04e+02;
8: Mismatches 3; Indels
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Pred. No. 1.04e+02;
4; Mismatches 4,
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W62047 standard; Protein; 364 AA.
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W69360 standard; Protein; 380 AA.
W69360;
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24-0CT-1996; US-029049.
(SMIK ) SMITHKLINE BEECHAM CORP.
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Best Local Similarity 35.3%;
Matches 6; Conservative
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Best Local Similarity 47.1%;
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1 MEKFMAEFGQGYVQTPF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
EP-849362-A2.
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N-PSDB; V37948.
                                                                                                                                                                                                                                38 AA;
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Query Match 42.8%;
Best Local Similarity 37.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure: Page 42-43: 59pp; English.

Disclosure: Page 42-43: 59pp; English.

This sequence is the E. coli glycerol dehydrogenase. The DNA can be used in a vector used in the method of the invention. The method is for the production of 1,2-propanediol (I), and comprises culturing a recombinant microorganism (A) that expresses enzymes(s) able to convert intracellular methylolyoxal (MG) to (I), in a medium convert intracellular methylolyoxal (MG) to (I), in a medium convert intracellular methylolyoxal (MG) to (I), in a medium companiety. Pharmaceuticals, confaining a sugar, other than a 6-deoxyhexose, as carbon source. (I) is used in manufacture of unsaturated polyester resins, inquid laundry detergents, pharmaceuticals, cosmetics, antiffreeze and de-icing compositions. By-products of the process (carbon dloxide, alcohols and compositions and provides production of (I) from renewable sources, without: (a) use of propylene oxide as intermediate; (b) generation of the convert waste; and (c) use of high temperature and pressure. Yields of (I) sequence 380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Kluyveromyces yeast with modified protease gene - esp. used for high yield prodn. of recombinant protein, also DNA encoding yeast protease and derived peptide(s)
Disclosure: Page 31-33; 49pp; English.

The protease gene is to be modified in order to render it (partially) incapable of producing the natural protein; or result in a nonfunctional protease or in a protease with modified proteolytic activity. The modifications can be introduced in vitro or in situ by standard genetic engineering techniques or by exposure to mutagenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Fermentative production of 1,2-propanediol from simple sugars - using recombinant microorganism that expresses enzymes that convert extracellular methylglyoxal, also new transformants and synthetic
                     Glycerol dehydrogenase.

1.2 Proparated production; intracellular methylglyoxal conversion; unsaturated polyester resin; liquid laundry detergent; antifreeze; de icing composition; animal feed; glycerol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 35; 1
Pred. No. 1.04e+02;
                                                                                                                                                                                                       /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of protease A encoded by gene PRAl. Protease; yeast; proteolysis. Kluyveromyces lactis. W09400579-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                              27-AUG-1998.
19-FEB-1998; U03271.
19-FEB-1997; US-801344.
(WISC.) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R48060 standard; Protein; 409 AA.
R48060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN 1994.
23-JUN-1993; FO0623.
25-JUN-1992; FR 007785.
(RHON ) RHONE POULENC RORER SA.
Fleer R, FOURTIER A, Yeh P;
WPI: 94-025215/03.
                                                                                                                                                                                                                                                                                                                                                           Altaras NE, Cameron DC, Shaw AJ; WPI; 98-480799/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 42.8%;
Local Similarity 37.5%;
  01-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 dkfvlgfaqstveksf 65
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                                                                                                                                                                              Misc_difference 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 AA;
                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q55348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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Elaim 11; Page 26-28; 40pp; English.

Claim 11; Page 26-28; 40pp; English.

The present sequence represents a spo/rel protein (spoT/relA family) which, consposing pneumoniae. The protein is of the spoT/relA family, which, in Escherichia coli, is involved in the stringent response to nutrient in Escherichia coli, is involved in the stringent response to nutrient considerable.

Inflation and regulate the accumulation of (p)ppGpp which is involved in the regulation of gene expression and other cellular processes.

Spo/rel proteins have a homology to e.g. S. equisimilis rel protein.

Spo/rel proteins can be used: (a) in the treatment of an individual in ceed of spo/rel protein, by administering to the protein to the patient;

(B) in the treatment of an individual having need to inhibit spo/rel protein, by administering an antagonist which inhibits the activity of inculating the mammal with spo/rel protein, or a fragment or variant of inculating the mammal with spo/rel protein, or a fragment or variant of it, adequate to produce antibody and/or T cell immune response to protect the animal from disease. Conditions which may be treated include otitis media, conjunctivitis, pneumonia, bacteraemia, meningitis, and compositions may be used as antibacterials.
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae spo/rel protein sequence.
Streptococcus pneumoniae: spo/rel; spoT/relA family; screening;
antibacterial; otitis media; conjunctivitis; pneumonia; bacteraemia;
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Streptococcus spoT/relA polypeptide(s) - useful in treatment ootitis media, conjunctivitis, pneumonia, bacteremia and especially
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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urinary stone; oxalate ion; detection; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 33; Length 740;
Pred. No. 1.04e+02;
4; Mismatches 4; Indels
Score 59; DB 9; Length. ...
Prod. No. 1.04e+02;
-hos 5; Indels
                                                                                                                                                                                                                                                                                         JT 7
W62045 standard; Protein; 740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olsen HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W22882 standard; Protein; 578 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1998.
23-CCT-1997; 308473.
24-CCT-1996; US-029049.
(SMIX ) SMITHKLINE BEECHAM CORP.
Gentry DR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human oxalyl-CoA decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO Saplens.
US5635G16-A.
03-JUN-1995; 458120.
02-JUN-1995; 458120.
(HUMA-) HUMAN GENOME SCI INC.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 emlmaqfqengyvankf 511
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                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EKFMAEFGQ-GYVQTPF 17
                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
EP-849362-A2.
                                                                                                                                                                                   2 EKFMAEFGOGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coleman TA,
                                                                                                                                                54 ekylnsfqraypqesf
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4

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      decarboxylase may be used to prevent urinary stone formation by reducing the plasma or urinary levels of the oxalate ion. It may also be used to prevent hyperoxaluria. Hyperoxaluria is characterised by either abnormal synthesis or hyper-absorption of oxalate which can be prevented by edgrading the oxalate ions. This sequence can also be used to identify other molecules with similar blological activity, and may be used as an immunogen to produce specific antibodies. The CDNA that encodes this sequence may be used in gene therapy and also for chromosome identification, e.g. fluorescent in situ hybridisation (FISH) of a cDNA clone to a metaphase chromosomal spread.
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "this region is given in fig 1, however, the mature protein is 578 amino acids in length"
                                                                                                                                                             The polynucleotide was identified in a cDNA library derived from the human pancreas. It contains an open reading frame encoding the mature protein, which is about 50-60% homologous to the oxalyl-CoA decarboxylase from the bacterium oxalobacter formigenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotide encoding oxaly1-COA decarboxylase - useful for protein prodn. for treating hyper:oxaluria Claim 5: Page 34-36; Sopp; English.
This sequence represents human oxaly1-COA decarboxylase. Oxaly1-C
                        produce enzymes, which can be used to prevent urinary stone produce enzymes, which can be used to prevent urinary stone formation or treat or prevent hyperoxaluria claim 1: Columns 17-22: 20pp; English.

The present sequence is human oxaly1-CoA decarboxylase, which can be used to prevent or treat hyperoxaluria or urinary stone formation by reducing the plasma or urinary levels of oxalate ion. The enzyme or the polymucleotide encoding it can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                            Length 578;
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Pred. No. 1.28e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                         Score 58; DB 23; I
Pred. No. 1.28e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxaly1-CoA decarboxylase.
Oxaly-CoA decarboxylase; hyperoxaluria;
fluorescent in situ hybridisation; FISH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
Adams MD, Coleman TA, Olsen H;
MPI: 95-207157/27.
                                                                                                                                                                                                                                                                                                                                                                                                T
R75085 standard; Protein; 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.0%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                         Query Match 42.0%;
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                      eqvmtafggkgyfvgtp 535
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 eqvmtafggkgyfvgtp 535
                                                                                                                                                                                                                                                                                                                                                  2 EKFMAEFG-QGY-VQTP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-1994; 003789.
30-MAY-1994; ZA-003789.
                                                                                                                                                                                                                              578 AA;
97-309885/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               090522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZA9403789-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams MD,
                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                R75085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
                                                                                                                                                                                                                                                                                                                      519
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P70647 standard; protein; 2721 AA.

RESULT

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The period fragments of apo:lipo:protein B-100 with anticoagulant activity - used for treating or preventing coagulation, inhibiting activity - used for treating or preventing coagulation, inhibiting and objects.

The adjogenesis, cell differentiation and apoptosis

Disclosure; Page 42-47; 60pp; English.

Disclosure; Page 42-47; 60pp; English.

This sequence represents the human apoliporptoein B-100 (apoB-100).

Tragments of this sequence can be used in the peptide of the invention, which has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100).

Tragments of apolipoprotein B-100 (apoB-100).

Tragments of apolipoprotein B-100 (apoB-100).

The N terminus of the peptide, or 1-47 amino acids (aa);

The Campositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, surgery or in cases of heart attack, stroke etc.) and to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form lipo-peptide complex
Claim 50; pp73-85; 123pp; English.
ApoB is a lipid-binding peptide adapted to bind to phospholipids at
one or more amphipatic alpha-helical peptide regions. ApoB gene is
pref. expressed in Chinese hamster ovary (CHO) cells and the gene is
introduced in an expression vector having a regulatable promoter
derived from the human metallothionein II gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                              04-0CT-1985; US-78418.
04-DEC-1985; US-804692.
27-FBB-1986; US-804692.
27-FBB-1986; US-804302.
PROTECH AA, Vigne JL, Mallory JB, Talmadge KD;
WPI; 87-108703/15.
PURIFIED 11014-binding peptide prodn. - by expression of recombinant system and adding lipid to obtd. peptide mixt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.0%; Score 58; DB 2; Length 2721; 23.5%; Pred. No. 1.28e+02; ative 7; Mismatches 5; Indels
17-APR-1991 (first entry)
Sequence of N-terminal apolipoprotein B (apoB).
Libid-binding peptide; apolipoprotein purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
Bruckdorfer KR, Ettelaie C;
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 11
W41262 standard; peptide; 4536 AA.
                                                                                                                                                                                                          87..167
/label= Signal
168..8247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2174 lqtymiqfdq-yikdsy 2189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKFMAEFGOGYVOTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1997; G01255.
09-MAY-1996; GB-009702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2721 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 98-008798/01.
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                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1986;
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                                                                                                                                                                                                                                                                                                                                     WO8702062-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Wrycolatopsis mediterranei rifamycin synthesis gene cluster - used

To produce rifamycin and rifamycin analogues

Claim 6; Page 126-151; 205pp; English.

To produce rifamycin and rifamycin analogues

Claim 6; Page 126-151; 205pp; English.

The present sequence represents a Amycolatopsis mediterranei rifamycin

Synthesis gene cluster ORF B protein from the present invention. The

DNA fragment comprises a DNA region involved directly or indirectly

in the gene cluster responsible for rifamycin synthesis, including

their function in connection with rifamycin biosynthesis, qualify

a constituents of this rifamycin gene cluster, and functional

fragments, derivatives or constituents of these. The Amycolatopsis

mediterranei rifamycin synthesis gene cluster DNA fragment can be used

for producing rifamycin, rifamycin analogues or precursors. It can also

be used for inactivating or modifying genes involved in ansamycin or

rifamycin biosynthesis. The DNA can be used for constructing mutant

critinomycetes strains from which the natural rifamycin or ansamycin

biosynthesis gene cluster has been partly or completely deleted. The

DNA fragment can be used for assembling a library of polyketide

crimonomycetes, which can be used for assembling a library of polyketides

synthases, which can be belosynthesis of ansamycins.
angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits activation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much smaller than apoB-100, they act more quickly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-1998 (first entry)
A. mediterranei rifamycin synthesis gene cluster fragment protein Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster; polyketide synthase; actinomycete; ansamycin.
Amycolatopsis mediterranei.
W09807868-A1.
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07-JAN-1997 (first entry)
Phage T4 ORFX gene product. gp34.
Phage T4; tail fibre protein; nanotechnology; nano-structure;
filter; molecular sleve.
                                                                                                                                                                                                          Score 58; DB 28; Length 4536;
Pred. No. 1.28e+02;
7; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 30; Length 5069
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1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W52846 standard; Protein; 5069 AA.
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R97371 standard; Protein; 65 AA.
                                                                                                                                                                                                          42.0%; s.larity 23.5%; E.Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
Engel N, Schupp T, Toupet C;
WPI; 98-169172/15.
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70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1998.
18-AUG-1997; E04495.
20-AUG-1996; EP-810551.
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                                                                                                                                                        4536 AA;
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                                                                                                                                                                Sequence
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AC R9
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                                                                                                                     No. 120.17. (Coldberg EB)

New Proper Taylors.

New Proteins derived from T4 phage tail fibre proteins - that can self assemble into nano-structure(s), useful as filters etc, also corresponding DNA

Claim 7: Fig 7: 83pp; English.

Claim 7: Fig 7: 83pp; English.

A protein (R97371) of unspecified function is the product of open reading frame x of the tail fibre protein gene region (see also C T9083) of phage T4. This gene region also includes open reading frames for tail fibre proteins (see also P8737071) of that the proteins (see also P8737071) of quantities in maturobial cells and used as building blocks of strong, general contractions and the produced in large contractions.
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08-JUL-1991; JP-193471.
08-JUL-1991; JP-193471.
08-JUL-1991; JP-193471.
NPID ASAHI CHEM IND CO LTD.
N-PSDB; Q46585.
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N-PSDB; Q46585.
N-PSDB; Q46585.
N-PSDB; Q46585.
N-PSDB; Q46586.
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HSV-2 strain SB5 Contig ID 15 ORF#32 protein.
HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor.
Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Pred. No. 1.57e+02;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 19; Pred. No. 1.57e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alkaligenes sp. No. 981 FERM BP-2570
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W72197 standard; Protein; 623 AA.
W72197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 14
R36268 standard; Protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDHase; clinical measurement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 87.5%; 7; Conservative
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13-OCT-1995; U13023.
13-OCT-1994; US-322760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carnitine dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stable nanostructures.
                                                                                          GOLDBERG E B.
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31-OCT-1997; U20016.
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Best Local Similarity
Matches 7; Conser
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PR 09-JUN-1997: US-049018.

PA (ANIK) SMITHKLINE BEECHAM CORP.

PI Chan JY. Dabrowski-Amaral CE, Delvecchio AM, Dillon SB,

Esser KM, Leary JJ;

DR WPI: 98-28684725.

PT Herpes Simplex virus type-2 sequences - useful in, e.g. prevention

PT and treatment of infection or inducing immunological response in

PT manmal

PS Claim 10.

PS Cla
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:08:32 1999; MasPar time 3.94 Seconds 172.832 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-17) from PCTUS9913024.pep (3 of 12) 138 1 MEKFWAEFGGGYVQTPF 17

Title: Description: Perfect Score: Sequence:

Scoring table:

122810 seqs, 40068593 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Mean 28.908; Variance 46.477; scale 0.622 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	ф			SUMMAKIES		
Ouery Match Length DB	eng	ţ.	DB	QI	Description	Pred. No.
55.8 860	8	0	7	F71000	hypothetical protein	3.00e-02
47.8 5	S	φ	~	S35168	cytochrome P450 (clon	2.24e+00
47.8 508	20	œ	7	164032	hypothetical protein	2.24e+00
~	230]	_	~	T02323		3.25e+00
	27	~	7	D70428		4.70e+00
	420	_	٦	TVUTG4	phosphoglycerate kina	4.70e+00
	440	_	٦	KIUTGG		4.70e+00
	440	_	ч	TVUTGB		4.70e+00
	505		H	TVUTZB		4.70e+00
	508		-	TVUT4B	phosphoglycerate kina	4.70e+00
46.4 509	209		Н	A45593		4.70e+00
	389		-	JS0443	alanine racemase (EC	6.76e+00
45.7 417	417		٦	TVCRGC	phosphoglycerate kina	6.76e+00
45.7 455	455			TVCRGG	phosphoglycerate kina	6.76e+00
	455		7	E71569	probable acyltransfer	6.76e+00
	603			W1WL8	El protein · human pa	6.76e+00
	645		7	F70825	probable PPE protein	6.76e+00
45.7 1215	121		N	S60904	hypothetical protein	6.76e+00
44.9 191	191		~	C69054	fuculose-1-phosphate	9.71e+00
44.9 421	421		-	KIUTGC	phosphoglycerate kina	9.71e+00
44.9 858	82	~	7	S68227	ubiquitin thiolestera	9.71e+00
44.2 605	9		7	S36592	El protein - human pa	1.39e+01
43.5 205	205		7	E69327	ribonuclease HII (rnh	1.97e+01

hypothetical protein 1.97e+01 probable membrane pro 1.97e+01 hemoglobin receptor h 1.97e+01 ATP-dependent transpo 1.97e+01 hypothetical protein 2.80e+01 glycerol dehydrogenas 2.80e+01 cellulose 1,4-beta-ce 2.80e+01 chitinase (EC 3.7.1. 2.80e+01 chitinase (EC 3.7.1. 2.80e+01 chitinase (EC 3.7.1. 2.80e+01 chitinase (EC 3.7.1. 2.80e+01 chitinase (Copper 2.80e+01 glucose transport pro 2.80e+01 glucose transport pro 2.80e+01 probable cytochrome C 2.80e+01 cytochrome c biogenes 3.80e+01 cytochrome c biogenes 3.80e+01 cytochrome c biogenes 3.95e+01 EI protein - human pa 3.95e+01 EI protein - human pa 3.95e+01 EI protein - human pa 3.95e+01 apolipoprotein B-100	#type complete   protein PH1302 - Pyrococcus horikoshii     sequence_revision 14-Aug-1998 #text_change     sequence_revision 14-Aug-1998 #text_change     sequence_revision 14-Baba, S.; Kosugi, H.; A.; Nagad, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Yamamoto, M.; Ohitu, Y.; Funahashi, T.;   K.; Yamazaki, J.; Kushida, N.; Oguchi, K.; Yamanchi, Y.; Sakamura, Y.; Robb, F.T.; Oguchi, Y.; Shizuya, H.; Kikuchi, H. Oguchi, Y.; Shizuya, H.; Kikuchi, H.; Maraton ordanization of the genome of a rmophilic archaebacterium, Pyrococcus horikoshii slation not shown   slation not shown     statah of N. Organization of the genome of a rmophilic archaebacterium, Pyrococcus horikoshii slation of shown     statah of N. Organization of the genome of a rmophilic archaebacterium, Pyrococcus horikoshii slation of shown     statah of N. Organization of the genome of a rmophilic archaebacterium, Pyrococcus horikoshii slation of shown     statah of N. Organization of the genome of a rmophilic archaebacterium, Pyrococcus horikoshii     statah of N. Organization of the genome of a recession for a ence replaced by GenBank     statah of N. Organization of the geneme of the shown     statah of N. Organization     statah of N. Organization     statah of Secore 77; DB 2; Length 860;     statah of Secore 77; DB 2; Length 860;     statah of Secore 77; DB 2; Length 860;     statah of Secore 77; DB 2; Indels 0; Gaps 0;     statah of Secore 77; DB 2; Indels 0; Gaps 0;     statah of Secore 77; DB 2; Indels 0; Gaps 0;     statah of Secore 77; DB 2; Indels 0; Gaps 0;     statah of Secore 77; DB 2;	nt 3) - Madagascar periwinkle (fragment) ) us roseus #common_name Madagascar
F71175 S52816 S66876 S66876 S49637 S64050 D74934 S36481 S36481 A74111 A71862 H71862 H71862 H71862 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199 A70199	#type complete   #type complete   Pytococcus hotise   #sequence_revision   #sequence_revision   #sequence_revision   #sequence_revision   Y.; Sawada, M.   Yamamoto, N.; Sawada, M.   Yamamoto, N. Yamamoto, N	e fragme (clone (EC 1 tharanth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzHugh, W.; Fields, C.; Gocayne, J.D.; Scott, J. Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C. Science (1995) 269:466-512 Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
#accession 164032
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hypothetical protein H11500 - Haemophilus influenzae (strain
Rd KW20)
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                                                                                         #authors Meijer, A.H.; Souer, E.; Verpoorte, R.; Hoge, J.H.C.
#journal Plant Mol. Biol. (1993) 22:379-383
#title Isolation of cytochrome P-450 cDNA clones from the higher plant Catharanthus roseus by a PCR strategy.
#cross-references MUID:93283641
                                                                                                                                                                                                                                                                                                                                                                    *binding_site heme iron (Cys) (axial ligand) *status
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                13-Jan-1995 #sequence_revision 09-May-1997 #text_change
17-Mar-1999
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18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
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Pred. No. 2.24e+00;
4; Mismatches 5; Indels
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#length 56 #checksum 2986
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Les 5; Conservative
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Best Local Similarity 43.8%;
Matches 7; Conservative
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##experimental_source strain VF5
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F13P17.19  #molecular-weight 253398 #checksum 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Alyay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392.353.358
#title The complete genome of the hyperthermophilic bacterium
#cross-references WID:98196666
#accession D70428
                                                                                                                                                                                                   Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
T02323 #type complete
hypothetical protein F13P17.19 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change
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hypothetical protein ed.1477 - Aquifex aeolicus
#formal_name Aquifex aeolicus
08.May-1998 #sequence_revision 08-May-1998 #text_change
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, July 1998
Arabidopsis thaliana chromosome II BAC F13P17 genomic
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*length 273  #molecular-weight 32949  #checksum 7504
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##cross-references EMBL:AC004481; NID:93337347; PID:93337366
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Pred. No. 3.25e+00;
3; Mismatches 5; Indels
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Pred. No. 4.70e+00;
6; Mismatches 2;
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Similarity 46.7%;
7; Conservative
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Best Local Similarity 38.5%;
Matches 5; Conservative
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##cross-references GB:X03370; NID:g10496; PID:g10498

IT This is one of the three isozymes of T. brucei phosphoglycerate kinase; it is transported to glycosomes, which belong to a group of subcellular organelles called microbodies.

FICATION #superfamily phosphoglycerate kinase AIP; gluconeogenesis; glycolysis; glycosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osinga, K.A.; Swinkels, B.W.; Gibson, W.C.; Borst, P.;
Veeneman, G.H.; Van Boom, J.H.; Michels, P.A.M.; Opperdoes,
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phosphoglycerate kinase (EC 2.7.2.3), glycosomal (allele 2)
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                    #journal EMBO J. (1985) 4:3811-3817

#title Topogenesis of microbody enzymes: a sequence comparison of the genes for the glycosomal (microbody) and cytosolic phosphoglycerate kinases of Trypanosoma brucei.
                                                                                                                                                                                           *authors le Blancg, S.M.; Swinkels, B.W.; Gibson, W.C.; Borst, P. *journal J. Mol. Biol. (1988) 200:439-447
*title Evidence for gene conversion between the phosphoglycerate kinase genes of Trypanosoma brucei.
                                                                                   #formal_name Trypanosoma brucei
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
05-Sep-1997
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ATP; gluconeogenesis; glycolysis; phosphotransferase
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##cross-references EMBL:x05890; NID:g10492; PID:g10494
##note the nucleotide sequence was submitted to
Library, September 1987
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6; Mismatches 5
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larity 35.3%;
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Best Local Similarity 35.3%;
Matches 6; Conservative
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#journal J. Mol. Biol. (1988) 200:439-447
#title Evidence for gene conversion between the phosphoglycerate
#tinss genes of Trypanosoma brucei.
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#length 505  #molecular-weight 55375  #checksum 4355
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##note the nucleotide sequence was submitted to the Library, September 1987
FICATION #superfamily phosphoglycerate kinase
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##note the nucleotide sequence was submitted to
Library, September 1987
EICATION #superfamily phosphoglycerate kinase
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6; Mismatches 5;
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#journal Mol. Biochem. Parasitol. (1991) 46:1-10
#title A phosphoglycerate Kinase-like molecule localized to
glycosomal microbodies: evidence that the topogenic signal
is not at the C-terminus.
#cross-references MUID:91304507
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##note the nucleotide sequence was submitted to the EMBL Data
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#title Evidence for gene conversion between the phosphoglycerate kinase genes of Trypanosoma brucei.
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#formal_name Trypanosoma brucei
22-Apr-1993 #sequence_revision 02-Jun-1994 #text_change
22-Jan-1999
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##cross-references GB:M37784; NID:g295366; PID:g295367
##experimental_source EATRO 164
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*superfamily phosphoglycerate kinase
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Matches 6; Conservative
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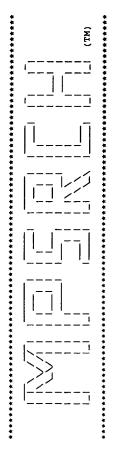
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#journal EMBO J. (1988) 7:1159-1165
#title The topogenic signal of the glycosomal (microbody)
phosphoglycerate kinase of Crithidia fasciculata resides in a carboxy-terminal extension.
#cross-references WUID:88296420
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#journal EMBO J. (1988) 7:1159-1165
#title The topogenic signal of the glycosomal (microbody)
phosphoglycerate kinase of Crithidia fasciculata resides in
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phosphoglycerate kinase (EC 2.7.2.3), glycosomal - Crithidia
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                                                                                                                                                                                                                                                                                                                                        TVCRGC #type complete
phosphoglycerate kinase (EC 2.7.2.3), cytosolic - Crithidia
*superfamily alanine racemase
cell wall synthesis; isomerase; phosphoprotein; pyridoxal
phosphate
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#formal_name Crithidia fasciculata
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
05-Sep-1997
                                                                      #binding_site pyridoxal phosphate (Lys). (covalent)
#status predicted
#length 389 #molecular-weight 43327 #checksum 9391
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ATP; gluconeogenesis; glycolysis; phosphotransferase
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#length 417 #molecular-weight 44602 #checksum 3677
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E/1569 #type complete
probable acyltransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
#formal_name Chlamydia trachomatis
13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
21.Nov-1998
##cross-references EMBL:X07459; NID:g6984; PID:g6985
##note the authors translated the codon GAC for residue 173 as
##note Thr, CAA for residue 292 as Lys, and GGC for residue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marath R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, F.L.; Zhao, O.; Koonin, E.V.; Davis, R.W. Science (1998) 282:754-759 Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.

#cross-references WIID:99000809
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 1 16:07:26 1999; MasPar time 2.71 Seconds 177.194 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-17) from PCTUS9913024.pep (3 of 12) 138 1 MEKFMAEFGGGYVQTPF 17 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 29.668; Variance 42.415; scale 0.699 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred No.		7.70e-01	7.70e-01	1.73e+00	1.73e+00	1.73e+00	1.73e+00	2.59e+00	2.59e+00	2.59e+00	2.59e+00	3.84e+00	3.84e+00	3.84e+00	3.84e+00	3.84e+00	3.84e+00	5.67e+00	5.67e+00	8.34e+00	8.34e+00	1.22e+01	1.22e+01	1,226+01
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### ALIGNMENTS

						BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;							MCKENNEI K., SUTTING G., FITZHOGH W., FIELDS C.A., GOCAYNE J.D.,	SCOLI J.D., SHINDER K., HU D. T., GLODEN A., KELLEY J.M., WEIDMAN J. F. DHILLIDG A. CODICG W HENDROLM F. COMMAN.	DEK D.M. BRANDON R.C.	FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.	GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,		Whole-genome random sequencing and assembly of Haemophilus		SCLENCE	oduced through a collaboration	between the Swiss Institute of Bioinformatics and the EMBL outstation	the European Bioinformatics Institute. There are no restrictions on its	by non-profit institutions as long as its content is in no way	Usage by and for commercial	regarres a trocuse agreement (see nuch://www.isb-sib.cn/announce/ in email to license@ish-sib ob:				2;	Tong+ 1, 508.	01:	4; Mismatches 5; Indels 0; Gaps 0;
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-DEC-1999 (REL. 37, LAST ANNOTATION UPDATE)
CYTOCHROME P450 72A1 (EC 1.14.14.1) (CYPLXXII) (PROBABLE GERANIOL-10-YTOCHROME P450 72A1 (EC 1.14.14.1) (CYPLXXII) (PROBABLE GERANIOL-10-CYP72A1 OR CYP72 OR P450CR3.
CYPTARANTHUS ROSEUS (ROSY PERIMINKLE) (MADAGASCAR PERIMINKLE).
EURARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; BUDPYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; GENTIANANAE; GENTIANALES; APOCYNACEAE; CATHARANTHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                        VETTER H.-P., MANGOLD U., SCHROEDER G., MARNER F.-J., WERCK-REICHHART D., SCHROEDER J.;
"MOICCLAIR analysis and heterologous expression of an inducible cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
PLANT PHYSIOL. 100:998-1007(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEIJER A.H., SOURE E., VERPOORTE R., HOGE J.H.C.;
"Isolation of cytochrome P-450 cDNA clones from the higher plant catharanthus roseus by a PCR strategy.";
PLANT MOL. BIOL. 22:379-383(1993).
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOCXYGENASES. MAY BE A GERANIOL-10-HYDROXYLASE.
-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + DATALYTIC PARTICLE PA
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OXIDOREDUCTASE: MONOOXYGENASE; ELECTRON TRANSPORT; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
HEME (BY SIMILARITY).
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5 -> D.
6 -> R.
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8 -> T.
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9 -> I.
1 -> I.
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4. FC0286BC CRC32;
                         524 AA.
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                      PRT;
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29.48;
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                         STANDARD;
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Best Local Similarity
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524 AA;
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VARIANT
                                               005047;
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MEDLINE; 86136022.
OSINGA K.A., SWINKELS B.W., GIBSON W.C., BORST P., VEENEMAN G.H.,
VAN BOOM J.H., MICHELS P.A.M., OPPERDOES F.R.;
"Topogenesis of microbody enzymes: a sequence comparison of the genes
                                                                                                                    TRYPANOSOMA BRUCEI BRUCEI.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                  -i- SUBGUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- IN T. BRUCEI, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE
ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
-i- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                   LE BLANCQ S.M., SWINKELS B.W., GIBSON W.C., BORST P.; "Evidence for gene conversion between the phosphoglycerate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE BLANCQ S.M., SWINKELS B.W., GIBSON W.C., BORST P.; "Evidence for gene conversion between the phosphoglycerate kinase
                                                              01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE KINASE, CYTOSOLIC (B) (EC 2.7.2.3) (ALLELE 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                Score 64; DB 1; Length 420;
Pred. No. 1.73e+00;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
19-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
TRYPANOSOMA BRUCEI BRUCEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSUVALLY,
PRAM; PRODIGE; PGK; 1.
PRAM; PRO1378; 13PK.
TRANSFASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY.
TRANSFASE; A20 AA; 45087 MW; DDFA3B80 CRC32;
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                 420 AA
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PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ALLELES 2 AND 4). MEDLINE; 88286728.
                 PRT;
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                                                  CREATED)
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                                                                                                                                                                                                                                      genes of Trypanosoma brucei
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Matches 6: Consolidation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                   STANDARD;
                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 88286728.
                                                                01-NOV-1988
01-FEB-1995
                                                  01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGKC_TRYBB
P07378;
                 PGKE_TRYBB
P08893;
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: the glycosomal (microbody) and cytosolic phosphoglycerate kinases Trypanosoma brucei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRYPANOSOMA BRUCEI BRUCEI.
EURARXOTA: EUGLENOZOA: KINETOPLASTIDA: TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                               Tn
                                                                                                                                                                                                                                                                                        -:- IN T. BRUCEI, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
-:- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
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LE BLANCO S.M., SWINKELS B.W., GIBSON W.C., BORST P.;
"Evidence for gene conversion between the phosphoglycerate kinase
genes of Trypanosoma Drucel.";
                                                                               BERNSTEIN B.E., MICHELS P.A.M., HOL W.G.J.;
"Synergistic effects of substrate-induced conformational changes
phosphoglycerate kinase activation.";
NATURE 386:275-278(1997).
                                                                                                                                                               BERGYEIN B.E., WILLIAMS D.M., BRESSI J.C., KUHN P., GELB M.H.,
BLACKBURN G.M., HOL W.G.;
"A bisubstrate analog induces unexpected conformational changes
phosphoglycerate kinase from Trypanosoma brucei.";
J. Mol. BIOL. 279:1137-1148(1998).
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP +
3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
-!- PATHMAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- SUBGELLULAR LOCATION: GLYCOSOMAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOSOME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64; DB 1; Length 440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE KINASE, A (EC 2.7.2.3) (ALLELE 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> D (IN ALLELE 4).
4A1F7393 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.73e+00;
                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 5-419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00111; PGLYCERATE_KINASE; 1.
                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
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SEQUENCE 440 AA; 47118 MW;
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                                  EMBO J. 4:3811-3817(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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PDB; 16PK; 25-NOV-98
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                                                                       MEDLINE; 97152496
                                                                                                                                                          MEDLINE; 98308020
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9
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PGKA_TRYBB
P08891;
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                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: NOT KNOWN.
-1- IN T. BRUCEI, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE
ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
-1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
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WEDLINE, 88286728.

WEDLINE, 88286728.

The LE BLANCO S.M., SWINKELS B.W., GIBSON W.C., BORST P.;

Evidence for gene conversion between the phosphoglycerate kinase of Trypanosoma brucei. 1

J. MOL. BIOL. 200:439-447(1988).

-I. CAPATUTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP +

3-PHOSPHO-D-GLYCEROYL PHOSPHATE.

-I. STALHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-I. SUBUNIT: MONOMER.

-I. SUBCELLULAR LOCATION: NOT KNOWN.

-I. SUBCELLULAR LOCATION: NOT KNOWN.

-I. SUBCELLULAR REGISTED CODE FOR PHOSPHOGLYCERATE KINASE

ISOZIMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PHOSPHOGINCERATE KINASE, A (EC 2.7.2.3) (ALLELE 4).
TRYPANOSOMA BRUCEI BRUCEI.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMAIIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
J. MOL. BIOL. 200:439-447(1988).
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
-!- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64; DB 1; Length 505;
Pred. No. 1.73e+00;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY. SEQUENCE 505 AA; 55376 MW; 9D2ACC09 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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PROSITE; PS00111; PCLYCERATE_KINASE; 1.
PFAM; PF00162; PGK; 1.
HSSP; P07378; 139K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.4%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 MAKILASYGDVYISDAF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKFMAEFGGGYVOTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X05889; G10489; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X05890; G10493; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00162; PGK; 1.
HSSP; P07378; 13PK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S00748; IVUT2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 88286728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKD_TRYBB
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PGKB OR PGK-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extension. EMBO J. 7:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                              MEDLINE;
        SO WENT THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation of an alanine racemase gene from Bacillus subtilis and its use for plasmid maintenance in B. subtilis."; BIOTECHNOLOGY 3:1003-1007(1985).
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                    BACILLUS SUBTILIS.
BACTERIA: FIRMICUTES: BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                            Score 64; DB 1; Length 508;
Pred. No. 1.73e+00;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KASAHARA Y., NAKAI S., LEE S., SADAIE Y., OCASAWARA N.; SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: L-ALANINE - D-ALANINE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: BELONGS TO THE ALANINE RACEMASE FAMILY.
TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY SEQUENCE 508 AA; 55668 MW; 7EB9B5FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V -> E (IN REF. 1).
V -> M (IN REF. 1).
V; AFEACC8C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 1; L
Pred. No. 2.59e+00;
2; Mismatches 4
                                                                                                                                                                                                                                                                   ALR_BACSU STANDARD; PRT; 389 AA. P10725; P96620: 01-201-1989 (REL. 11, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) ALANINE RACEMASE (EC 5.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00395; ALANINE_RACEMASE; 1.
PFAM; PF00842; Ala_racemase; 1.
HSSP; P10724; 1SFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERRARI E., HENNER D.J., YANG M.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOMERASE; PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: AB001488; D1020054; -. EMBL: Z99106; E1182430; -. PIR, JS0443; JS0443; SUBTILIST; BG10950; ALR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                              Query Match 46.4%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                              240 MAKILASYGDVYISDAF 256
                                                                                                                                                                      | |::| :|: |: |
| MEKFMAEFGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 MDQFMVELDQEY 324
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66
389 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKFMAEFGOGY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
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PGKB_CRIFA
P08966;
                                                                                                                                                                                                                                                                                                                                                                                                  ALR OR DAL
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                           SWINKELS B.W., EVERS R., BORST P., The topogenic signal of the glycosomal (microbody) phosphoglycerate kinase of Crithidia fasciculata resides in a carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88296420.
SWINKELS B.W., EVERS R., BORST P.;
"The topogenic signal of the glycosomal (microbody) phosphoglycerate
"The topogenic signal of the glycosomal (microbody) phosphoglycerate
kinase of Crithidia fasciculata resides in a carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                  EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; CRITHIDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRITHIDIA FASCICULATA.
EURARYOTA: EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; CRITHIDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 7:1159-1165(1988).

-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP +
3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
-!- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- SUBDNIT: MONOMER.
-!- SUBCELLULAR LOCATION: GLYCOSOMAL.
-!- DOMAIN: THIS GLYCOSOMAL PGR HAS A C-TERMINAL EXTENSION OF 38
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 1; Length 417;
Pred. No. 2.59e+00;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCKC_CRIFA STANDARD; PRT; 455 AA.
P08967;
01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE KINASE, GLYCOSOMAL (C) (EC 2.7.2.3).
01-NOV-1988 (REL. 09, CREATED)
01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE KINASE, CYTOSOLIC (B) (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSFERASE, KINASE, GLYCOLYSIS, MULTIGENE FAMILY SEQUENCE 417 AA; 44602 MW; 89E19A31 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X07458; G6983; -.
PIR; S00486; TVCRGC.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 MAKVLAAYGDVYVSDAF 164
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HSSP; P07378; 13PK.
                                                                                                                                                CRITHIDIA FASCICULATA.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      88296420
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50.08;

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6; Conservative
     Best Local Similarity
Matches 6; Conser
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Q27683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGKB_TRYBB
P07377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WHICH IS NOT PRESENT IN THE CYTOSOLIC ISOENZYME. THIS DOMAIN MOST
LIKELY SENES AS TOPOGENIC SIGNAL TO DIRECT THE GLYCOSOMAL PKG TO
THE GLYCOSOME.
SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic sequence and comparative analysis.";
J. VIROL. 58:626-634(1986).
I- VIROL. 58:626-634(1986).
VIROL. DA REPLICATION. TI FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN PAPILLOMAVIRUS TYPE 8.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A03656; WIWLB.
PFAM; PF00519; E1; 1.
PFAM; PF00524; E1_N: 1.
EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUCHS P.G., IFTNER T., WENINGER J., PFISTER H., "Epidermodysplasia verruciformis-associated human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFERSE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY; GLYCOSOME.
DOMAIN 417 455 TOPOGENIC SIGNAL (POTENTIAL).
DOMAIN 422 427 POLY-ALA.
SEQUENCE 455 AA; 47843 MW; C5062442 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 1; Length 455; Pred. No. 2.59e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
E7BCC22E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UT 10
VEL_HPV08 STANDARD; PRT; 603 AA.
V60420;
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
REPLICATION PROTEIN EI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                               PIR; S00487; TVCRGG.
PROSITE: PSOOILI, PGLYCERATE_KINASE; 1.
PFAM; PFOOIL62; PGK; 1.
HSSP; P07378; 13PK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M12737; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 MAKVLAAYGDVYVSDAF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKFMAEFGQGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                      EMBL; X07459; G6985; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86200410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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DB 1; Length 603;

45.7%; Score 63;

Query Match

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01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PHOSPHOGINCERATE KINASE, CYTOSOLIC (B) (EC 2.7.2.3) (ALLELE 2).
TRYPANOSOMA BROCEI BRUCEI.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEISHWANIA MAJOR.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; LEISHMANIA.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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LE BLANCQ S.M., SWINKELS B.W., GIBSON W.C., BORST P.;

"Evidence for gene conversion between the phosphoglycerate kinase genes of Trypanosoma brucei.";

J. Mol. BIOL. 200:439-447(1988).
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Pred. No. 3.84e+00;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHOGLYCERATE KINASE, CYTOSOLIC (B) (EC 2.7.2.3).
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Pred. No. 2.59e+00;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                          417 AA
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PROSITE; PS00111; PGLYCERATE_KINASE; 1.
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Best Local Similarity 41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 MAKVLASYGDVYVSDAF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEKFMAEFGOGYVOTPF 17
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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HSSP; P07378; 13PK.
                                                                                                                           166 MAKFKEAFGDGF 177
                                                                                                                                                                                                        1 MEKFMAEFGOGY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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UBP5_HUMAN
P45974;
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P50808;
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       S X S S S S
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                                                          OSINGA K.A., SWINKELS B.W., GIBSON W.C., BORST P., VEENEMAN G.H., VAN BOOM J.H., MICHELS P.A.M., OPPERDOES F.R.;
"Topogenesis of microbody enzymes: a sequence comparison of the genes for the glycosomal (microbody) and cytosolic phosphoglycerate kinases of Trypanosoma brucei.";
EMBO J. 4:3811-3817(1985).
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PESSPHOGLYCERATE KINASE, GLYCOSOMAL (C) (EC 2.7.2.3).
PESSHOGLYCERATE KINASE, GLYCOSOMAL (C) (EC 2.7.2.3).
LEISHMANIA MAJOR.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; LEISHMANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP + 3-PHOSPHO-D-GLYCEROYL PHOSPHATE.

13-PHOSPHO-D-GLYCEROYL PHOSPHATE.

1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.

1- SUBGELLULAR LOCATION: CYTOPLASMIC.

1- SUBCELLULAR LOCATION: CYTOPLASMIC.

1- IN T. BRUCEL, THREE GENES CODE FOR PHOSPHOGLYCERATE KINASE ISOZYMES, WHICH ARE TRANSPORTED TO DIFFERENT CELL COMPARTMENTS.

1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
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STRAIN-ISOLATE FRIEDLIN, LONDON;
STRAIN-ISOLATE FRIEDLIN, LONDON;
SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP
3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 1; Length 421;
Pred. No. 3.84e+00;
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM: PF00162; PGK: 1.
HSSP; P07378; 13PK.
TRANSFERASE; KINASE; GLYCOLYSIS; MULTIGENE FAMILY.
SEQUENCE 421 AA; 45154 MW; 54901A08 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 AA.
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PIR; A25119; KIUTGC.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.9%;
Similarity 29.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 MAKILSSYGDVYISDAF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X03370; G10497; -.
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P50312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELIUS H.;
SUBMITTED (CCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INTITATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /IRUSES; DSDNA VIRUSES, NO RNA STAGE; PAPOVAVIRIDAE; PAPILLOMAVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00514; E1; 1.
PFAM; PF00524; E1_N; 1.
EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
UBIOUTIN CARBOXYL-TEMINAL HYDROLASE 5 (EC 3.1.2.15) (UBIQUITIN TARGOXYL-TEMINAL HYDROLASE 5 (EC 3.1.2.15) (UBIQUITIN SPECIFIC PROCESSING PROFEASE 5)
(DEUBIQUITINATING ENZYME 5) (ISOPEPTIDASE T).
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
EMBL; L25121; G499643; -.
PROSITE: PS00111; PGLYCERATE_KINASE; 1.
PFAM; PF00162; PGK; 1.
HSSP; P07376; 13PK.
HSSP; P07376; 13PK.
SEQUENCE 479 Aa; 51575 MW; 7506ECC5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.9%; Score 62; DB 1; Length 604; 58.3%; Pred. No. 3.84e+00; rative 2; Mismatches 3; Indels
                                                                                                                                                                                                  Score 62; DB 1; Length 479;
Pred. No. 3.84e+00;
4; Mismatches 6; Indels
                                                                                                                                                                                                     Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 439 ATP (POTENTIAL).
604 AA; 68972 MW; 3BCCEFFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
12-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
REPLICATION PROTEIN EI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 AA
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                                                                                                                                                                                                  Score 62;
Pred. No. 3
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                                                                                                                                                                                               Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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Conservative
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1 MEKFMAEFGQGYVQTPF 17
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NP_BIND 432
SEQUENCE 604 AA
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BY SIMILARITY.

BY SIMILARITY.

GSLGFYGNEDEDSFCSPHFSSPTS -> A (IN SHORT FORM).

EL -> DV (IN REF. 1).

I -> V (IN REF. 1).

K -> R (IN REF. 3).

G -> D (IN REF. 3).

MW: IFOBB3C9 CRC32;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TASHAYEV V.L., O'CONNOR L.B., LARSEN C.N., KASPEREK E., PICKART C.M.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 96303695.
MEDLINE; 96303695.
MALLEY T., GIBBS R.A.;
MALLEY T., GIBBS R.A.;
"A gene-rich cluster between the CD4 and triosephosphate isomerase genes at human chromosome 12pi3.";
GENOME RES. 6:314-326(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00627; UBA; 2.
UBIQUITIN CONJUGATION; HYDROLASE; THIOL PROTEASE; MULTIGENE FAMILY;
                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                        JATON J.-C.;

"A human de-ubjquitinating enzyme with both isopeptidase and peptidase activities in vitro.";

FEBS LETT. 359:73-77 (1955).

-!- FUNCTION: CLEAVES LINEAR AND BRANCHED MULTUBIQUITIN POLYMERS WITH A MARKED PREFERENCE FOR BRANCHED POLYMERS.

-!- CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)0 - UBIQUITIN + A THYOL.

-!- COFACTOR: ZINC; REQUIRED FOR CATALYTIC ACTIVITY.

-!- COFACTOR: ZINC; REQUIRED FOR CATALYTIC ACTIVITY.

-!- THE N-TERMINAL IS BLOCKED.
                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 96105388.
FALQUET L., PAQUET N., FRUTIGER S., HUGHES G.J., HOANG-VAN K.,
JATON J.-C.,
"CDNA cloning of a human 100 kDa de-ubiquitinating enzyme: the SkDa human de-ubiquitinase belongs to the ubiquitin C-terminal hydrolase family 2 (UCH2).";
FEBS LETT. 376:233-237(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWN AS FAMILY 2 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95154450.
FALQUET L., PAQUET N., FRUTIGER S., HUGHES G.J., HOANG-VAN K.,
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U47927; G1208744; -.
EMBL; U47924; G1203896; -.
EMBL; U35116; G1008542; -.
MIM; 601447; -.
PROSITE: PS00972; UCH_2_1; 1.
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681
858 AA;
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95786 MW;

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Gaps
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Score 62; DB 1; Lengtn occ, Pred. No. 3.84e+00;
                                                                                                                                        Search completed: Wed Sep 1 16:07:37 1999 Job time: 11 secs.
          Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                  47 MNTFLG-FGKQYVERHF 62
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1 MEKFMAEFGQGYVQTPF 17
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protein . protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:07:53 1999; MasPar time 5.37 Seconds 172.884 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-17) from PCTUS9913024.pep (3 of 12) 138 1 MEKFWAEFGGGYVQTPF 17 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searchec:

Post-processing: Minimum Match 0% Listing first 45 summaries

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 28.183; Variance 44.286; scale 0.636 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

		Pred. No.	2.01e-02	5.40e-01	8.03e-01	1.76e+00	2.59e+00	3.80e+00	3.80e+00	3.80e+00	3.80e+00	3.80e+00	5.56e+00	5.56e+00	5.56e+00	5.56e+00	8.10e+00	1.17e+01	1.70e+01	1.70e+01	1.70e+01	1.70e+01
		Description	860AA LONG HYPOTHETICA	MANNOSE-1-PHOSPHATE GU	HYPOTHETICAL 19.4 KD P	CYTOCHROME P450 (EC 1.	F13P17.19 PROTEIN.	HYPOTHETICAL 32.9 KD P	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	PHOSPHOGLYCERATE KINAS	CYTOCHROME P450 (EC 1.	SIMILAR TO FAMILY 1 OF	ACYLTRANSFERASE.	PPE-FAMILY PROTEIN.	DNA FOR SEROTYPE B CAP	FUCULOSE-1-PHOSPHATE A	E6, E7, E1, E2, E4, L2	RIBONUCLEASE HII (RNHB	ALGI.	ALGI.	558AA LONG HYPOTHETICA
SUMMARIES		ID	059003	074624	060074	042701	080784	067454	037744	937745	037743	042700	023003	084013	053818	048232	027457	056954	029634	052196	051392	058315
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		Length DB	860	364	178	516	2301	273	420	440	509	524	355	455	645	1215	191	605	202	499	520	558
	% Query	Match	55.8	50.0	49.3	47.8	47.1	46.4	46.4	46.4	46.4	46.4	45.7	45.7	45.7	45.7	44.9	44.2	43.5	43.5	43.5	43.5
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01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE (EC 2.7.7.13).
HYPOCREA JECORINA.

RESULT 1D 07 AC 07 DT 01 DT 01 DE MA

HEMOGLOBIN BINDING PRO ATP DEPENDENT PERMEASE CHROMOSOME XV READING SIMILAR TO HUMAN PROTE OPRO2-LIKE PORIN PRECU BETA - 1.4 - XYLARES PREC ES, EY, EI, EZ, E4, L2 CYTOCHROME C BIOGENESI KINESIN MOTOR PROTEIN.	26 HYPOTHETICAL 118.2 KD 2.44e+01 814 HYPOTHETICAL 168.8 KD 2.44e+01 815 SZK PROTEIN. 3.50e+01 815 SZK PROTEIN. 3.50e+01 816 SZK PROTEIN. 3.50e+01 817 PROJEIN B-48 (F 3.50e+01 818 PROBABLE PROTEIN B-48 (F 3.50e+01 818 APOLIPOPROTEIN B-100 (3.50e+01 819 APOLIPOPROTEIN B-100 (3.50e+01 810 APOLIPOPROTEIN B-100 (3.50e+01 811 APOLIPOPROTEIN B-100 (3.50e+01 812 PROTEIN B-100 (3.50e+01 813 PROLIFOR SYNTHASE. 3.50e+01 814 PROMETIDE SYNTHASE. 3.50e+01 815 PROMETIDE SYNTHASE. 3.50e+01 816 PROMETIDE SYNTHASE. 3.50e+01 817 PROMETIDE SYNTHASE. 3.50e+01 818 PROMETIDE SYNTHASE. 3.50e+01	ALIGNMENTS PRT; 860 AA. CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)	LES; THERMOCOCCACEAE; PYR A H., HAIKAWA Y., HINO Y. AWA H., TARAMIYA M., OHFU YAMAZAKI J., KUSHIDA N., RIKOSHI K., MASUCHI Y., S ation of the Genome of a	Pyrococcus horikoshi F868 CRC32; 7; DB 1; Length 860 0. 2.01e-02; smatches 3; Indels
	2 06/726 2 05/734 2 05/589 14 011416 4 01377 5 019753 11 070395 5 023388 4 01378 4 01378 2 052545 2 052545	ALIGNY PRT 07, CREAT 07, LAST 09, LAST PROTEIN.	HERM ., H ABA R., KUDO B T.	bacter ". MW; Sco; Pre
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SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY
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BINDING
SEQUENCE
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                                                                                   STRAIN-EDITOR: 98309839.
MEDLINE: 98309839.
KRUSZENGKA J.S., SALOHEIMO M., PENTTILA M., PALAMARCZYK G.;
KRUSZENGKA J.S., SALOHEIMO M., PENTTILA M., PALAMARCZYK G.;
ISOJATION OF a Trichoderma reesei cDNA encoding GTP:
alfa-d-mannose-1-phosphate guanyltransferase involved in early steps
of protein glycosylation.";
cURR. GENET. 33:445-450(1998).
TRANSFERASE; NUCLEOTIDYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; GENTIANANAE; GENTIANALES; APOCYNACEAE; CATHARANTHUS.
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LYNE M., WOOD V., RAJANDREAM M.A., BARRELL B.G., BADCOCK K.,
CHURCHER C.M.;
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
HYPOCREALES; HYPOCREACEAE; HYPOCREA.
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MANGOLD U., EICHEL J., BATSCHAUER A., LANZ T., KAISER T.,
SPANGENBERG G., WERCK-REICHHART D., SCHROEDER J.;
PLANT SCI. 96:129-136(1994).
                                                                                                                                                                                                                                                                                                                                         Score 69; DB 3; Length 364;
Pred. No. 5.40e-01;
                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
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                                                                                                                                                                                                                                                                                              364 AA; 40284 MW; 95D4573B CRC32;
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01-AUG-1998 (TREMBLREL. 07, Li
01-AUG-1998 (TREMBLREL. 07, Li
HYPOTHETICAL 19.4 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                         50.0%;
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tes 8; Conservative
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| MEKFMAEFGOGYVOTPF 17
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EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VF5;
MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CY. COLUMBIA;
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
"Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AC004481; G3337366; --
SEQUENCE 2301 AA; 253398 MW; FB931E6C CRC32;
EMBL; L19075; G404690; -.
PROSITE: PS00086; CYTOCHROME_P450; 1.
PRAM: PF00067; P450; 1.
MENDEL; 11605; CATICO:113:14.
OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME.
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                                                                                                                                                                         Length 516;
                                                                                                                                                                       Score 66; DB 10; Length 516
Pred. No. 1.76e+00;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 10; Length 230
Pred. No. 2.59e+00;
3; Mismatches 5; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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08, LAST ANNOTATION UPDATE)
                                                                                                             459 459 HEME (BY SIMILARITY).
516 AA; 59720 MW; AD63FB23 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA.
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01-AUG-1998 (TREMBLREL. 07, CR
01-AUG-1998 (TREMBLREL. 07, LA
01-NOV-1998 (TREMBLREL. 08, LA
HYPOTHETICAL 32.9 KD PROTEIN.
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Best Local Similarity 46.7%;
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                                                                                                                                                                                                               5; Conservative
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01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
F13F17.19 PROTEIN.
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Best Local Similarity
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SEQUENCE FROM N.A.
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AQUIFEX AEOLICUS
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PCT-US99-13024-2-03.rspt

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[1]
SEQUENCE FROM N.A.
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037743
037743;
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MEDLINE: 91101667.

ALEXANDER K.A., PARAIL A.C., PARSONS M.;

ALEXANDER K.A., PARAIL A.C., PARSONS M.;

ALEXANDER W. A.C., PARAIL A.C., PARSONS M.;

An allele of Trypanosoma brucei cytoplasmic phosphoglycerate kinase is a mosaic of other alleles and genes.",

MOL. BIOCHEM. PARASITOL. 42:293-296(1990).

-!- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE - ADP +

3-PHOSPHO-D-GLYCEROYL PHOSPHATE.

-!- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.

-!- SUBUNIT: MONOMER. (BY SIMILARITY).
          DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SHEAD M.A., KELLER M., AUJAY M., HUBER R., SHELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. ABGONGA42; G2983869; -
HYPOTHETICAL PROTEIN.
SEQUENCE Z73 AA: 32949 MM; 4B858AZF CRC32;
                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-EATRO 164;
MEDLINE; 91101667.
ALEXARDER K.A., PARAIL A.C., PARSONS M.;
"An allele of Trypanosoma brucel cytoplasmic phosphoglycerate kinase is a mosaic of other alleles and genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION.
EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA.
                                                                                                                                        Gaps
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                                                                                                               Length 273;
                                                                                                                                       2; Indels
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Pred. No. 3.80e+00;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
2.7.2.3).
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                                                                                                            Score 64; DB 2; Lo
Pred.. No. 3.80e+00;
6; Mismatches 2.
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EC
                                                                                                              Query Match 46.4%;
Best Local Similarity 38.5%;
Matches 5; Conservative
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Best Local Similarity 35.3%;
Matches 6; Conservative
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1 MEKFMAEFGGGYVQTPF 17
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                             01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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 STRAIN=VF5;
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EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; GENTIANANAE; GENTIANALES; APOCYNACEAE; CATHARANTHUS.
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A phosphoglycerate kinase-like molecule localized to glycosomal microbodies: evidence that the topogenic signal is not at the C-terminus.
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MOL. BIOCHEM. PARASITOL. 42:293-296(1990).
-1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-PHOSPHATE.
-3-PHOSPHO-D-GLYCEROYL PHOSPHATE.
-1- PATHWAY: SCOOLD STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-1- SUBUNIT: MONOMER (BY SIMILARITY).
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
PRAM: PF00162; PGK: 1.
TRANSFERASE; MITOCHONDRION; KINASE; GLYCOLYSIS.
SEQUENCE 440 AA; 47231 MM; 09EF6813 CRC32;
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-1- CATALITIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE = ADP + 3-PHOSPHATE.
-1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- PROSITE; PSG0111; PGLYCERATE_KINASE; 1.
-- PRAM: PF00162; PGK: 1.
-- MITOCHONDRION; TRANSFERASE; KINASE; GLYCOLYSIS.
-- SEQUENCE 509 AA; 55747 MM; AF7895A4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 440;
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LAST ANNOTATION UPDATE)
2.7.2.3).
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Pred. No. 3.80e+00;
6; Mismatches 5.
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Best Local Similarity 35.3%;
Matches 6; Conservative
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Similarity 35.3%;
6; Conservative
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1 MEKFMAEFGQGYVQTPF 17
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Matches 6; Conser
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MEDLINE; 91304507
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Thu Sep

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STRAIN-BRISTOL N2;
XX MEDLINE, 94150/18.
ANDLINE, 94150/18.
MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., AINSCOUGH R., CONNELL M., COPERT J., COOPER J., COULSON A.,
BONFIELD J., BUBTON J., LONDELL M., COPERT T., COOPER J., COULSON A.,
CRAYTON M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
CARDINER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., SHOPIBES D., SHOWNKEEN R.,
A SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIEBRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATENSTON R.,
A WATSON A., WEINSTOCK L., WILKINSON SPROAT J., WOHLDWAN P.;
T. = 12 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                              EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                         Length 524;
                                                                                                                                                                                                                                                                                      4; Indels
      MANGOLD U., EICHEL J., BATSCHAUER A., LANZ T., KAISER T., SPANGENBERG G., WERCK-REICHHART D., SCHROEDER J.;
PLANT SCI. 96:129-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 5; Length 355;
Pred. No. 5.56e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
MILLER N., BRADSHAW H.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATERSTON R.; SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U64843; G1458290; -. PFAM; PF00001; 7tm_1; 1. SEQUENCE 355 AA; 40972 MW; 92BB3B7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
SIMILAR TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                     Score 64; DB 10; I
Pred. No. 3.80e+00;
8; Mismatches 4;
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Best Local Similarity 29.4%;
Matches 5; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                488 LORFIFDVAPSYVHAPF 504
                                                                                                                                                                                                                                                                                                                                  1 MEKFMAEFGOGYVQTPF 17
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NATÚRE 368:32-38(1994).
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Q23003
Q23003;
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STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                            STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L., MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                       DAVIS R.W.;
"Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
SCIENCE 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 2; Length 455;
Pred. No. 5.56e+00;
9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AE001275; G332898; --
TRANSFERASE; ACYTRANSFERASE
SEQUENCE 455 AA; 52058 MW; 18AB7CEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMLIN N., CHURCHER C.M.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                           CHLAMYDIA TRACHOMATIS.
BACTERIA; CHLAMYDIALES; CHLAMYDIACEAE; CHLAMYDIA.
                                                                                455 AA.
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                                                                               PRT;
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08,
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MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 45.7%;
Best Local Similarity 29.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 LORFLIEFGEFYADASL 359
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264 KFINLFSHNYVQFQF 278
                                                                               PRELIMINARY;
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01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
PPE-FAMILY PROTEIN.
                 3 KFMAEFGQGYVQTPF 17
                                                                                                                     01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                        01-NOV-1998 (TREMBLREL.
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084013
084013;
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053818
053818;
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"Region II of the Haemophilus influenzae type be capsulation locus is involved in serotype-specific polysaccharide synthesis.";
MOL. MICROBIOL. 15:107-118(1995).
EMBL: X78559; G471236;
SEQUENCE 1215 AA: 142323 MW; DF50121E CRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-DELTA H;
MEDLINE; 98037514.
SMITH D.R., DOUCETTE-STAWM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
JIMANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Mechanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FUCULOSE-1-PHOSPHATE ALDOLASE.
MTH1406.
METHANOBACTERIUM THERMOAUTOTROPHICUM.
ARCHAEA: EURYARCHAEOTA; METHANOBACTERIACEAE;
                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                          HAEMOPHILUS INFLUENZAE.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1215;
                                                                                            Length 645;
                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deltaH: functional analysis and comparative genomics.";
J. BACTERIOL. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DNA FOR SEROTYPE B CAPSULATION LOCUS.
                           PRÓC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
EMBL: AL021958: E1253293; -.
SEQUENCE 645 AA; 62693 MW; 04F5F7FI CRC32;
                                                                                           DB 2; Le
5.56e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63; DB 2; L
Pred. No. 5.56e+00;
                                                                                                                        4; Mismatches
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                                                                                           Score 63;
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 45.7%;
Local Similarity 52.6%;
les 10; Conservative
                                                                                       / Match
Local Similarity 46.7%;
nes 7; Conservative
                                                                                                                                                       592 FMSGFGNTGFLQSGF 606
                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE; 95272382
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                                                                                            Query Match
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048232
048232;
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027457
027457;
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Search completed: Wed Sep 1 16:08:14 1999 Job time : 21 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 5.59 Seconds 213.200 Million cell updates/sec Wed Sep 1 16:11:25 1999; Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-56) from PCTUS9913024.pep (4 of 12) 402 1 MEKFMAEFGQGYVQTPFLSE.....STAGPSYVKFQDNPVGSQTF Description: Perfect Score: Sequencé: Title:

PAM 150 Gap 11 Scoring table:

170751 seqs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part13 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part14 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Mean 25.232; Variance 100.718; scale 0.251 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	1.93e-20	1.51e+01	1.51e+01	1.820+01	1.82e+01	1.82e+01	1.82e+01	1.826+01	1.826+01	1.82e+01	1.82e+01	1.82e+01	1.82e+01	1.82e+01	1.826+01	1.82e+01
Description	Phage T4 ORFX gene pr	Hepatitis C virus gen	HCV genomic amino aci	Sequence of hepatitis	Sequence encoded in t	HCV NS5 domain antige		_	CKS-	_	HCV CKS-NS5E recombin	HCV CKS-NS5E - DHCV-4	CKS-NS5 EF	~	Protein sequence of h	Peptide encoded by co
£ £	R97371	R66995	R40120	P90150	P92033	R90934	W67010	R33441	R33633	R33575	R33595	R21566	R33630	P92041	P90158	P90164
DB	19	12	œ	-	Н	16	38	9	7	9	9	4	7		-	٦
Query Match Length DB	65	3011	3011	170	170	411	499	516	516	516	516	516	798	1766	1786	2261
Query Match	74:6	20.1	20.1	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9	19.9
Score	300	81	81	80	80	80	80	80	80	80	80	80	80	80	80	80
Result No.	1	7	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16

Sequence encoded in t 1.82e+01 HCV polypeptide 1. Sequence encoded in t 1.82e+01 HCV amino acid sequen 1.82e+01 HCV amino acid sequen 1.82e+01 HCV-1 polyprotein 1.82e+01 HCV-1 polyprotein 1.82e+01 HCV polyprotein 2.19e+01 Variant vitamin D bin 2.19e+01 Variant vitamin D bin 2.19e+01 Variant vitamin D bin 2.19e+01 Human NMDA R2A recept 2.19e+01 Human NMDA R2A recept 2.19e+01 HCV sequence 3.19e+01 HCV sequence 3.19e+01 Human excitatory amin 3.19e+01 Human excitatory amin 3.19e+01	chnology; nano-struc ail fibre proteins - , useful as filters nction is the produc otein gene region (s on also includes ope also and be produced as bulding blocks	0; DB 19; Length 65; v. 1.93e-20; Longth 65; matches 7; Indels 0; Gaps 0; gscplstagpsyvkfqdnpvgsqtf 56 i
P92047 R25135 P92050 R28582 P90288 R34009 R24440 R34480 R346931 R40038 R40038 R40038 R2279 R22779 R22779 R22779 R22779 R22779 R25529 R75534 R40119 R40119 R40119 R40119 R55529 R75534 R40119 R77338	ALIGNM 65 AA. 7 gp34. 11n; nan 1sh. 1sh. 1sh. 1sh. 1sh. 1sh. 1sh. 1sh.	Score 300; Pred. No. 3; Misma snsvrykisiags
23301 24436 24436 24436 24436 24436 24462 1 28946 29946 3011 4588 1116 4588 1116 4588 1116 4588 1116 4588 1116 11464 3011 11464 3011 11464 3011 11464 3011 11464 3011 11464 3011 11464 3011 11464 3011 3011 3011 3011 3011 3011 3011 301	Prot. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1
	standard; (fi. 1997 (fi. 1997) (fi. 1997) (fi. 1995) (f	atch cal Similarity 82 45; Conservat 46; Conservat mekfmaeiwtricpnai        : :: MEKFMAEFGGGYVQTPF 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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02-MAR-1990 (first entry)
Sequence encoded in the hepatitis C virus (HCV) cDNA insert in clone 14c.
Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and associated nucleic acids and polypeptide(s)
Claim 13; Figure 18; 139pp; English.
It is the sequence encoded in the hepatitis C virus (HCV) cDNA insert in clone 14c. Tag a = the region of overlap with the HCV antigen encoded in clone 25c. It is an epitope which could be used as immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis.
                                                                                                                                                                                                                                               D 26-JUL-1989.

F 18-NOV-1989; G27024.

F 18-NOV-1987; US-122714.

A (CHIR) Chiron Corporation.

Houghton M. Choo QL, Kuo G;

MPT: 89-215054/30.

T MPT: 89-215054/30.

T MPT: 89-215054/30.

T POIVPEPTIAGE(s) and antibodies for diagnosis, prevention and Treatment of infection.

T Lreatment of infection.

C The sequence is the peptide encoded by the hepatitis C virus (HCV) cDNA insert in clone 14c (see N90319). The polypeptides (C are used to diagnose HCV induced NAMBH, to raise antibodies for immunoassay or treatment, or to produce vaccines.

C The region shown overlaps with clone 25c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB 1; Length 170;
Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                       1-NOV-1989 (first entry)
Sequence of hepatitis C virus cDNA insert in clone 14c
Hepatitis C virus; clone 14c; clone 25c; probe; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsg 106
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14-NOV-1988; US-271450; US-122714.
P90150 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r 5
P92033 standard; protein; 170 AA
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Houghton M, Choo q-L, Kuo G;
WPI; 89-159274/22.
N-PSDB; N92089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 19.9%;
Similarity 37.8%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
19.9%;
Best Local Similarity 37.8%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..71
/*tag= a
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Sequence 170 AA;
                                                                                                                                                           Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New plasmid pHCV-162 is a mammalian expression systems for HCVD proteins - useful for diagnosing HCV infection and as vaccines proteins - useful for diagnosing HCV infection and as vaccines proteins - useful for diagnosing HCV infection and as vaccines is Example 1; Page 39-49; 100pp; English.

Example 1; Page 39-49; 100pp; English.

C Gesignated from the plasma of a HCV seropositive human (designated "LG") and cDNA was prepared from it. The cDNA sequence (ERNANK M62321). Further amplification using nested primers resulted in 7 adjacent HCV DNA fragments which could be assembled into a full-length sequence. The CDNA sequence. Comparison of the LG genomic amino acid sequence with that from HCV-1 showed 134 amino acid differences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               HCV genes and the corresponding proteins - used in the production of anti-HCV antibodies and the detection of HCV infection colaim 11; Pages 18-32; 35pp; Japanese. (74770 encodes R66995 the HC-J1/protein, the cDNA can be used in the construction of an expression vector for the transformation of a host cell, ran then be used in the production of proteins and peptides, useful in the preparation of monoclonal and polyclonal HCV-specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ន
01-AUG-1995 (first entry)
Hepatitis C virus gene HC-01/protein.
Hepatitis C virus; HCV gene HC-01/protein; specific antibodies.
Hepatitis c virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77-JAN-1994 (first entry)
HCV genomic amino acid sequence isolated from infected human I
Hepatitis C Virus; Non-A, non-B hepatitis Virus; HCV; NANBHV;
human growth hormone; HGH; secretion signal; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 20.1%; Score 81; DB 12; Length 3011; Local Similarity 40.0%; Pred. No. 1.51e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 20.1%; Score 81; DB 8; Length 3011; Local Similarity 40.0%; Pred. No. 1.51e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2116 vpspeffteldgvrlh-rfappckpllreevsfrvglhdypvgsq 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2116 vpspeffteldgvrlh-rfappckpllrdevsfrvglhdypvgsg 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1993.
29-JAN-1993: U00907.
31-JAN-1992: US-830024.
(ABBOT Labort Labort Labort Labort Labort Labort Labort Labort Labort J, Zeck BJ;
WPI; 93-258673/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R40120 standard; Protein; 3011 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
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                                                                                                                                                                                                                                                                                 (IMMO ) IMMUNO JAPAN KK.
WPI; 94-362594/45.
N-PSDB; Q74770.
                                                                                                                                                                                       11-OCT-1994.
10-DEC-1993; 345753.
10-DEC-1992; JP-360705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9315193-A.
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R40120;

Matches

a

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vaccine

4

Gaps

4

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Gaps
                                          4
Score 80; DB 1; Length 170;
Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                                        vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 106
                                                                                                                54
                                                                                                           13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ
                                                                                                             å
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Sequence

Matches

음 ò RESULT

4

R90934;

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Hepatitis C virus; NANBH; non-A, non-B hepatitis; CMP-KDO synthetase; non-structural protein; pHCV-45; diagnosis; CKS fusion protein; CTP:CMP-3-deoxy-manno-octulosonate cytidylyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibodies to hepatitis C virus NS5 proteins - used in diagnosing hepatitis C infections and differentiation studies Disclosure; Page 27; 38pp; English.
The sequence is that of an E. coli derived fragment of Hepatitis C virus NS5. The sequence may be used to raise monoclonal antibodies which specifically bind HCV NS5 antigen and to produce the hybridoma See also R33442-4.
Sequence 516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant NS5 region antigens - for hepatitis C assay for detecting hepatitis C virus infections
Example 7: Rage Sc5-57: 164pp: English.
Bight oligonucleotides representing amino acids 1932-2191 of the HCV genome were ligated together and cloned as a 793bp EcoRI/BamHI fragment into the CKS fusion vector pJ0200. The complete DNA sequence of this plasmid is designated pHCV-45. The resultant fusion protein HCV CKS-NS5E consists of 239 amino acids contributed by linker DNA sequences and 260 amino recombinant HCV CKS-NS5E antigen was immunoractive with human serum samples containing HCV antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80; DB 6; Length 516;
Pred. No. 1.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 80; DB 7; Length 516; Pred. No. 1.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1993 (first entry)
HCV NS5 encoded by pHCV45 clone.
Monoclonal antibody; hybridoma; E.coli; diagnosis.
Wepstitis C virus.
WO9304084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq
                                                                                                                                                                                                                                                      04-MAR-1993.
21-AUG-1992; U06865.
21-AUG-1991; US-748563.
(ABBO) ABBOTT LAB.
Dalley SH, Desal SM, Devare SG, Johnson JE,
WPI; 93-093937/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-1993 (first entry)
HCV CKS-NS5E fusion protein pHCV45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalley SH, Desal SM, Devare SG; WPI; 93-093942/11.
N-PSDB; Q38267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 9
R33633 standard; Protein; 516 AA.
T 8
R33441 standard; protein; 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%;
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Local Similarity 37.8%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 37.8%;
les 17; Conservative
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21-AUG-1992; U06964.
21-AUG-1991; US-748565.
(ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1mmunoassay; ss.
Hepatitis C Virus.
WO9304089-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                    윱
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of antibody in sample - uses peptide analog absorbed or chemically bound on carrier as antigen Disclosure; Page 5: 13pp. Japanese.

This sequence represents the Hepatitis C virus (HCV) non-structural (NS4) protein. The invention relates to peptide analogues derived from HCV protein. The invention relates to peptide analogues derived antibodies in a sample. Preferably the peptide analogues contain one or more thioamide peptide bonds where at least one oxygen atom of the peptide bond is replaced by sulphur atom. The peptide analogues analogues can be adsorbed or chemically bound to a carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The antigens may in the form of a fusion protein, a simple physical mixture, or the individual antigens commonly bound to a solid matrix. They are pref. prepd. by recombinant DNA techniques (primers are given in T12711-T12716), but can be synthesised or isolated from
                                                                                                                                                                                                                                                                                                                                                               CHIR ) CHIRON CORP.
CHOO Q, Houghton M, Kuo G;
WPI; 96-117956/13.
Combinations of synthetic Hepatitis C Virus antigens - provide more effective diagnosis of Non-A, Non-B Hepatitis
Claim 8; Fig 1(A-Y); 53pp; English.
The combination comprises an HCV antigen from the C domain (pref. C22 - R90936) and at least one HCV antigen from the NS3 (pref. C33c - R90932), NS4 (pref. C100 - R90933), S (pref. S2 - R909955) or NS5 (R90934) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                         TO MAIN 1399 (LITEL GILLY)

NON-A NON-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis; antibodies.

Repatitis C virus.

24-378-741.

24-378-1991; 114016.

04-APR-1990; US-504352.
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Pred. No. 1.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsg 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 16; Dred. No. 1.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV using affinity chromatography.
                       R90934 standard; Protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W67010 standard; protein; 499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 19.9%;
Local Similarity 37.8%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.9%;
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                        15-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1999 (first entry)
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19-FEB-1997; JP-034702.
(KYOW ) KYOWA MEDEX KK.
WPI; 98-515103/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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Query Match Best Local 3 Sequence

Matches

a ò W67010;

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Gaps

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4

Gaps

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Sequence

48

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Query Match
Best Local Similarity
                                                         Local Similarity
les 17; Conser
  516 AA;
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  Sequence
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                                                                                    R21566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region
                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repatitis C assay using recombinant NSI region antigens - for detecting antibodies and antigen in body fluids from individuals exposed to hepatitis C virus because the partitis C virus C vir
                                                                                                                                                                                                                                                                                                                                                                                                    Eight oligonucleotides representing amino acids 1932-2191 of the HCV genome were ligated together and cloned as a 793 base pair EcotF BamHI fragment into the CKS fusion vector pu0200. The control of the lac promoter. The recombinant antigen consists of 239 amino acids of CKS, nine amino acids contributed by linker DNA sequences and 260 amino acids from the HCV NS4/NS5 region (1932-2191). The recombinant antigen can be used to detect antibodies and antigen in body fluids from individuals exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1932-2191). The recombinant antigen can be used to detect antibodies and antigen in body fluids from individuals exposed to
                                                                                                                                                                                                                                                                                                                        Hepatitis C assay using recombinant C-100 region antigens - for detecting antibodies and antigen in body fluids from individuals exposed to hepatitis C virus Example 7; Page 92-94; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1993 (first entry)
HCV CKS-NSSE recombinant antigen.
HEPALITIS C VITUS: NON-A, NON-B hepatitis virus; NANBH;
NON-Structural protein; CMP-KDO synthetase; CKS fusion protein;
CTP:CMP-3-deoxy-manno-octulosonate cytidylyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
;
                                                       01-JUL-1993 (first entry)
HCV CKS-NSSE recombinant antigen.
HPPATITIS C VITUS: NS3: C100 antigen: CKS fusion protein;
CMP-KDO synthetase; immunodot assay; Non-A, non-B hepatitis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 80; DB 6; Length 516;
Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casey JM, Desai SM, Devare SG, Rupprecht KR; WPI; 93-093940/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-1993.
21-AuG-1992. U07188.
21-AuG-1991: US-748561.
(ABBO ) ABBOTT LAB.
Dailey SH. Desai SM. Devare SG:
WPI: 93-093941/11.
T 10
R33575 standard; Protein; 516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R33595 standard; Protein; 516 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.9%;
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                         04-MAK-1993.
21-AUG-1992; U07187.
21-AUG-1991; US-748566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoassay; pHCV-45.
Hepatitis C Virus.
                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 AA;
                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                         N-PSDB; Q38237
                                                                                                                                                            WO9304087-A
                                                                                                                                                                                   04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Hepatitis C virus; NANBH; non-A, non-B hepatitis; CMP-KDO synthetase; non-structural protein; pHCV-59; dlagnosis; immunoassay; CTP:CMP-3-deoxy-manno-octulosonate cytidylyl transferase.

W09304089-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                    09-JUN-1992 (first entry)
HCV CKS-NS5E - PHCV-45.
Hepatitis C virus; antigen; diagnosis; inhibitor; CMP-KDO synthase;
CKS; HCV CKS-NS5E; NANBHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: according to the diagramatic illustration of this sequence, Note: according to the diagramatic illustration of this sequence, both linkers comprise 9 amino acids.

The polypeptide (mol.wt. 55 kD) represents a distinct antigenic region of the HCV genome and can be used for the detection of antibodies and antigens for early diagnosis of HCV infection. The polypeptide can also be used to develop specific inhibitors of viral replication and for therapeutic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= NS5-E
/note= "HCV region NS4/NS5, amino acids 1932-2191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant heptatitis C virus antigens · produced as fusion proteins and representing distinct antigenic regions of the HCV
                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
Score 80; DB 6; Length 516; Pred. No. 1.82e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80; DB 4; Length 516;
Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'-NOV-1990; US-572822.
(ABBO) ABBOTT LABORATORIES.
Devare SG, Desai SM, Casey JM, Dawson GJ, Lesniewski RR;
Dailey SH, Gutierrez RA, Stewart JL;
N-PSDB; Q21679.
Recomhim---
                                                                                                    433 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 476
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                                                                                                                                   13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ 54
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 13
R33630 standard; protein; 798 AA.
                                                                                                                                                                                                                                                     R21566 standard; Protein; 516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240..248
/label= linker
/note= "see CC"
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/label linker
/note "see CC"
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37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- CKS
     19.98;
                          larity 37.8%;
Conservative
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c virus composite cDNA

10-NOV-1989 (first entry)
Protein sequence of hepatitis
Hepatitis C virus; vaccine.

troglodytes

26-JUL-1989. 18-NOV-1988; G27024 18-NOV-1987; US-122714 (CHIR) Chiron Corporation. Houghton M; Choo QL; Kuo G. WPI; 89-215054/30 N-PSDB; N90327.

PCT-US99-13024-2-04.rag

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                                                                                               New recombinant NSS region antigens - for hepatitis C assay for detecting hepatitis C virus infections

Claim 1, Page 36-318, 164pp; English.

Claim 1, Page 36-318, 164pp; English.

Claim 1, Page 36-318, 164pp; English.

Eight oligonucleotides representing amino acids 2188-2481 of the HCV genome were ligated together and cloned as a 895bp EcoRI-BamHI fragment in the vector DAC200 (i.e. pBR322 having a modifited lac promoter fused to part of the CKS gene and contg. a synthetic linker) to produce pHCV-48. The construct pHCV-45 was prepared by cloning a 793bp fragment representing HCV amino acids 1932-2191 into pJC300.

The Sall-BamHI fragment from pHCV-48 was ligated into the Sall-BamHI vector backbone of pHCV-45 to give an insert representing AAs 1932-2491 of HCV. The resulting 1650bp EcoRI-BamHI fragment was cloned into pJC300 to produce pHCV-59. The amino acid sequence of the resultant fusion antigen HCV KKS-NKS EF consists of 239 amino acids of CKS, 9 linker amino acids and 550 amino acids from the NS5 region of the HCV genome. The fusion protein is useful in immunoassays, for detecting anti-HCV antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     It is the sequence encoded in the open reading frame of hepatitis C virus CDNA inserts in clones 141,m 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, a33f, 33g and 39c. It is antigenic and could be used in immunoassay reagents and vectines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - and associated nucleic acids and polypeptide(s)
Claim 13; Figure 26-1, 26-2, 26-3, 26-4, 26-5, 26-6; 139pp; English.
14: 11b; 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 31, 33g and 39c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1990 (first entry) Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB 7; Length 798; Pred. No. 1.82e+01; 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ 54
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18-NOV-1988; 310922.

14-NOV-1988; US-271450; US-122714.

(CHIR) Chiron Corp.

HOUGHCON M, Choo q-L, Kuo G;

WPI; 89-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P92041 standard; protein; 1766 AA
                                                    (ABBO ) ABBOTT LAB.
Dailey SH, Desal SM, Devare SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h
Similarity 37.8%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purified hepatitis C virus
                                 US-748565.
                21-AUG-1992; U06964
21-AUG-1991; US-748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                798 AA;
                                                                                    93-093942/11
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Gaps

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1380 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsg 1423

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Best Local Similarity Matches 17; Conserv

Query Match

or 15 P90158 standard; protein; 1786 AA.

RESULT ID PO

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 Score 80; DB 1; Length 1786;
Pred. No. 1.82e+01;
11; Mismatches 13; Indels
                                                          1400 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 1443
                                                                            Wed Sep 1 16:12:13 1999
Query Match
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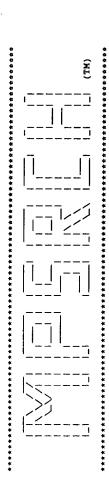
These antigens

Hepatitis C virus gene - used for prodn. of polynucleotide probes, polypeptide(s) and antibodies for diagnosis, prevention and treatment of infection.

Disciosure: fig 26; 30pp; English.

The sequence is encoded by the composite cDNA of N90327. These anticreact with antibodies in patients with non-A non-B hepatitis (NANBH). They can be used to diagnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines.

Sequence 1786 AA;



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 1 16:10:51 1999; MasPar time 5.66 Seconds 396.641 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-56) from PCTUS9913024.pep (4 of 12) 402 1 MEKFWAEFGQGYVQTPFLSE.....STAGPSYVKFQDNPVGSQTF 56 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

122810 seqs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 35.616; Variance 63.166; scale 0.564 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

*accession

24 76 18.9 821 2 B70199 25 75 18.7 18.7 18.2 100022 28 75 18.7 575 2 5018818 29 75 18.7 575 2 5018818 30 73 18.2 18.4 171 2 B381818 31 73 18.2 139 2 139818 33 73 18.2 139 2 139818 33 73 18.2 18.2 10.2 5065 34 73 18.2 10.2 5065 34 73 18.2 10.2 5065 34 73 18.2 201 2 570826 35 72 17.9 260 1 VCCWW 39 72 17.9 347 2 J01903 41 72 17.9 347 2 J01903 41 72 17.9 347 2 J01903 41 72 17.9 347 2 J01903 42 72 17.9 347 2 J01903 41 72 17.9 476 1 VYRTD 44 72 17.9 476 1 VYRTD 44 72 17.9 476 1 VYRTD 44 72 17.9 476 1 VYRTD 45 17.9 476 1 VYRTD 46 676 676 1 VCCWW 31 10.0 17.9 17.5 Fristrom, disc morphogenesis is effective mRNA afformal_name Drosophila melanoga formal_name Excherich formal_name Drosophila melanoga formal_name Excherich formal_name Drosophila melanoga formal_name Drosophila function of horse-reference formal_name Excherich formal_name Drosophila melanoga function function of horse-reference formal_name Excherich formal_name Drosophila melanoga function function of horse-reference function fun	outer membrane protei 4.70e+00 subtilisin inhibitor 6.48e+00 hemagglutinin precurs 6.48e+00 bNA directed DNA poly 6.48e+00 hypothetical protein 8.30e+00 ribosomal protein 8.12e+01 catalase (EC 1.11.1.6 1.22e+01 ribonucleotide reduct 1.22e+01 probable membrane pro 1.22e+01 probable membrane pro 1.22e+01 probable membrane pro 1.22e+01 probable membrane pro 1.22e+01 probable protein 1.22e+01 protein 1.66e+01 drypothetical protein 1.66e+01 hemagglutinin 1 inf 1.66e+01 coproporphyrinogen ox 1.66e+01 hypothetical protein 1.66e+01 hypothetical protein 1.66e+01 rec protein-tyrosine 1.66e+01	NTS	ete ane protein IMP-E3 - fruit fly	) lanogaster sion 31-Dec-1993 #text_ch		; Hammonds -309 :3, a qene	rosophila melanogaster.		01255	r-weight 36583 #checksum 8221	85; DB 2; Length 331; No. 2.31e-01; Mismatches 18; Indels 2; Gaps 2;	SIAGKKRVPPTKP-YVDF 235      : :        SIAGSCPLSTAGPSYVKF 46	lete r - Escherichia coli plasmid NTP113 hia coli _revision 05-Jan-1996 #text_change	G.A.; van der Zeijst, B.A.; Gaastra,	-263 de sequence of region 1 of the CFA/I human enterotoxigenic Escherichia coll.
24 76 18.9 821 2 25 75 18.7 575 2 28 75 18.7 575 2 28 74 18.4 171 2 29 74 18.4 171 2 30 73 18.2 18.2 18.2 33 73 18.2 18.2 17.9 34 73 18.2 18.2 2301 2 35 73 18.2 2301 2 36 72 17.9 347 2 44 72 17.9 347 2 44 72 17.9 347 2 44 72 17.9 347 2 44 72 17.9 347 2 44 72 17.9 347 2 45 72 17.9 347 2 46 72 17.9 347 2 47 72 17.9 476 1 44 72 17.9 476 1 44 72 17.9 476 1 44 72 17.9 66104  **ESCULT 1 16-Feb-1997 **ACCESSIONS A61046 **FSTERENCE A610493 **FYYYY **FYYY **ITLE TENTEMARERGOCYVOTPFLESES **NATRY CFGC Protein PYNY **ITLE AUTHORS A5617 **TYPE AFTY ACCESSIONS A5617 **FYYNY **FOURNAL AND	100022 506218 506518 501882 501882 501882 838162 838162 838162 139818 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665 570665	ALIGNMENTS	pe complete ed membrane	melanoga rosophil equence_		ristrom, 990) 11:	enesis in	abel MOO	e:FBgn000125			<b>«</b>	oe complete recursor - scherichia		:257 2011 0f
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                                               ##cross-references GB:M55661; NID:g145507; PID:g145510
##experimental_source enterotoxigenic strain, CFA/I-ST plasmid NTP113
##note sequence extracted from NCBI backbone (NCBIN:108960, NCBIP:108971)
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Pred. No. 6.47e-01;
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Hum. Mol. Genet. (1994) 3:897-901
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Hum. Mol. Genet. (1994) 3:897-901
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#map_position 4p12-4p12
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Best Local Similarity 32.4%;
Matches 11; Conservative
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SH2 homology; SH3
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Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.
#journal J. Biol. (1995) 270:1928-1934
#title Identification of rlk, a novel protein tyrosine kinase with predominant expression in the T cell lineage.
#cross-references WIDD:95130578
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protein-tyrosine kinase (EC 2.7.1.112) rlk - mouse
resting lymphocyte kinase
#formal_name Mus sp. #common_name mouse
23.4mr-1995 #sequence_revision 23.4mr-1995 #text_change
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#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#reqion protein kinase APP-binding motif
#length 527 #molecular-weight 61108 #checksum 785
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#domain protein kinase homology #label KIN
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Pred. No. 6.47e-01;
7; Mismatches 8; Indels
                                                                                                     *Superfamily protein-tyrosine kinase homology; protein kinase homology; homology
                                                                                                                                                                                                                           ##cross-references GDB:377329; OMIM:600058
#map_position 4p12-4p12
CLASSIFICATION #superfamily protein-tvrosine k
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                                            to 4p12.
#cross-references MUID:95038742
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Matches 12; Conservative
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##experimental_source isolate HC-J1
CLASSIFICATION #superfamily hepatitis C virus genome polyprotein; DEAD/H box
helicase homology
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##residues 1-3011 ##label OKA
##cross-references EMBL:D10749; NID:g221586; PID:d1002057; PID:g221587
NOE PC1284
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The 5'-terminal sequence of the hepatitis C virus genome. PC1285
  Txk - mouse #formal_name Mus musculus *common_name house mouse 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 12-Feb-1899
                                                                                                                      #authors Haire, R.N.; Litman, G.W.
#journal Mamm. Genome (1995) 6:476-480
#title The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5.
#cross-references MUID:9605936
#accession 149133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyprotein precursor - hepatitis C virus #formal_name hepatitis C virus 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Sep-1998
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#region nucleotide-binding motif A (P-loop)
#length 3011 #molecular-weight 327114 #checksum 5911
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#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase APP-binding motif
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No. 9.06e-01;
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Pred. No. 9.06e-01;
10; Mismatches 13; Indels
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##residues 1-513 ##label OK2
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Matches 18; Conservative
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GNWVC3 *type complete
genome polyprotein - hepatitis C virus (strain HCV-1)
capsid protein C; envelope protein M; major envelope protein
E; nonstructural protein NS1; nonstructural protein NS2;
nonstructural protein NS3; nonstructural protein NS2;
nonstructural protein NS4; nonstructural protein NS5
#formal_name hepatitis C virus
30-Sep-1992 *sequence_revision 30-Sep-1992 *text_change
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##cross_references GB:D37935; NID:g1235749; PID:d1007731; PID:g1235750
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#length 802 #molecular-weight 90438 #checksum 7656
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                                                                                                                  #formal_name Saccharomyces cerevisiae
02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
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                                           NAB3 protein - yeast (Saccharomyces cerevisiae)
probable RNA/ssDNA-binding protein HMD1; protein P1945;
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#title Dosage suppressors of the dominant Gl cyclin mutant C identification of a yeast gene encoding a putative RNA/ssDNA binding protein.
#cross-references #UID:96069710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
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NCE S60122
                        #type complete
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                                                                                          protein YPL190c
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'n,

2116 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHDYPVGSQ 2159

24-Oct-1997

A35327

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ALTERNATE_NAMES ORGANISM
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213-381
400-472
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                                         RESULT
ENTRY
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                                                                                                                                                                                                                                                         Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L.; Simmonds, P.
J. Gen. Virol. (1992) 73:1131-1141
Analysis of a new hepatitis C virus type and its phylogenetic relationship to existing variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary
##molecule_type genomic RNA
##residues 1577-1633 ##label CH2
##experimental_source isolates E-b17
##superfamily hepatitis C virus genome polyprotein; DEAD/H box
helicase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *product capsid protein C *status predicted *label CPC\
*product envelope protein M *status predicted *label BPN\
                              #authors Choo, O.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.;
Dong, C.; Gallegos, C.; Coit, D.; Mediner, A.J.; Bradley, D.W.; Kuo, G.; Houghton, M.
Fjournal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2451-2455
#cross-references MuID:91172826
#accession A39166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; P-loop; polyprotein; transmembrane
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#product nonstructural protein NS4a #status predicted
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*product nonstructural protein NS3 *status predicted *label NS3\
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#label MEE\
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predicted
#length 3011 #molecular-weight 327199 #checksum 8610
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#region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B\
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                                                                                                                                                                                                              ##residues 1-3011 ##label CHO
##cross-references GB:M62321; NID:9329873; PID:9329874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 1; L
Pred. No. 1.27e+00;
                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type genomic RNA
##residues 1577-1633 ##label CHA
##cross-references DDBJ:D10128
                                                                                                                                                                                                                                                                                                                                                                                                                                                     **experimental_source isolates E-bl6 cession PQ0404
22-May-1998
A39166; PQ0403; PQ0404
A39166
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#product nonst
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Best Local Similarity 37.8%;
Matches 17; Conservative
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448,476,532,540,
556,576,623,645,
1213,1255,2041,
2077,2240,2364,
2550,2789
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1616-1862
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                ACCESSIONS
REFERENCE
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Yang, F.; Bergeron, J.M.; Linehan, L.A.; Lalley, P.A.; Sakaguchi, A.Y.; Bowman, B.H. Genomics (1990) 7:509-516 Mapping and conservation of the group-specific component gene
                                                                                                                                                                                                                                ##residues 1-472 ##label YAN
##cross-references GB:M55413; GB:J04762; NID:g193445; PID:g193446

## DBP is a multifunctional protein found in plasma ascitic fluid, cerebrospinal fluid, and urine and on the surface of many cell types. In plasma, it carries the vitamin D sterols and prevents polymerization of actin by binding its monomers. DBP associates with membrane-bound immunoglobulin on the surface of B-lymphocytes and with 19G Fc receptor on the membranes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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#domain serum albumin repeat homology #label SA2\
#domain serum albumin repeat homology #status atypical
#label SA3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily serum albumin; serum albumin repeat homology
actin binding; duplication; globulin; glycoprotein; liver;
plasma; polymorphism; vitamin D
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#product vitamin D-binding protein #status predicted
#label MAT\
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#blnding_site carbohydrate (Asn) (covalent) #status
predicted #length 472 #checksum 7326
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vitamin D-binding protein precursor (allele Gc2) - human
DBP; Gc-globulin; group-specific component
fformal.name Homo sapiens #common_name man
28-May-1986 #sequence_revision 28-May-1986 #text_change
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Yang, F.; Brune, J.L.; Naylor, S.L.; Cupples, R.L.;
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19.7%; Score 79; DB 1; L.
Best Local Similarity 30.4%; Pred. No. 1.77e+00;
Matches 14; Conservative 12; Mismatches 17
                                                                                                                                                  cross-references MUID:90353947
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                                                                                                                         in mouse
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                                                                                                                                                                                                       ##molecule_type mRNA
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107-118,141-186,
185-194,216-262,
261-269,282-296,
295-307,331-372,
371-380,403-449,
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CLASSIFICATION
KEYWORDS
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#authors
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Yang, F.: Naberhaus, K.H.; Adrian, G.S.; Gardella, J.M.;
Brissenden, J.E.; Bowman, B.H.
Gene (1987) 54:285-295
The vitamin D-binding protein gene contains conserved
nucleotide sequences that respond to heavy metal, adipocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                             Witke, W.F.; Gibbs, P.E.M.; Zielinski, R.; Yang, F.; Bowman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence not shown; translation not shown
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DBP is a multifunctional protein found in plasma, ascitic fluid,
cerebrospinal fluid, and urine and on the surface of many cell
types. In plasma, it carries the vitamin D sterols and prevents
polymerization of actin by binding its monomers. DBP associates
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##cross-references GB:M12654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.H.; Dugalczyk, A.
Genomics (1993) 16:751-754
Complete structure of the human Gc gene: differences and
similarities between members of the albumin gene family
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Schoentgen, F.; Metz-Boutigue, M.H.; Jolles, J.; Constans, J.; Jolles, P.
J.; Jolles, P.
Biochim. Blophys. Acta (1986) 871:189-198
Complete amino acid sequence of human vitamin D-binding protein (group-specific component): evidence of a three-fold internal homology as in serum albumin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
##residues
1-19 ##label YA2
##cross-references GB:M17156
A92765
A92767
A9
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#journal Biochemistry (1979) 18:1611-1617
#title Molecular basis for the three major forms of human serum vitamin D binding protein (group-specific component).
#cross-references MUID:79145448
Naberhaus, K.H.; Bowman, B.H.
Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7994-7998
Human group-specific component (Ge) is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **residues 1-474 ##label YAN
##cross-references GB:M11321; NID:9183005; PID:9183006
Phose
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#*molecule_type protein
##residues 17-474 ##label SCH
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*cross-references MUD:8621623
*accession A24066
                                                                                                                          albumin family. #cross-references MUID:86068030
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A94076
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A46759
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with membrane-bound immunoglobulin on the surface of B-lymphocytes and with IgG Fc receptor on the membranes of T-lymphocytes.

Over 80 variants of human DBP have been identified. The three most common alleles are called Gclf, Gcls, and Gc2.
                                                                                                                                                                                                                                                                                            #domain signal sequence #status predicted #label SIG\
#product vitamin D-binding protein #status experimental
#label MPT\
#domain serum albumin repeat homology #label SAI\
#domain serum albumin repeat homology #label SA2\
#domain serum albumin repeat homology #status atypical
#label SA3\
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                                                                                                                                                                                                                 *superfamily serum albumin; serum albumin repeat homology actin binding; duplication; globulin; glycoprotein; liver;
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predicted
#length 474 #molecular-weight 52963 #checksum 5462
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Blochim. Biophys. Acta (1993) 1216:385-394
Sequence and organization of the human vitamin D-binding
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#domain serum albumin repeat homology #label SA2
#length 474 #molecular-weight 52949 #checksum 6044
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Pred. No. 1.77e+00;
12; Mismatches 12; Indels
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Pred. No. 1.77e+00;
                                                                                                                                                                                                                                                         plasma; polymorphism; vitamin D
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##molecule_type DNA
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Best Local Similarity 35.7%;
Matches 15; Conservative
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Best Local Similarity 35.7%;
Matches 15; Conservative
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189-198,220-266,
265-273,286-300,
299-11,335-376,
375-384,407-453,
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217-385
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217-385
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17-474
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##cross-references GB:AP000006; NID:g3236133; PID:d1031349; PID:g3257723
##experimental_source strain OT3
##experimental_source strain OT3
##note this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                            Rawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Outuka, R.;
Nakazawa, H.; Takamiya, M.; Ohtuku, Y.; Funahashi, R.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Rushida, N.; Oquchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.

Complete sequence and gene organization of the genome of a
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                                                                                                                                                                                                                                                                                                                                                                                         hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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##molecule_type DNA
##residues 1-70 ##label BLAT
##cross-references GB:AE000137; GB:U00096; NID:g2367108; PID:g1786500;
##cross-references GB:AE000137; GB:U00096; NID:g2367108; PID:g1786500;
                       F71000 *type complete
hypothetical protein PH1302 - Pyrococcus horikoshii
*formal_name Pyrococcus horikoshii
14.Aug-1998 *sequence_revision 14-Aug-1998 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein b0309 - Escherichia coli
probable membrane protein b0309 - Escherichia coli
fromal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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; 1.77e+00;
.....a 8; Indels
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Pred. No. 1.77e+0
10; Mismatches
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ilarity 28.0%;
Conservative
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Best Local Similarity 44.0%;
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Aunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessiores, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessiorer, L.;
Bolotlin, A.; Borchert, S.; Borriss, R.; Boursiler, S.;
Bolotlin, M.; Brignell, S.C.; Bron, S.; Broutlier, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Enrighton, J.; Enriam, K.D.; Errington, J.;
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Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Erjita,
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S.Y.; Glaser, P.; Goffeau, A.; Golightil, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harvood,
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
Kasahara, Y.; Kaerr-Blanchard, M.; Klein, C.; Kobayashi,
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Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Persoc,
M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,
V.; Rody, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.;
Schowska, A.; Seror, S.J.; Seror, P.; Shin, B.S.; Soldo,
B.; Sorokia, S.; Stacorn, P.; Shin, B.S.; Soldo,
B.; Sorokia, M.; Tamakoshi, A.; Tanaka, T.;
Tarkemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;
Wanters, P.; Wipat, A.; Yasanotti, A.; Wana, K.; Yata, K.;
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##cross-references GB:Z99116; GB:AL009126; NID:g2634723; PID:e1185714;
Gaps
                                                                                                                                                                                                Xaa-Pro #type complete
Xaa-Pro dipeptidase homolog yqhT - Bacillus subtilis
#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
24-Sep-1998
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19.4%; Score 78; DB 2; Length 353;
Best Local Similarity 29.7%; Pred. No. 2.45e+00;
Matches 11; Conservative 14; Mismatches 12; Indels
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Conservative
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Matches
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QY 1 MEKFMAEFGQGYVQTPFLSESNSVRYKISIAGSCPLS 37

Search completed: Wed Sep 1 16:11:07 1999 Job time : 16 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:09:43 1999; MasPar time 3.74 Seconds 422.797 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-56) from PCTUS9913024.pep (4 of 12) 402 1 MEKFWAEFGGGYVQTPFLSE.....STAGPSYVKFQDNPVGSQTF 56 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot37 1:swissprot

Mean 36.535; Variance 57.714; scale 0.633 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	. No.	4.61e-49	6.62e-02	2.04e-01	96e-01	1.27e-01	4.27e-01	14e-01	14e-01	8.81e-01	8.81e-01	8.81e-01	1.26e+00	1.26e+00	1.79e+00	2.54e+00	2.54e+00	2.54e+00	54e+00	54e+00	3.60e+00	5.07e+00	5.07e+00	5.07e+00
	Pred.	4	9	7	7	4	4	6.1	9	8	8	8	7	7	1.	2	2.5	2.5	2.5	2.5	6	S	ν. Ο	50
	Description	HYPOTHETICAL 7.3 KD PR	CFA/I FIMBRIAL SUBUNIT	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	NUCLEAR POLYADENYLATED	GENOME POLYPROTEIN (CO	VITAMIN D-BINDING PROT	VITAMIN D-BINDING PROT	PUTATIVE PEPTIDASE IN	VITAMIN D-BINDING PROT	GENOME POLYPROTEIN [CO	GLUTAMATE [NMDA] RECEP		TOXIN CORREGULATED PIL	HEMAGGLUTININ PRECURSO	EYES ABSENT HOMOLOG 1.	EYES ABSENT HOMOLOG 1.	DNA POLYMERASE (EC 2.7	DNA POLYMERASE (EC 2.7	0	FLEXIBLE CUTICLE PROTE	30S RIBOSOMAL PROTEIN	DEOXYRIBODIPYRIMIDINE
SUMMARIES	ΙD	Y15A_BPT4	CFAC_ECOLI	TXK_HUMAN	TXK_MOUSE	NAB3_YEAST	POLG_HCV1	VTDB_MOUSE	VTDB_HUMAN	YQHT_BACSU	VTDB_RABIT	POLG_HCVH	NME1_MOUSE	NME1_RAT	TCPF_VIBCH	HEMA_INBBO	EYA1_MOUSE	EYA1_HUMAN	DPOL_NPVAC	DPOL_NPVBM	YCB2_PSEDE	CU12_HYACE	RS8_METVA	PHR_BACFI
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ф	Query Match	74.6	21.1	20.4	20.1	19.9	19.9	19.7	19.7	19.4	19.4	19.4	19.2	19.2	18.9	18.7	18.7	18.7	18.7	18.7	18.4	18.2	18.2	18.2
	Score	300	82	82	81	80	80	79	79	78	78	78	77	77	92	7.5	75	75	75	75	74	73	73	73
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CATALASE HPII (EC 1.11 RIBONUCLEOSIDE-DIPHOSP INSULIN-LIKE PEPTIDE R NON-STRUCTURAL POLYPRO COAT PROTEIN. HYPOTHETICAL PROTEIN M GUANINE NUCLEOTIDE-BIN HEMAGGLUTININ (FRAGMEN HEMAGGLUTININ PRECURSO COPROPORPHYRINGEN III LATE EMBRYGERESIS ABU VITAMIN D-BINDING PROT TYROSINE-PROTEIN KINAS PUTATYVE GLUCOSAMINE THIOREDOXIN REDUCTASE NADH-UBLQUINONE OXIDOR HEMAGGLUTININ PRECURSO CANDIDAPEPSIN 7 PRECURSO CANDIDAPEPSIN 7 PRECURSO CANDIDAPEPSIN (DNA POLY HYPOTHETICAL 108.4 KD GENOME POLYPROTEIN (CO	RGENIC REGION. PHAGES; MYOVIRIDA ANK.  Length 65; 9; 7; Indels 0; PSYVKFQDNPVGSOTF	9 AA. ATE) PDATE) ONISATION FACTOR ANTIG SION; ENTEROBACTERIACE WO genes of the CFA/I
CATE_MYCAV RIRI_YEAST LILER_BRALA POLN_HEYMY COAT_WDV Y 2455_MYCPN GBA4_DICDI HEMA_INBFU HEMA_INBFU HEMA_INBFG TEC_HUMAN TEC	PRT; 65 AA.  EATED) S.T SEQUENCE UPDATE) EIN IN GP34-GP35 INTE NO RNA STAGE; TAILED  THE SWISS-PROT DATA B  MW; C2D7CE2D CRC32; %; Score 300; DB 1; %; Pred. No. 4.61e-4 e 3; Mismatches ESNSVRXISIAGSCPLSTAG	PRT; 86 WTED) C SEQUENCE UPD C ANNOTATION U PRECURSOR (COL GAMMA SUBDIVI GAMMA G.A., K LESHAW G.A., K STRA W.;
7006 11898 11898 11898 2603 12802 12802 13802 13802 13902 13918 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13185 13	STANDARD; P L. 31, CREATED) L. 31, LAST SEQU L. 31, LAST SEQU S. AST ANNO 3 KD PROTEIN IN 4. VIRUSES, NO RNA VIRUSES, NO THE SWI OTEIN. A. 74.6%; SCO 114y 82.1%; Pre nservative 3; RICPNAILSESNSVRY STYQTPFLSESNSVRY	ANDARD; PR 22, CREATED) 22, LAST SEQUE 23, LAST ANNOT BUNIT C PRECURS ACTERIA; GAMMA A.M., WILLSHAW A.M., GAASTRA W equence of the
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Y15A_BPT4 STANDARD; P39509; P39509; P39509; O1-FEB-1995 (REL. 31, LA ONTGER ON A ONTGER ON A ONTGER E.M.;	CFAC_ECOLI STANDARD; PS733, 01-MXY-1992 (REL. 22, CREA 01-MAY-1992 (REL. 22, LAST 01-MAY-1992 (REL. 23, LAST 01-MAY-1992 (REL. 23, LAST 01-MAY-1992 (REL. 23, LAST CFA,T FIMBRIAL SUBUNIT C P SUBUNIT C). ESCHERICHIA COLI. PLASMID NTPS13. BACTERIA; PROTEOBACTERIA; ESCHERICHIA. [1] SEQUENCE FROM N.A. STRAIN-ENTEROPYGGENIC; MEDLINE; 89330163. HAMERS A.M., PEL H.J., WILL VAN DER ZEIJST B.A.M., GAA "The nucleotide sequence o
24 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CEAC_ECOL P15773. 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-19 01-MAY-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAIRE R.N., OHTA Y., LEWIS J.E., FU S.M., KROISEL P.M., LITMAN G.W.; "TXK a novel human tyrosine kinase expressed in T cells shares sequence identity with Tec family kinases and maps to 4p12."; HUM. MOL. GENET. 3:897-901(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96197775.
OHTA Y., HAIRE R.N., AMEMIYA C.T., LITMAN R.T., TRAGER T., RIESS O.,
LITMAN G.W.;
                                                                                      JORDI B.J.A.M., WILLSHAW G.A., VAN DER ZEIJST B.A.M., GAASTRA W.; "The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
TISSUE SPECIFICITY: EXPRESSED IN T CELLS AND SOME MYELOID CELL
                                                                                                                                           DNA SEQ. 2:257-263(1992).
-!- FUNCTION: MAY SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human Txk: genomic organization, structure and contiguous linkage with the Tec gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85; DB 1; Length 869;
Pred. No. 6.62e-02;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONCOGENE 12:937-942(1996).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                              CFA/I FIMBRIAL SUBUNIT C.
operon of human enterotoxigenic Escherichia coll.";
MICROB. PATHOG. 6:297-309(1989).
                                                                                                                                                                                                                                                                                                                                                          EMBL; M55661; G145510; -.
ANTIGEN; SIGNAL; FIMBRIA; OUTER MEMBRANE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                               7AF76347 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TXK_HUMAN STANDARD; PRT; 527 AA. P42681; Q14220; C1-NOY-1995 (REL. 32, CREATED) C1-FED-1996 (REL. 33, LAST SEQUENCE UPDATE) TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 AFIQSQTINLSDSGKYKRLSISGNSALGITDTSY 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GYVQTPFLSESNSVRYK-ISIAGSCPLSTAGPSY 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN. BELONGS TO THE BIK SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                 97830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.4%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                               869 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE; 95038742.
                                                    SEQUENCE FROM N.A. MEDLINE; 92329981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                              MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

H -> R (IN REF. 2).

BDF019E3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-THYMUS; MEDLINE; 96059536. HAIRE R.N., LITMAN G.W.; "The murine form of TXK, a novel TEC kinase expressed in thymus maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOY-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING
                                                                                                                                                                                                                                                                                                                                                                                  HSSP, Q06187; 1AWW.
TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN; PHOSPHORYLATION.
DOMAIN; PHOSPHORYLATION.
14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82; DB 1; Len
Pred. No. 2.04e-01;
7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527
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                                                                                                                                                                                                                                                                                                PROSITE; PSO107; PROTEIN_KINASE_ATP; PROSITE; PSO109; PROTEIN_KINASE_IYR; PROSITE; PSS0101; PROTEIN_KINASE_DOM; PROSITE; PSS0001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 LRYPVGLMGSCLPATAGFSYEKWEIDP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                EMBL, 127071; G684986; -.
EMBL, U34379; G1161364; -.
EMBL, U34367; G1161364; JOINED.
EMBL, U34369; G1161364; JOINED.
EMBL, U34379; G1161364; JOINED.
EMBL, U34371; G1161364; JOINED.
EMBL, U34372; G1161364; JOINED.
EMBL, U34373; G1161364; JOINED.
EMBL, U34373; G1161364; JOINED.
EMBL, U34374; G1161364; JOINED.
EMBL, U34375; G1161364; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            U34378; G1161364; JOINED.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61239
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                                                                                                                                                                                                                                                             G1161364;
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MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
527 AA;
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nes 12; Conser
                                                                                                                                                                                                                                                             034377
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P42682;
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CONFLICT
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NP_BIND
BINDING
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                                                                                                                                                                                                                                                                          EMBL;
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Gaps

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Indels

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Mismatches

Conservative

PCT-US99-13024-2-04.rsp

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12;
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYATION (AUTO-) (BY SIMILARITY).
LS -> SF (IN REF. 3).
                                                                                                                                                                                                                   HU O. DAVIDSON D., SCHWARTZBERG P.L., MACCHIARINI F.,
LENAROO M.J., BLUESTONE J.A., MATIS L.A.;
"Identification of Rlk, a novel protein tyrosine kinase with
predominant expression in the T cell lineage.";
J. BIOL. CHEN. 270:1928-1934(1995).
-1. CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-1. SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-1. TISSUE SPECIFICITY: EXPRESSED IN EARLY THYMOCYTES, T CELLS AND
MAST CELLS.
                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE BTK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: U16145; G562125; -..
R EMBL: U19607; G643065; -..
R EMBL: D43969; G604884; -..
R EMBL: D435268; G623443; -..
R MGD: MGI:102960; TXK.
R PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
R PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
R PROSITE: PS500011; PROTEIN_KINASE_DOM; 1.
R PROSITE: PS500011; PROTEIN_KINASE_DOM; 1.
R PROSITE: PS500011; SH2; 1.
R PROSITE: PS500013; SH3; 1.
R PRAM: PF000018; SH3; 1.
R PFAM: PF000069; Pkinase; 1.
R HSSP; Q06187; 1AWW.
R HSSP; Q06187; 1AWW.
TRANSFERASE; TYRONINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUB-LIVER;
HIGASHITCH H., NONGGUCHI K., ARII S., FURUTANI M., KANEKO Y.,
NAKAYAMA H., FUUITA J.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                   SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-THYMUS;
SOMMERS C.L., HUANG K., GRINBERG A., CHARLICK D.A., KOZAK C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 527;
                                                                         LOVE P.E.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LS -> SF (IN REF. 3).
Y -> D (IN REF. 3).
A -> T (IN REF. 3).
F -> S (IN REF. 3).
5B39DA78 CRC32;
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Pred. No. 2.96e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-CYS.
to chromosome 5.";
MAMM. GENOME 6:476-480(1995).
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527 AA;
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MEDLINE; 95130578.
                                                                                                                                                                                   SEQUENCE FROM N.A.
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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NP_BIND
BINDING
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44.48;

Best Local Similarity

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                                                                                                                                                                                                                                                                              NAB3 OR YPL190C.
SECHAROWYCES CERVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI: ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                 ., OBERDORF A.M., DATAR K.V., SWEDLOW J.R., PADDY M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 1; Length 802;
Pred. No. 4.27e-01;
10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
RIEGER M., MUELLER-AUER S., SCHAEFER M.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SUBMCELLULAR LOCATION: NUCLEAR.
-1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 QGYGSQPPIPMNQSYG-RYQTSIPPPPPQQQIPQGYGRYQAGP 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 QGX-VQTPF-LSESNSVRYKISIAGSCPLSTAGPSYVKFQDNP
                                                                                                                                                                                                        01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLU.
POLY-ASP.
POLY-ASP.
POLY-ASP.
POLY-GLU.
POLY-GLU.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-CLN.
POLY-PRO.
POLY-CLN.
POLY-CLN.
POLY-CLN.
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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                        802 AA
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  268
                                             20
                          24 VRYKISIAGSCPLSTAGPSYVKFQDNP
242 LRYPIGLLGSCLPATSGFSYEKWEIDP
                                                                                                                                                                              01-FEB-1995 (REL. 31, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90438 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U05314; G476220; -.
EMBL; Z73546; E246917; -.
PIR; S48529; S48529.
SGD; L0001228; NAB3.
PFAM; PF00076; rrm; 1.
RNA-BINDING; NUCLEAR PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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765
769
7892 AA;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SWANSON M.S
                                                                                                                                   NAB3_YEAST
P38996;
                                                                                                                                                                                                                                                                                                                                                                                                                    WILSON S.M
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POLG_HCV1
P26664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELLULAR AMINOPERTIDASE.
CARSID PROTEIN ( POTENTIAL).
MATRIX PROTEIN ( POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/PE (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/PE (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/PE (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (SUPELOPE PROTEIN); MATRIX PROTEIN SUPPORTEIN BY MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5); HERATITIS C YIRUS (ISOLATE 1) (HCV). VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE; HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                        MEDLINE; 91172826.
CHOO Q.-L., RICHMAN K.H., HAN J.H., BERGER K., LEE C., DONG C.,
CHOO Q.-L., RICHMAN K.H., HAN J.H., BERGER K., LEE C., DONG C.,
BRADLEY D.W., KUO G., HOUGHTON M.;
Genetic organization and diversity of the hepatitis C virus.";
Genetic organization and diversity of the hepatitis C virus.";
FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHORIC, SOGGESTING A POSSIBLE MEMBRARAR-REALFED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
I-SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN BURNELOPE. CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-DIRECTED RNA POLYMERASE (NS5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP (POTENTIAL).
DECH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL).
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1862
2013
3011
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2041
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2240
                                                                                              SEQUENCE FROM N.A.
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-1- FUNCTION: MULTIFUNCTIONAL PROTEIN FOUND IN PLASMA, ASCITIC FLUID, CEREBROSPINAL FLUID, AND URINE AND ON THE SURFACE OF MANY CELL TYPES. IN PLASMA, IT CARRIES THE VITAMIN D STEROLS AND PREVENTS POLYMERIZATION OF ACTIN BY BINDING ITS MONOMERS. DBP ASSOCIATES WITH MEMBRANE-BOUND IMMUNGLOBULIN ON THE SURFACE OF B-LYMPHOCYTES. AND WITH IGG FC RECEPTOR ON THE MEMBRANES OF T-LYMPHOCYTES.
-1- SUBCELLULAR LOCATION: EXTRACELLULAR DOMAINS.
-1- DOMAIN: COMPOSED OF THERE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
VITAMIN D-BINDING PROTEIN PRECURSOR (DBP) (GROUP-SPECIFIC COMPONENT)
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The isolation, characterization and amino terminal sequence of the vitamin_D-binding protein (group specific component) from mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00273; transport_prot; 1.
ALBUMIN; GLYCOPROTEIN; VITAMIN D; TRANSPORT; PLASMA; ACTIN-BINDING;
REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YANG F., BERGERON J.M., LINEHAN L.A., LALLEY P.A., SAKAGUCHI A.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUMMAN B.H.;
"Mapping and conservation of the group-specific component gene in mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BORKE J.L., LITWILLER R.D., BELL M.P., FASS D.N., MCKEAN D.J., KUMAR R.;
                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                       Length 3011;
                                                                                                                                                                                                                                           2116 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 2159
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                                                                                                                                                                                                                                                                              13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFQDNPVGSQ 54
                                                                                                                    Score 80; DB 1; Len-
Pred. No. 4.27e-01;
11; Mismatches 13;
                                     POTENTIAL.
MW; 0726BB84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              472 AA
      POTENTIAL
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2364 2364
2789 2789
3011 AA; 327197
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                                                                                                                       19.98;
                                                                                                                                                   Local Similarity 37.8%;
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENOMICS 7:509-516(1990).
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MGD; MGI:95669; GC.
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VTDB_MOUSE
P21614;
                                  CARBOHYD
SEQUENCE
      CARBOHYD
                                                                                                                       Query Match
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SIGNAL
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                                                                                                                                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
VITAMIN D-BINDING PROTEIN PRECURSOR (DBP) (GROUP-SPECIFIC COMPONENT)
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVASTI J., KUROSKY A., BENNETT A., BOWMAN B.H.; "Molecular basis for the three major forms of human serum vitamin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRAUN A., KOFLER A., MORAWIETZ S., CLEVE H.; "Sequence and organization of the human vitamin D-binding protein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete amino acid sequence of human vitamin D-binding protein (group-specific component): evidence of a three-fold internal homology as in serum albumin and alpha-fetoprotein."; BIOCHIM. BIOPHYS. ACTA 871:189-198(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE: 86068030.
XANG F., BRUNE J.L., NAYLOR S.L., CUPPLES R.L., NABERHAUS K.H.,
BOWMAN B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human group-specific component (Gc) is a member of the albumin
                                                                                                                                                                                                       ë
                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHOENTGEN F., METZ-BOUTIGUE M.-H., JOLLES J., CONSTANS J.,
                                                                                                                                                                                 Length 472;
                                                                                                                                                                                                     12; Mismatches 17; Indels
                                                                                                                                                                                                                      153 DQFLYEYSSNYGQAPLPLLVAYTKNY-LSMVGSCCTSANPTVCFVK 197
                                                                                                                                                                                                                                    PROC. NATL. ACAD. SCI. U.S.A. 82:7994-7998(1985).
                    Y SIMILARITY.
Z SIMILARITY.
Z SIMILARITY.
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Z SIMILARITY.
                                                                                                                                                                               Score 79; DB 1; Lr
Pred. No. 6.14e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha fetoprotein gene family.";
J. CLIN. INVEST. 76:2420-2424(1985).
   53085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 17-31 AND 431-441.
                                                                                                                                                                               19.78;
30.48;
                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
 HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                          (GC-GLOBULIN) (VDB).
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92
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107
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                                                                                                                                                                                          Local Similarity
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MEDLINE; 86216223.
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                                                                                                                                                                                                                                                                             LT 8
VTDB_HUMAN
P02774;
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**MOLECULAR A. BICHLAMIER R., CLEVE H.;

**MOLECULAR AND SPECIFIC COMPONENT): allelic differences of the common protein (group-specific component): allelic differences of the common genetic G types.";

**CERENCE G TYPES. IS 1401-406(1992).

**CERENCE SPICE FOUND IN PLASMA, ASCITIC FLUID, CERENCESPINAL FOUND IN PLASMA, ASCITIC FLUID, CERENCOSPINAL FLUID, AND URINE AND ON THE SURFACE OF MAY CELL. TYPES. IN PLASMA, IT CARRIES THE VITAMIN D STEROLS AND PREVENTS POLYMERIZATION OF ACTIN BY BINDING ITS MONOMERS. DBP ASSOCIATES WITH MEMBRANE'S BOUND INVOICEDULIN ON THE SURFACE OF B-LYMPHOCYTES.

**AND WITH IGG FC RECEPTOR ON THE MEMBRANES OF T-LYMPHOCYTES.**

**AND WITH LIGG FC RECEPTOR ON THE MEMBRANES OF T-LYMPHOCYTES.**

**AND WITH LIGG FC RECEPTOR ON THE MEMBRANES OF T-LYMPHOCYTES.**

**ID DOMAIN IS COMPOSED OF THREE HOMOLOGOUS DOMAINS.**

**IT DOMAIN COMPOSED OF THREE HOMOLOGOUS DOMAINS.**

**IT THREE MOST COMMON ALLEES ARE CALLED GCIF, GCIS, AND GC2. THE SEQUENCE SHOWN IS THAT OF THE GC2 ALLEED.**

**ITH ALLEATY: BELONGS TO THE ALB ARPLY FAMILY.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                          SEQUENCE OF 1-19 FROM N.A.
MEDILINE; 88005794.
YANG F., NABERHAUS K.H., ADRIAN G.S., GARDELLA J.M., BRISSENDEN J.E.,
BOWMAN B.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.
D; TRANSPORT; PLASMA; ACTIN-BINDING;
                                                                                                 "The vitamin D-binding protein gene contains conserved nucleotide sequences that respond to heavy metal, adipocyte and mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITAMIN D-BINDING PROTEIN
binding protein (group-specific component)."; BIOCHEMISTRY 18:1611-1617(1979).
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JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S67474, G455970, JOINED.
S67476, G455970, JOINED.
S67478, G455970, JOINED.
S67479, G455970, JOINED.
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                                                                                                                                                                         VARIANTS GC2; GC1F AND GC1S.
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                                                                                                                              signals.";
GENE 54:285-290(1987).
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                                                                                                                                                                                        MEDLINE; 92316509
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(GC-GLOBULIN) (VDB).
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REPEAT
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
VITAMIN D-BINDING PROTEIN PRECURSOR (DBP) (GROUP-SPECIFIC COMPONENT)
                                                                                                                                                  Gaps
                                                                                                                                                                                                                            YQHT_BACSU STANDARD; PRT; 353 AA.
P54518:
01-00T-1996 (REL. 34, CREATED)
01-00T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-00T-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE PEPTIDASE IN GCVT-SPOILIAA INTERGENIC REGION (EC 3.4.-.-).
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                                                                             AND GCIS ALLELES).
                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                          KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S., SATO T., TAKEUCHI M., SUBNITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                              Length 474;
                                                                                                                                      Pred. No. 6.14e-01;
12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 1; Length 353;
Pred. No. 8.81e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches 12; Indels
                                                                                                                                                                   157 NQFMWEYSTNYGQAPLSLLVSYTKSY-LSMVGSCC-TSASPT 196
                                                                                                                                                                               EKFMAEFGGGYVQTPF-LSESNSVRYKISIAGSCPLSTAGPS 42
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
POTENTIAL.
D -> E (IN GC1S ALLEI
K -> T (IN GC1F AND G
G -> E (IN REF. 2).
E -> R (IN REF. 2).
F -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00557; pep_M24; 1.
HYPOTHETICAL PROTEIN; HYDROLASE.
SEQUENCE 353 AA; 38120 MW; C433A088 CRC32;
                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LEKLRNLFGQLGIDGMLITSNTNVRYMTGFTGSAGLA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBTILIST; BG11708; YQHT.
PROSITE; PS00491; PROLINE_PEPTIDASE; 1.
                                                                                                                             Score 79;
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                                                                                                          52963 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.7%;
Matches 11; Conservative
                                                                                                                           Match 19.7%;
Local Similarity 35.7%;
les 15; Conservative
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 286
299
335
375
407
452
288
432
168
168
327
474 AA;
                                                                                                                                                                                                                                                                                                                                      STRAIN-168 / JH642;
                                                                                                                                                                                                                                                                                                  SACILLUS SUBTILIS
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P53789;
                                                          CARBOHYD
VARIANT
                               DISULFID
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                 D-binding protein (Gc globulin)...

BIOCHEM. MOL. BIOL. INT. 34:1003-1009(1994).

-I-FUNCTION: MULTIFUNCTIONAL PROTEIN FOUND IN PLASMA, ASCITIC FLUID,
-I-FUNCTION: MULTIFUNCTIONAL PROTEIN FOUND IN PLASMA, ASCITIC FLUID,
-I-FUNCTION: MULTIFUNCTIONAL PROTEIN FOUND IN PLASMA, IT CARRIES THE VITAMIN D STEROLS AND PREVENTS
FOLYMERIZATION OF ACTIN BY BINDING ITS MONOMERS. DBP ASSOCIATES
WITH MEMBRANE-BOUND IMMUNOSTOBULIN ON THE SURFACE OF B-LYMPHOCYTES
-I-SUBCELLULAR LOCATION: EXTRACELLULAR.
-I-DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-I-SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PFAM; PF00273; transport_prot; 1.
ALBUMIN; GLYCOPROTEIN; VITAMIN D; TRANSPORT; PLASMA; ACTIN-BINDING;
                                                                                                                                                   OSAWA M., TSUJI T., YUKAWA N., SAITO T., TAKEICHI S.; *Cloning and sequence analysis of cDNA encoding rabbit vitamin
GC OR DBP.
ORYCOLÁGUS CUNICULOS (RABBIT).
ENGRATOTA, METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTÓLAGUS.
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VITAMIN D-BINDING PROTEIN.
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(REL. 23, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
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                                                                                           SEQUENCE FROM N.A.
STRAIN-NEW ZEALAND WHITE; TISSUE-LIVER;
MEDLINE; 95218682.
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15-DEC-1998 (
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Р27958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN ( POTENTIAL).
MATIX PROTEIN ( POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).
HELICASE (NS3) ( POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 ( POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A ( POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A ( POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A ( POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (NS5).
                                                                                                                                                                                                       GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN B); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NSI, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE [CC 2.7, 7.48] (NS5)].
HEPATITIS C VIRUS (ISOLATE H) (HCV).
VIRUSES; SSRNA POSITIVE_STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A36814; GNWCH.

PDB: 1HEI; 25-NOV-98

PFAM: PF01009; HCV_RARP: 1.

PFAM: PF01001; HCV_NS4B: 1.

PFAM: PF01006; HCV_NS4B: 1.

POLYPROTEIN; GLYCOPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; CORE PROTEIN; GLYCOPROTEIN; ENVELOPE PROTEIN; HELICASE; ATP-BINDING; TRANSMEMBRANE; NONSTRUCTURAL PROTEIN; 3D-STRUCTURE.

INIT_MET 1 1 REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                             "Genomic structure of the human prototype strain H of hepatitis virus: comparison with American and Japanese isolates."; PROC. NATL. ACAD. SCI. U.S.A. 88:10292-10296(1991).
                                                                                               SEQUENCE FROM N.A.
MEDILIE: 92052236.
INCHAUSPE G., ZEBEDEE S., LEE D.H.H., SUGITANI M., NASOFF M.,
PRINCE A.M.;
                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1207-1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
DECH BOX.
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                                                                          HEPATITIS C-LIKE VIRUSES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI 95820; GRINZA.
PFRM; PF00060; 11g_chan; 1.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed from cloned cDNAS.";
NATURE 357.70-74 (1992).
-1- FUNCTION: NADA RECEPTOR SUBTYPE OF GLUTAMATE-GATED ION CHANNELS
POSSESSES HIGE CALCIUM PERMEABILITY AND VOLTAGE-DEPRNDENT
POSSESSES HIGE CALCIUM PERMEABILITY AND VOLTAGE-DEPRNDENT
-1- SUBJUITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.
-1- SUBJUIT: HETERODIMER OF AN EPSILON SUBJUIT AND A ZETA SUBJUIT.
-1- SUBJUIT: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDIINE: 92244361.
MEGURO H., MUSHIYA E., KUTSUWADA T.,
TAMAZARI M., KURANISHI T., ARAKAWA M., SAKIMURA K., MISHINA M.;
"Functional characterization of a heteromeric NMDA receptor channel
                                                                                                                                                                                                                                                                                01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBUNIT 20) (NRZA) (NMDARZA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1.
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2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
FUNCTIONAL DETERMINANT OF NWDA
RECEPTORS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                     Length 3011;
                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                           12; Mismatches 13;
                                                                                           MW; 49643481 CRC32;
                                                                                                                                 Pred. No. 8.81e-01;
                                                                                                                      Score 78; DB 1;
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TRANSMEMBRANE; CALCIUM; MAGNESIUM.
                                                                                           AA; 327142
                                                                                                                      19.4%;
                                                                                                                                                 16; Conservative
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68D725B1 CRC32;

1464 AA; 165468 MW;

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                            MONYER H., SPRENGEL R., SCHOEPFER R., HERB A., HIGUCHI M., LOMELI H., BURNASHEV N., SAKMANN B., SEEBURG P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M91561; G2905806; -.
PFAM; PF00060; lig_chan; l.
RECEPTOR; POSTSYNAPTIC MEMBRANE; IONIC CHANNEL; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                     "Heteromeric NMDA receptors: molecular and functional distinction
                                                                                                                                                                                    01-UUN-1994 (REL. 29, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR (N-METHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
GLUTAMATE (NMDA) RECEPTOR SUBUNIT
                                                                    ö
                                                                                                                                                                                                                                                                       EUKARYOTA; META2OA; CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA: SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                          Score 77; DB 1; Length 1464;
Pred. No. 1.26e+00;
10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSILON 1. EXTRACELLULAR (POTENTIAL)
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FUNCTIONAL DETERMINANT OF
RECEPTORS (BY SIMILARITY)
                                                                                                                                                                                                                                    D-ASPARTATE RECEPTOR SUBTYPE 2A) (NR2A) (NMDAR2A).
         POTENTIAL.
W: 7CF0BA85 CRC32;
                                                                                                                                                                 1464 AA
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                                                                                          727 AFIYDAAVLNYKAGRDEGCKLVTIGSGYI 755
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                                                                                                           16 PFLSESNSVRYKISIAGSCPLSTAGPSYV 44
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                      165490 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS TO 595 AND 597-598
                                                                                                                                                                                                                                                                                                                                                                                 subtypes.";
SCIENCE 256:1217-1221(1992).
                                           Query Match 19.2%;
Best Local Similarity 27.6%;
Matches 8; Conservative
                                                                                                                                                                 STANDARD;
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                      1464 AA;
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Q00959;
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                      SEQUENCE
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                                                                                                                                                                                        01-APR-1993 (REL. 25, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
TOXIN CORREGULATED PILUS BIOSYNTHESIS PROTEIN F PRECURSOR (TCP PILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 93231536.
MEDLINE; 93231536.
MEDLINE; B12031536.

"Biogenesis and requiation of the Vibrio cholerae toxin-coregulated plus: analogies to other virulence factor secretory systems."; glus: analogies to other virulence factor secretory systems."; GENE 126:43-49(1993).
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                 HIGGINS D.E., NAZARENO E., DIRITA V.J.;
"The virulence gene activator ToxT from Vibrio cholerae is a member of the AraC family of transcriptional activators.";
J. BACTERIOL. 174:6974-6980(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CLASSICAL 01 / 217561;
MEDLINE; 93231537.
MCIERMAN M.A., ZABIHI S., MOURTZIOS L., MANNING P.A.;
"Genetic organization and sequence of the promoter-distal region of the top gene cluster of Vibrio cholerae.";
GENE 126:51-60(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    SACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO
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H
 Score 77; DB 1; Length 1464; Pred. No. 1.26e+00;
                                   11; Indels
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D -> E (IN REF. 2).
D -> E (IN REF. 2).
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                                  10; Mismatches
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                                                                 727 AFIYDAAVLNYKAGRDEGCKLVTIGSGYI 755
                                                                                    16 PFLSESNSVRYKISIAGSCPLSTAGPSYV 44
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   19.2%;
llarity 27.6%;
Conservative
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EMBL; X64098; G48417; -.
EMBL; M93963; G155281; -.
PIR; S23273; S23273.
PIR; A45247; PA45247.
PIR; JN0528; JN0528.
                                                                                                                                                                                                                                                        SIOSYNTHESIS PROTEIN TCPF).
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Best Local Similarity 33.3%;
Matches 11; Conservative
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338 AA;
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93015761
                                                                                                                                                                                                                                                                                       VIBRIO CHOLERAE
                                                                                                                                            RESULT 14
ID TCPF_VIBCH
AC P29488;
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                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
RITCHIE L.R., AIR G.M.;
SUBMITTED (JAN-1989) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPPORS AND FOR INITIATING INFECTION.
-!- SUBBUIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS (HAI AND HAZ) LIRKED BY A DISCULFIDE BOND.
-!- SUBBUIT: HOMOTRIMED BY A DISCULFIDE BOND.
-!- AND HAZ) LIRKED BY A DISCULFIDE BOND.
-!- AND HAZ) LIRKED BY A DISCULFIDE BOND.
-!- AND HAZ) LIRKED BY A DISCULFIDE BOND.
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                                                                                                                                                                                             INFLUENZA B VIRUS (STRAIN B/BONN/43).
VIRUSES; SSRNA NEGATIVE-STRAND VIRUSES; ORTHOMYXOVIRIDAE;
INFLUENZA VIRUS A AND B GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Match 18.7%; Score 75; DB 1; Length 575; Local Similarity 50.0%; Pred. No. 2.54e+00; es 9; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X13550; G758202; -.

PIR; S01882; S01882.

PFAM; PF00509; Hemagglutinin; 1.

HSSP; P03437; 5HMG.

ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.

NON_TER

SIGNAL

9 351 HA1 CHAIN.
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E31DFFE5 CRC32;
                                                                                  HEMA_INBBO STANDARD; PRT; 575 AA. P10448; 01-MAR-1989 (REL. 10, CREATED) 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST SHNOTATION UPDATE) HEMAGGLUTININ PRECURSOR (FRAGMENT).
146 KLSTALNQEYITGRFLTKENG-RYDIVNVGGVP 177
                 3 KFMAEFGGGYVQTPFLSESNSVRYKISIAGSCP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAI CHAIN.
HAZ CHAIN.
HAZ CHAIN.
POTENTIAL.
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Search completed: Wed Sep 1 16:09:53 1999 Job time: 10 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:10:10 1999; MasPar time 7.61 Seconds 401.470 Million cell updates/sec Run on:

not generated. rabular output >PCT-US99-13024-2 (1-56) from PCTUS9913024.pep (4 of 12) 402 1 MEKFMAEFGGGYVQTPFLSE.....STAGPSYVKFQDNPVGSQTF Description: Perfect Score:

Scoring table:

Sequence:

PAM 150 Gap 11

26

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19

Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 34.913; Variance 62.861; scale 0.555 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

SUMMARIES

					SUMMARIES		
		dР					
Result		Query					
No.	Score	Match	Length	BB	ΠD	Description	Pred. No.
-	81	20.1	3011	14	003463	GENOME POLYPROTEIN.	1.086+00
7	80	19.9	275	14	068468	POLYPROTEIN (FRAGMENT)	1.50e+00
m	80	19.9	275	14	068467	_	1.50e+00
4	80	19.9	275	14	068469	_	1.50e+00
'n	80	19.9	357	'n	001993	VC27A7L.1 PROTEIN.	1.50e+00
9	80	19.9	802	m	007034	RNA BINDING PROTEIN.	1.50e+00
7	80	19.9	2436	14	081756	POLYPROTEIN (FRAGMENT)	1.50e+00
80	79	19.7	542	'n	017456	SIMILAR TO GLUTAMATE D	2.10e+00
σ	79	19.7	860	-	029003	860AA LONG HYPOTHETICA	2.10e+00
10	78	19.4	70	7	P75688	FROM BASES 311709 TO 3	2.91e+00
11	78	19.4	3011	14	036610	POLYPROTEIN.	2.91e+00
12	78	19.4	3011	14	036608	POLYPROTEIN.	2.91e+00
13	78	19.4	3011	14	036609	POLYPROTEIN.	2.91e+00
14	78	19.4	3011	14	036579	POLYPROTEIN.	2.91e+00
15	77	19.2	418	~	056631	LECITHINASE.	4.04e+00
16	77	19.2	470	ď	087325	LECITHINASE.	4.04e+00
17	77	19.2	266	~	084354	HYPOTHETICAL 63.5 KD P	4.04e+00
18	77	19.2	196	~1	054123		4.04e+00
19	77	19.2	1464	11	063728	N-METHYL-D-ASPARTATE R	4.04e+00
20	77	19.2	1464	Ξ	008948	N-METHYL-D-ASPARTATE R	4.04e+00

4.004e+000 5.58e+000 5.58e+000 5.58e+000 5.58e+000 7.70e+000 1.06e+001 1.45e+01 1.45e+01 1.45e+01 1.45e+01 1.45e+01 1.45e+01 1.45e+01 1.66
N.METHYL-D-ASPARTATE R ZKI067.2 PROTEIN. SIMILARITY TO HUMAN GT FRUCTOFURANOSIDASE (EC OUTER MEMBRANE PROTEIN B120. F2552.2 (FRAGMENT). MANNOSE-1-PHOSPHATE GU HYPOTHETICAL 19.4 KD P C34B7.2 PROTEIN. L1 PROTEIN. L1 PROTEIN. L2 PROTEIN. L3 PROTEIN. L4 PROTEIN. HYPOTHETICAL 49.3 KD P TAIL PROTEIN. FAIL PROTEIN. FAIL PROTEIN. FAIL PROTEIN. HARMAGGLUTININ (FRAGME HARMAGGLUTININ (FRAGME HEMAGGLUTININ (FRAGMEN HEMAGGLUTININ (FRAGMEN HEMAGGLUTININ (FRAGMEN) POLYPROTEIN (FRAGMENT)
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ALIGNMENTS

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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN.
WIRDATITIS C VIRUS (ISOLATE HC-J1) (HCV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKAMOTO H., KANAI N., MISHIRO S.;
Full-length nucleotide sequence of a Japanese hepatitis C virus
isolate (HC-J1) with high homology to USA isolates.";
NUCLEIC ACIDS RES. 20:6410-6410(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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OKRAMOTO H., OKADA S., SUGIYAMA Y., YOTSUMOTO S., TANAKA T., YOSHIZAWH H., TSUDA F., MIYAKAWA Y., WAXUMI M.;

THE 5'-terminal sequence of the hepatitis C virus genome.";

JRN J. EXP. MED. 60:167-177(1990).

PEMBL; D10749; G221587;

PEMBL; PFO09999; HCV_RGRP; I.

PFAM; PF01091; HCV_NSAP; I.

PPRM; PF01001; HCV_NSAP; I.
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20.1%; Score 81; DB 14; Length 3011;
Best Local Similarity 40.0%; Pred. No. 1.08e+00;
Matches 18; Conservative 10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2116 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHDYPVGSQ 2159
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                                                PRT; 3011 AA
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ID Q68468 PRELIMINARY; PRT;

AC Q68468;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE; 93117120.
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VC27A7L.1 PROTEIN.
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01-JUL-1997
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                                                Best Loca
Matches
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                                                                                                                                                                           Gaps
     01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
HEPATITIS C VIRUS (HCV).
HEPATITIS C-LIKE VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 4

068469 PRELIMINARY: PRT; 275 AA.

068469; (TREMBLREL. 01, CREATED)

01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)

POLYPROTEIN (FRAGMENT).

HEPATITIS C VIRUS (HCV).

HEPATITIS C LIKE VIRUSES.
                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
HEPATITIS C VIRUS (HCV).
VIRUSES; SSRNA POSITIVE STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                      Score 80; DB 14; Length 275; Pred. No. 1.50e+00; 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80; DB 14; Length 275; Pred. No. 1.50e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches 13; Indels
                                                                                                                                                                                           140 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 183
                                                                                                                                                                                                      54
                                                                  STEALN-PATIENT #2675;
VIZMANOS J.L.;
THEREIS (1996), GENETICS DEPT., UNIVERSITY OF NAVARRA.
POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-PATIENT #2675;
VIZMANOS J.L.;
THESIS (1996), GENETICS DEPT., UNIVERSITY OF NAVARRA.
POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEPT., UNIVERSITY OF NAVARRA
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1
275 275
275 AA; 30423 MW; 6DE9E548 CRC32;
                                                                                                                                    6D967905 CRC32;
                                                                                                                                                                                                                                                  PRT;
                                                                                                                            275 275
275 AA; 30504 MW;
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                      Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-PATIENT #2675;
VIZMANOS J.L.;
FHESIS (1996), GENETICS DIEMBL, U37646; GIL73779; POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                          HEPATITIS C-LIKE VIRUSES
                                                                                                                                                                                                                                                   PRELIMINARY;
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                               SEQUENCE FROM N.A.
                                                                                                                              NON_TER
SEQUENCE
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NON_TER
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAZTON M., DEAR S., DUZ., DUREIN R., FAVELLO A., FULTON L.,
GARDNER M., KERSHAW J., KIRSTEN J., HANTILER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAINSTER N., LATREILLE P.,
FARSONS J., FERCY C., MCMURRAY A., MORTHORFS B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFER L., STADEN R., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
SUGINCT K., MATSUMOTO K., KORNBERG R.D., REED S.I., WITTENBERG C.;
"HMD1 of the yeast Saccharomyces cerevisiae encodes a putative
RNA/single strand DNA-binding protein, whose overexpression reduces
the expression of a G1 cyclin, CLN3.";
SUBMITTED (AUG-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOY-1996 (TREMBLREL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
RNA BINDING PROTEIN.
SACCHAROMYCES CREEVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                  ..
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                                                                                                             Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 80; DB 5; Length 357; Larity 45.8%; Pred. No. 1.50e+00; Conservative 7; Mismatches 6; Indels
                                                                                                                                                               Indels
                                                                                                                                                                                                               140 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 183
                                                                                                                                                                                                                                                13 VQTP-FLSESNSVRYKISIAGSC-PLSTAGPSY-VKFODNPVGSO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                       Score 80; DB 14; Le
Pred. No. 1.50e+00;
11; Mismatches 13;
1 1
275 275
275 AA: 30495 MW; 9BEIEE8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 368:32-38(1994).
EMBL: 295621; E1349927; - .
SEQUENCE 357 AA; 41307 MW; D2FB4683 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       802 AA
                                                                                                                                                                                                                                                                                                                                                                              357
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 QGYVQTPFLSESNSVRYKISIAGS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                 04,
09,
                                                                                                       Match 19.9%;
Local Similarity 37.8%;
nes 17; Conservative
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Best Local Similarity '
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SEQUENCE
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P75688;
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                                                        Gaps
                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYPROTEIN (FRAGMENT).
VIRDATITIS C VINUS (HCV).
VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
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                                   Score 80; DB 3; Length 802;
Pred. No. 1.50e+00;
10: Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                          1666 VPSPEFFTELDGVRLH-RFAPPCKPLLREEVSFRVGLHEYPVGSQ 1709
                                                                                                                                                                                                                                                                                                                                                                    CHOO Q.L., RICHMAN K., HAN J.;
SUBMITTED (MAY-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; M32084; G329876; -.
PFAM; PF00998; HCV_RARP; I.
PFAM; PF01001; HCV_NS4D; I.
                                                                      622 QGYGSQPPIPMNQSYG-RYQTSIPPPPPQQQIPQGYGRYQAGP 663
                                                                                 10 QGY-VQTPF-LSESNSVRYKISIAGSCPLSTAGPSYVKFQDNP 50
                                                                                                                                                                                                                                                                                                                                                                                                                   017456, 01786 (TREMBLREL. 01, CREATED) 01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01.NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) SIMILAR TO GLUTAMATE DECARBOXYLASE.
                                                                                                                                                                                                                                                                                              2436 2436
2436 AA; 264734 MW; 3CF4508C CRC32;
                    54BFODFF CRC32;
                                                                                                                             Ą
                                                                                                                                                                                                                                                                                                                                                                                                              542 AA
                                                                                                                            PRT; 2436
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; D37935; D1007731; -. PFAM; PF00076; rrm; 1. SEQUENCE 802 AA; 90437 MW;
                                   Query Match 19.9%;
Best Local Similarity 32.6%;
Matches 14; Conservative
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans.";
NATURE 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             POLYPROTEIN.
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SEQUENCE
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081756
081756;
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FIRAIN-OT3;
MEDLINE; 98344137.
MEDLINE; 98344137.
MEDLINE; 98344137.

KANARABATASI Y., SAWADA M., HORIKAWA H., HAIKAWA A., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., NARAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).

EMBL; AP000006; D1031349; -. SEQUENCE 860 AA; 95455 MW; B336F868 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
FROM BASES 311709 TO 323910
(SECTION 27 OF 400) OF THE COMPLETE GENOME (SECTION 27 OF 400).
ESCHERICHIA COLI.
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                                                                                                                                                                                                                                                                                Query Match
19.7%; Score 79; DB 5; Length 542;
Best Local Similarity 30.3%; Pred. No. 2.10e+00;
Matches 10; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.7%; Score 79; DB 1; Length 860; 28.0%; Pred. No. 2.10e+00; active 10; Mismatches 8; Indels
STRAIN-BRISTOL N2;
DU Z., GATTUNG S.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                 TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA
EMBL; U50312; G125312; -.
PFAM; PF00282; pyridoxal_dec; 1.
SEQUENCE 542 AA; 61133 MW; A7C148AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 A.A.
                                                                                                                                                                                                                                                                                                                                                                      309 GFLL-PFLEE-DEIRYDFRVPGVSSISADSHKY 339
                                                                                                                                                                                                                                                                                                                                                                                                 CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKFLTDFSNAFIRVAFKYNSYEAR 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TREMBLREL. 07, LAST
01-JAN-1999 (TREMBLREL. 09, LAST
860AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.0%;
Matches 7; Conservative
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01-AUG-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYROCOCCUS HORIKOSHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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MEDLINE; 97426617
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BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;

"The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277.1453-1474(1997).

EMBL, 86000137; 31786500; -
SEQUENCE 70 AA; 7854 MW; B754D938 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLYPROTEIN.

POLYPROTEIN.

YERPATITIS C VIRUS STRAIN H77.

VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;

HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 12
036608
036608
03.001-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYTROTEIN
TOUXYPROTEIN
VIRUS STRAIN H77.
VIRUSES, SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C -LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 97385173.

YANACI M., PURCELL R.H., EMERSON S.U., BUKH J.;

"Transcripts from a single full-length cDNA clone of hepatitis C virus are infectious when directly transfected into the liver of
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"Transcripts from a single full-length cDNA clone of hepatitis C
virus are infectious when directly transfected into the liver of
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Pred. No. 2.91e+00;
12; Mismatches 13; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 70;
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036510
036510
036510;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
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PROC. NATL. ACAD. SCI. U.S.A. 94:8738-8743(1997).
EMBL, AF011753; G2327075;
PFAM; PF01001; HCV_RGRP; 1.
PFAM; PF01001; HCV_NS4D; 1.
PFAM; PF01006; HCV_NS4D; 1.
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EMBL; AF011751; G2327071; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78; DB 2; LA
Pred. No. 2.91e+00;
9; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||||::||::|: || :::|: || QCYVQTPFLSESNSV-RYKISIAGS 33
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Local Similarity 35.6%;
les 16; Conservative
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Local Similarity 44.0%;
nes 11; Conservative
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MEDLINE; 97385173.
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
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HEPATITIS C VIRUS (HCV).
VIRUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; FLAVIVIRIDAE;
HEPATITIS C-LIKE VIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YANAGI M., PURCELL R.H., EMERSON S.U., BUKH J.;
"Transcripts from a single full-length cDNA clone of hepatitis C
virus are infectious when directly transfected into the liver of
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SCIENCE 277:570-574(1997).
EMBL. AF00996 (G2316098). -.
PFAM: PF01001; HCV_RARP; 1.
PFAM: PF01001; HCV_NS4b; 1.
PFAM: PF01006; HCV_NS4b; 1.
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Pred. No. 2.91e+00;
12; Mismatches 13; Indels 4
                                                                                                              Length 3011;
                                                                                                        Score 78; DB 14; Length 301
Pred. No. 2.91e+00;
12; Mismatches 13; Indels
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                         01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimpanzee.";
PROC. NATL. ACAD. SCI. U.S.A. 94:8738-8743(1997).
EMBL; AF011752; G2327073; --
PFAM; PF00998; HCV_RGRP; 1.
PFAM; PF01001; HCV_NS4b; 1.
PPAM; PF01006; HCV_NS4b; 1.
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                                                                       3011 AA; 327114 MW; A987CA50 CRC32;
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PFAM; PF00998; HCV_RdRP; 1.
PFAM; PF01001; HCV_NS4b; 1.
PFAM; PF01006; HCV_NS4a; 1.
                                                                                                            Query Match 19.4%;
Best Local Similarity 35.6%;
Matches 16; Conservative
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Best Local Similarity 35.6%;
Matches 16; Conservative
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                                                    POLYPROTEIN.
SEQUENCE 3
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SEQUENCE
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036609;
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO.
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                                                                                                                               Query Match 19.4%; Score 78; DB 14; Length 3011; Best Local Similarity 35.6%; Pred. No. 2.91e+00; Matches 16; Conservative 12; Mismatches 13; Indels 4
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19.2%; Score 77; DB 2; Length 418;
Best Local Similarity 29.0%; Pred. No. 4.04e+00;
Matches 9; Conservative 14; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-E7946 EL TOR;
FIORE A.E., KAPER J.B.;
SUBMITTED (FEB-1996) DEMBL/GENBANK/DDBJ DATA BANKS.
BRBL; U50004; G123642; -..
PFAM; PF00657; Lipase_GDSL; 1.
SEQUENCE 418 AA; 47600 MW; 408D6983 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
POLYPROTEIN.
SEQUENCE 3011 AA; 327184 MW; BB4B08D3 CRC32;
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
LECITHINASE.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:14:29 1999; MasPar time 5.88 Seconds 281.992 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 1 MEKFWAEFGGGYVQTPFLSE.....GLHLRVFDPSTGALVDSKSY Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

170751 segs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part8 10:part10 11:part11 12:part12 13:part13
14:part19 20:part10 11:part15 16:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38

Mean 26.730; Variance 108.537; scale 0.246 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description	Pred. No.
: -	300	54.4	65	19	R97371	Phage T4ORFX.cone	1 220-19
7	96	17.4	1693		W76368	Hematitis E virus hol	1.666+00
٣	87	15.8	623	35	W75773	Amino acid sequence o	9.05e+00
4	86	15.6	1693		R51264	HEV strain protein en	1.090+01
S	86	15.6	1693	36	W80196	Protein encoded by OR	1.09e+01
9	86	15.6	1693		R91813	Hepatitis E virus str	1.096+01
7	86	15.6	1693		W71209	Protein encoded by OR	1.09e+01
ထ	98	15.6	1693	37	W81519	Hepatitis E virus (HE	1.09e+01
σ	82	15.4	633	32	W75774	Amino acid seguence o	1.316+01
10	84	15.2	1693	٣	R14618	Protein encoded by OR	1.57e+01
11	82	14.9	633	35	W75775	Amino acid sequence o	2.27e+01
12	81	14.7	3011	12	R66995	Hepatitis C virus gen	2.72e+01
13	81	14.7	3011	ထ	R40120	HCV genomic amino aci	2.72e+01
14	80	14.5	170	П	P92033	Sequence encoded in t	3.26e+01
15	80	14.5	170	-	P90150	Sequence of hepatitis	3.26e+01
16	80	14.5	411	16	R90934	HCV NS5 domain antige	3.260+01

RESULT 2 ID W76368 standard; Protein; 1693 AA.

HCV non-structural pr 3.26e+01 Brassica napus micros 3.26e+01 HCV CKS-NS5E recombin 3.26e+01 HCV CKS-NS5 EF fusion 3.26e+01 Sequence encoded in 1.26e+01 Protein sequence of h.3.26e+01 Protein sequence of h.3.26e+01 Protein sequence of h.3.26e+01 Peptide encoded by co.3.26e+01 HCV amino acid sequen 3.26e+01 HCV-1 polyprotein. 3.26e+01 Hepatitis C virus pol 3.26e+01 Hepatitis C virus (HC 3.26e+01	S CS - S GS - S
W67010 W08378 R08378 R08378 R338519 R338441 R338532 R38532	ALIGNA 29p34 f. phace acture sh. citfle ciffle or mc or mc or mc or mc sh. cor ciffle sh. ciffle s
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	1 standard; Protein; 1; N-1997 (first entry 14 ORFX gene produc 14; tail fibre produc 17-1995; U3-322760. 17-1997;
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Query Match
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This is the amino acid sequence of a novel Bacillus thuringlensis toxin used in the method of the invention, to control lepidopteran pests.

The new toxins are useful as pestlides, especially for the control of ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynuclectide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1998 (first entry)
Amino acid sequence of lepidoteran-active HD573 toxin.
HD573 toxin: PCR: primer; amplification; Bacillus thuringlensis; probe; lepidoptera; pest; pesticide: Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringlensis.
                                                                                                                                                                                                                                            Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation of Laim 10: Page 17-24: 29pp: Japanese.

This sequence represents a Hepatitis E viral hollow particle protein. This polypeptides can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 frtsfydgavleangperynlsfdasgstmaagpfsptyaasaaglevryvaagldhrav 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 96; DB 35; Length 1693;
Pred. No. 1.66e+00;
21; Mismatches 25; Indels 3; Gaps
          03-DEC-1998 (first entry)
Hepatitis E virus hollow particle protein #1.
Hollow particle protein; virus; antibody; detection; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New insecticidal Bacillus thuringiensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea
                                                                                                             /note= "Partial sequence"
                                                                                                                                                                                     (DENK-) DENKA SEIKEN KK. (KKUV.) KOKURITSU YOBO EISEI KENKYUSHO. WPI: 98-555037/46. N-PSDB: V61687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1998. U05081.
13-MAR-1998. U05081.
13-MAR-1997. US-040512.
(MYCO ) MYCOGEN CORP.
MULIER-COhn J, Narva KE, Schnepf HE;
WPI: 98-506734/43.
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W75773 standard; Protein; 623 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 17.4%;
Local Similarity 26.9%;
nes 18; Conservative
                                                                                                                                            08-SEP-1998.
28-FEB-1997; 062445.
28-FEB-1997; JP-062445.
                                                                     Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632 fapgvsp 638
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                                                                                                                             J10234383-A
                                                      infection
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Disclosure; Page 57-62; 114pp; English.
The sequences given in R51264-66 are encoded by the hepatitis E virus (HEV) strain SAR-55. The clonk sequence contains three open reading frames (ORFS). These proteins can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins SAR-55 CDNA mas isolated from diagnosis of HEV infection. The HEV suspensions obtained from hepatitis E patients.
                                                                                                                                                              502 fisekygnggdslrfelsnttarytlrgngnsynlylrvssigsstirvtingrvytanv 561
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                                                                                                                                                                                                                     12 YVQTPFLSESNSYRXKIS-IAGSCPLSTAGPSYVKF-QDNPVGSQTFSAGLHLRVFDPST 69
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Protein encoded by ORF1 of ET-NANB (HEV) Burma strain DNA sequence.
Enterically transmitted non A non B hepatitis virus; ET-NANB;
Hepatitis E virus; HEV; Burma HEV isolate; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ë,
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HEV strain protein encoded by ORF-1.
HEV strain protein encoded by ORF-1.
antibody; detection; diagnosis; primates; stool suspension.
Hepatitis E virus strain SAR-55.
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    Length 623;
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Pred. No. 1.09e+01;
22; Mismatches 25; Indels
                                                                                     26; Mismatches 26; Indels
Score 87; DB 35;
Pred. No. 9.05e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R51264 standard; Protein; 1693 AA.
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W80196 standard; Protein; 1693 AA.
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Non A non B Hepatitis virus.
US5824649-A.
Ouery Match 15.8%;
Best Local Similarity 18.2%;
Matches 12; Conservative
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Matches 17; Conservative
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US-208997.
US-336672.
US-367486.
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07-JUN-1995; 475807,
25-JUL-1994; US-27982
17-JUN-1988; US-20899
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Disclosure; Pages 9-13; 121pp; English.

The present sequence is the protein prod. of ORF-1 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the etection of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than
                                                                                                                     Claim 22; Columns 57-66; 47pp; English.

W80196-98 are encoded by the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB)

(hepatitis E virus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORFI sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB.
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                                                                                     N-PSDB; V66321.
Hepatitis E virus proteins - useful for diagnosis or vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 ORF-1.
Hepatitis E virus; HEV; SAR-55 strain; enteric transmission; structural region; antigen; detection; antibody; vaccine;
                                                                                                                                                                                                                                                                                                        Score 86; DB 36; Length 1693;
                                                                                                                                                                                                                                                                                                                      Pred. No. 1.09e+01;
22; Mismatches 25; Indels
                                          Bradley DW, Fry KE, Krawczynski K2, Reyes GR, Tam A,
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3-00T-1995; U13102.
03-00T-1994; US-316765.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Emerson SU, Purcell RH, Tsarev SA;
WPI: 96-209320/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                           (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 6
R91813 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunisation; infection.
Hepatitis E virus.
05-JUL-1990; US-505888.
07-JUN-1995; US-475807.
                                                                                                          production the virus
Claim 22; Columns 57
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                                                        Yarbough PO;
WPI; 98-582599/49.
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                                                                                                                                                                                                                                                                              Sequence
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Disclosure; Columns 55-64; 45pp; English.
W/1209-11 represent the proteins encoded by the open reading frames (OREs) of the DNA sequence of the Burmese isolate of an enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV). detecting ET-NANB in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in
                                                                                                                                                                                                                      572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
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                                                                                                                                                                                                                                                    Gaps
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30-0CT-1998 (first entry)
Protein encoded by ORF 1 of the Burmese isolate of ET-NANB.
Enterically transmitted nonA/nonB hepatitis virus; identification;
HEV; ET-NANB; detection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis E virus DNA - useful for e.g. virus detection and viral
50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 confg. baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781. Sequence 1693 AA,
                                                                                                                                                                          'n
                                                                                                                          Length 1693;
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                                                                                                                                                                          25; Indels
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11-ARR-1989; US-336672.

19-JUN-1989; US-420921.

05-ARR-1990; US-505888.

25-JUL-1994; US-279888.

25-JUL-1994; US-279828.

Bradley DW, Fry KE, Krawczynski KZ, Reyes GR, Tam A,
                                                                                                                       Score 86; DB 19; I
Pred. No. 1.09e+01;
22; Mismatches 25;
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Best Local Similarity 25.4%; Pred. No. 1.09e+01;
Matches 17; Conservative 22; Mismatches 25;
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Misc_difference 1552
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Misc_difference 1514
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
ID W71209 standard; Protein; 1693 AA.
                                                                                                                       Query Match 15.6%;
Best Local Similarity 25.4%;
Matches 17; Conservative
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US-681078.
US-208997.
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WPI; 98-446186/38.
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25-JUN-1994; 2
05-APR-1991; U
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WPI; 91-325242/44.
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Matches
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                                                                                                                                                                                                                                                                                                                                               reg. developing products for diagnosis of, and vaccination against hepatitis E virus infection

Personal and products for diagnosis of, and vaccination against hepatitis E virus infection

Disclosure; Pages II-15: 20 kpp; English

This represents a hepatitis E virus (HEV) open reading frame (ORF)-1

Protein encoded by a DNA sequence designated SAR-55. SAR-55 also encodes

HEV MRF-2 and ORF-3 proteins. A host conganism transformed or transfected

With a recombinant expression vector containing the SAR-55 nucleic acid

can be used to produce the HEV proteins, especially ORF-2 protein. The

recombinant HEV proteins can be used as diagnostic agents and as vaccines

for use against HEV infection. The detection of antibodies specific for

HEV, and for monitoring the progression of such diseases. Such methods are

also useful for monitoring the efficacy of therapeutic agents during the

course of treatment of HEV infection and disease in a mammal. The

antibodies can be used for detection or for passive immunisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of lepidoteran-active HD525 toxin.
HD525 toxin, PCR: primer; amplification: Bacillus thuringlensis; probe; lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens; Helicoverpa zea; hybridisation.
Bacillus thuringlensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 frtsfydgavletngperhnlsfdasgstmaagpfsltyaasaaglevryvaagldhrav 631
        WB1519 standard; Protein; 1693 AA.
WB1519 (first entry)
Hepatitis E virus (HEV) ORF-1 protein.
Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                      New hepatitis E virus DNA from Pakistani strain SAR-55 - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۳
ښ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86; DB 37; Length 169:
Pred. No. 1.09e+01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                Emerson SU, Purcell RH, Robinson RA, Tsarev SA; WPI; 98-568733/48.
                                                                                    passive immunisation; open reading frame; ORF
                                                                                                                                                                                                                                                                   11-APR-1997; US-840316.
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                 /note= "encoded by CAG"
                                                                                                                                     'note- "encoded by CAG"
                                                                                                                                                                                         /note= "encoded by GTG"
                                                                                                                                                                                                                   /note= "encoded by GGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1998, U05081.
13-MAR-1997, US-040512.
(MYCO ) WYCOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W75774 standard; Protein; 633 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 15.6%;
Local Similarity 25.4%;
Les 17; Conservative
                                                                                                                                                   Misc_difference 1244
                                                                                                                                                                              Misc_difference 1352
                                                                                                                                                                                                       Misc_difference 1662
                                                                                                                            Misc_difference 1238
                                                                                                                                                                                                                                                           09-APR-1998; U07418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1693 AA;
                                                                                                   Hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 fapgvsp 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 FDPSTGA 71
                                                                                                                                                                                                                                                                                                           WPI; 98-568733/
N-PSDB; V71604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9840490-A1.
                                                                                                                                                                                                                                             22-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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controlling lepidopteran pests, especially Ostrinia nubilalis, Heliothis virescens and Helicoverpa zea Heliothis virescens and Helicoverpa zea Claim 14, Pages 32-34; 50pp; English.
This is the amino acid sequence of a novel Bacillus thuringiensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pestficides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression of the toxins and the primers, together with probes derived from the new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 15; 117pp; English.

A positive clone ET1.1 was identified in a library prepared from blie of cynomolgus monkeys infected with the Burma strain of ET-NANB. Both strands of ET1.1 were sequenced indentity of the sequence with sequences in etiologic agents has been confirmed by locating a similar sequence in a viral strain isolated in Burma. This protein is encoded by the longest ORF (ORF 1) of the Burma strain. Sequence 1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 fisekfgngsdalrfegsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by ORF 1 of Burmese ET-NANB viral strain.
enterically transmitted non-A, non-B hepatitis virus; hepatitis C;
HCV; E.coli strain BB4; ATCC deposit number 67717; Burma.
Enterically transmitted non-A, non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New viral proteins from non A-non-B hepatitis agent - used to treat and prevent enterically-transmitted non-A non-B hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 15.2%; Score 84; DB 3; Length 1693; Local Similarity 26.6%; Pred. No. 1.57e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 85; DB 35; Length 633
Pred. No. 1.31e+01;
20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reyes GR, Yarbough PO, Bradley DW, Krawczynski KZ, Tam A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 10
R14618 standard; Protein; 1693 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W75775 standard; Protein; 633 AA. W75775; 02-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.4%;
Best Local Similarity 23.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1990; US-505888.
(GENE-) GENELABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1991,
05-APR-1991, U02368,
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02-MAR-1990 (first entry)
Sequence encoded in the hepatitis C virus (HCV) cDNA insert in clone 14c.
Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH).
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and associated nucleic acids and polypeptide(s)

Claim 13: Figure 18: 139pp; English.

It is the sequence encoded in the hepatitis C virus (HCV) cDNA insert in clone 14c. Tag a = the region of overlap with the HCV antigen encoded in clone 25c. It is an epitope which could be used as immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive sequence 170 AA;
                                                                                                                                                                                                                                                                                                                     Example 1: Page 39-49; 100pp: English.

RNA was isolated from the plasma of a HCV seropositive human (designated "LG") and cDNA was prepared from it. The cDNA was PCR amplified using specific primers with sequences based on the prototype HCV-1 cDNA sequence (GENBANK M6231). Further amplification using nested primers resulted in 7 adjacent HCV DNA fragments which could be assembled into a full-length sequence. The DNA sequence was determined and translated into the genomic amino acid sequence. Comparison of the LG genomic amino acid sequence.

With that from HCV-1 showed 134 amino acid differences.
    HCV genomic amino acid sequence isolated from infected human LG. Hepatitis C Virus; Non-A, non-B hepatitis Virus; HCV; NANBHV; human growth hormone; HGH; secretion signal; fusion protein;
                                                                                                                                                                                                                                                                                 New plasmid pHCV-162 is a mammalian expression systems for HCVD proteins - useful for diagnosing HCV infection and as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2116 vpspeffteldgvrlh-rfappckpllrdevsfrvglhdypvgsq 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 vpspeffteldgvrlh-rfappckpllreevsfrvglheypvgsq 106
                                                                                                                               05-AUG-1993.
29-ANN-1993; U00907.
31-JAN-1992; UG-830024.
(ABBO ) ABBOTT LAB.
Bode SL, Casey JM, Desai SM, Devare SG, Frail DE;
Yamaguchi J, Zeck BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1989.

18-NOV-1988; 310922.

14-NOV-1988; US-271450; US-122714.

(CHIR) Chiron Corp.

Houghton M, Choo q-L, Kuo G;

WPI; 89-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P92033 standard; protein; 170 AA P92033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 14.7%;
Local Similarity 40.0%;
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..71
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3011 AA;
                                                                                         Hepatitis C Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; N92089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
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                                                                                                                                                                                                                                                                      New insecticidal Bacillus thuringlensis toxins - useful for controlling lepidopteran pests, especially Ostrinia nubilalis, that other controlling lepidopteran pests, especially Ostrinia nubilalis, that other controlling lepidopteran pests. Claim 5: Pages 36-38: 50pp; English.

This is the amino acid sequence of a novel Bacillus thuringlensis toxin used in the method of the invention, to control lepidopteran pests. The new toxins are useful as pesticides, especially for the control of Ostrinia nubilalis, Heliothis virescens, and Helicoverpa zea. The polynucleotide coding sequences are useful for recombinant expression new sequences, are useful for the identification and characterisation of novel genes that encode pesticidal toxins.
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Amino acid seguence of lepidoteran-active 8612 toxin.
8612 toxin; PCR; primer; amplification; Bacillus thuringlensis; probe;
lepidoptera; pest; pesticide; Ostrinia nubilalis; Heliothis virescens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 fisekfgnggdslrfegsnttarytlrgngnsynlylrvssignstirvtingrvytas 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV genes and the corresponding proteins - used in the production of anti-HCV antibodies and the detection of HCV infection claim 11; Pages 18-32; 35pp; Japanese.

Q74770 encodes R66995 the HC-JI/protein, the CDNA can be used in the construction of an expression vector for the transformation of a host cell. The host cell can then be used in the production of proteins and peptides, useful in the preparation of monoclonal Sequence 3011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1995 (first entry)
Hepatitis C virus gene HC-J1/protein.
Hepatitis C virus; HCV gene HC-J1/protein; specific antibodies.
Hepatitis c virus.
J06284887-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 2.72e+01;
10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 633;
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Pred. No. 2.27e+01;
                                                                                                                             17-SEP-1998. U05081.
13-MAR-1998. U05081.
13-MAR-1999; US-040512.
(MYCO ) MYCOGEN CORP.
Muller-Cohn J, Narva KE, Schnepf HE;
WPF: 98-506734/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 12
R66995 standard; Protein; 3011 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ
                                                                 Helicoverpa zea; hybridisation.
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Local Similarity 22.0%;
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-1994.
10-DEC-1993; 345753.
10-DEC-1992; JP-360705.
(IMMO ) IMMUNO JAPAN KK.
WPI; 94-36259445.
N-PSDB; Q74770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                       Bacillus thuringiensis.
                                                                                                         WO9840490-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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a ò NAME OF THE PART O

윱 ò 라오타

4

Gaps

4

54

Score 81; DB 8; Length 3011; Pred. No. 2.72e+01; 10; Mismatches 13; Indels 4

Gaps

4

Score 80; DB 1; Length 170; Pred. No. 3.26e+01; 11; Mismatches 13; Indels

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Tegion 1.71

GB2212511-A.

D 5-JUL-1989.

R GB2212511-A.

GB2312511-A.

GB2312511-A.

GB2312511-A.

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                               p90150;
1-NOV-1989 (first entry)
Sequence of hepatitis C virus cDNA insert in clone 14c
Hepatitis C virus; clone 14c; clone 25c; probe; vaccine.
Pan troglodytes
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   P90150 standard; protein; 170 AA.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 1 16:13:51 1999; MasPar time 6.25 Seconds 500.410 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 Title: Description: Perfect Score: Sequence:

1 MEKFMAEFGGGYVQTPFLSE......GLHLRVFDPSTGALVDSKSY 78 PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 37.846; Variance 68.015; scale 0.556 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Š.	7.69e-02 2.14e-01 3.14e-01 1.13e-01 1.13e-01 1.13e-01 1.13e-00 2.15e-00 2.1	226100
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SUMMARIES	S61248 MONWHE A61046 C56617 S38913 D70928 D70928 138375 S55092 164483 G70447 A55631 149133 S40770 S48529 S48529 S48529 GNWVC3 S69718	
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1 VYHUD 2 S39787 2 E712053 2 E712053 2 E64757 2 C69960 2 C700758 2 C700758 2 C700758 2 C700758 2 C700758 2 C700758 2 C700758 2 C700758 2 C70758 2 C70758	ype com protein sequence sequence the EMB the EMB the EMB the EMB 1 genor 1 genor ary ary label VI 248053; 248053;	Score 3 9; M 9; M 9; M 1111: 1111: 11-HLRVFD 1-HL
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#journal Virology (1991) 185.120-131

#title Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.

#cross-references MUID:92024067

#accession A40778
                                                                                ##residues 1-566 ##label ARN ##cross-references GB:AE001308; GB:AE001273; NID:g3328766; PID:g3328771 ##experimental_source serotype D, strain UM-3/Cx
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#title hepatitis E virus (HEV): strain variation in the nonstructural gene region encoding consensus motifs for an #RNA-dependent RNA polymerase and an ATP/GTP binding site.
                                                                                                                                                                                                                                                                                                              63 IAESYLQQSFLSEDTYIR-KSAIIGA-GLSGSSEA-LELLSEAIETQDLYEQL-L-ILNA 117
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##residues 967-1693 ##label FRY
##cross-references GB:M32400; NID:g330021; PID:g330022
##note sequence extracted from NCBI backbone (NCBIN:104572,
NCBIP:104573)
FINITE ##note #*superfamily hepatitis E virus nonstructural protein
RICATION #superfamily hepatitis E virus nonstructural protein
ATP; nonstructural protein; nucleotidyltransferase
#length 1693 #molecular-weight 185191 #checksum 6520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 FRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
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genome polyprotein - hepatitis E virus (strain Burma)
RNA-directed RNA polymerase (EC 2.7.7.48)
#formal_name hepatitis E virus
30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
29-May.1993
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22; Mismatches 25; Indels
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##residues 1-1693 ##label TAM
##cross-references GB:M73218; NID:9330024
RWCE A48547
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Pred. No. 2.14e-01;
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#cross-references MUID:99000809
#accession G71525
                              ##molecule_type DNA
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Best Local Similarity 26.2%;
Matches 17; Conservative
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The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.
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Jordi, B.J.; Willshaw, G.A.; van der Zeijst, B.A.; Gaastra,
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Characterization of IMP-E3, a gene active during imaginal disc morphogenesis in Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cfaC protein precursor - Escherichia coli plasmid NTP113 *formal_name Escherichia coli 05-Jan-1996 *sequence_revision 05-Jan-1996 *text_change 20-Mar-1998
A61046 *type complete ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster) *fromal_name brosophila melanogaster 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change
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##cross-references FlyBase:FBqn0001255
DS membrane protein
tX #length 331 #molecular-weight 36583 #checksum
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*length 869 #molecular-weight 97830 #checksum
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Pred. No. 8.12e-01;
14; Mismatches 8;
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Pred. No. 8.12e-01;
12; Mismatches 18
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Best Local Similarity 31.9%;
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                                                                                                        Wu, D.; Cao, X.L.; Bai, Y.Y.; Aronson, A.I.
FEMS Microbiol. Lett. (1991) 81:31-36
Sequence of an operon containing a novel delta-endotoxin gene
from Bacillus thuringiensis.
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hypothetical protein Rv2913c - Mycobacterium tuberculosis
(strain H37Rv)
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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                                                                                                                                                                                                                                                                                                            delta-endotoxin
#length 622 #molecular-weight 69729 #checksum 8205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83; DB 2; Length 281; Pred. No. 1.56e+00;
                                                                                                                                                                                                                                                                                                                                                                                                      26; Mismatches 26; Indels
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                                                                                                                                                                                                                                    ##residues 1-622 ##label WUD
##cross-references EMBL:X57252; NID:940283; PID:940286
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17-Jul-1998 #sequence_revision 17-Jul-1998
17-Jul-1998
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Best Local Similarity 18.2%; Pred. No. 1.13e+00;
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delta-endotoxin
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Best Local Similarity 24.1%;
Matches 14; Conservative
                                                 09-Sep-1997
S17402
S17400
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S38913
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##residues 1-6;
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homology; protein kinase homology; SH2 homology; SH3
homology
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Hum. Mol. Genet. (1994) 3:897-901

TXK, a novel human tyrosine kinase expressed in T cells shares sequence identity with Tec family kinases and maps
##cross-references GB:Z74024; GB:AL123456; NID:g3250700; PID:e1301028;
PID:g3250707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain protein kinase homology (fragment) #label KIN #length 81 #checksum 7751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138375 *type fragment
tyrosine kinase - human (fragment)
*formal_name Homo sapiens *common_name man
29.May-11998 *sequence_revision 29-May-1998 *text_change
10-Jul-1998
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#length 611 #molecular-weight 67204 #checksum
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##cross-references EMBL:U07794; NID:9508219; PID:9508224
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Pred. No. 1.56e+00;
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. No. 2.15e+00;
Mismatches 8; Indels
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##cross-references GDB:377329; OMIM:600058
#map_position 4p12-4p12
                                                                                                                                                                                                                                              translation not shown
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Pred. No.
                                                                                                                                                                                                                                                                                                                              ##experimental_source strain H37Rv
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44 VKFQDNPVGSQTFSAGLHLRVFD 66
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#accession I38375
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Best Local Similarity 43.5%;
Matches 10; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
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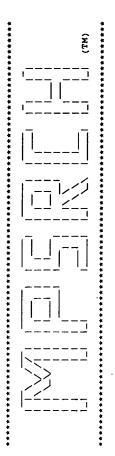
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#map_position 4p12-4p12
CLASSIFICATION #superfamily protein-tyrosine kinase tec; pleckstrin repeat
homology; protein kinase homology; SH2 homology; SH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184483 #type complete
tyrosine kinase - human
#formal_name Homo sapiens #common_name man
29-May-1998 #sequence_revision 29-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                       227 YMMGFSLGASIMTNYLGEESDRTKIECAISVSNPFDLYNSAYF-INSTPMGSRFYSPAL 284
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Hum. Mol. Genet. (1994) 3:897-901
TXK, a novel human tyrosine kinase expressed in T cells
shares sequence identity with Tec family kinases and n
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#domain SH2 homology #label SH3\
#domain protein Kinase homology #label KIN
#length 527 #molecular-weight 61239 #checksum 7997
          s55092  #type complete
hypothetical protein YMR210w - yeast (Saccharomyces
cerevisiae)
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submitted to the EMBL Data Library, June 1995
S55092
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18; Mismatches 22; Indels
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Pred. No. 2.15e+00;
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                                                           hypothetical protein YM8261.04
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-1995 #
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Local Similarity 44.4%;
les 12; Conservative
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Best Local Similarity 27.1%;
Matches 16; Conservative
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CLASSIFICATION #sup
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##residues
1-16 ##!abel AQF
##cross-references GB:AE000752; NID:g2984021; PID:g2984027; GB:AE000657
##experimental_source strain VF5
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Lenardo, M.J.; Bluestone, J.A.; Matis, L.A.
    J. Biol. Chem. (1995) 270:1928-1934
#title Identification of rlk, a novel protein tyrosine kinase with predominant expression in the T cell lineage.
#cross-references MUID:95130578
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                                                                                                                                                                                                                                   Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670447 *type complete
flagellar L-ring protein FlgH - Aquifex aeolicus
*formal_name Aquifex aeolicus
08-May-1998 *sequence_revision 08-May-1998 *text_change
08-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resting lymphocyte kinase
#formal_name Mus sp. #common_name mouse
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
17-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                 #title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum 9605
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#region protein kinase ATP-binding motif
#length 527 #molecular-weight 61108 #checksum 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) rlk
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#domain SH2 homology #label SH2\
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##residues 1-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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*residues 1. 1-513 **label OK2
*experimental_source isolate HC-J1
ICATION *superfamily hepatitis C virus genome polyprotein; DEAD/H box
helicase homology
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The 5'-terminal sequence of the hepatitis C virus genome. PC1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-527 ##label RES
##cross-references EMBL:U16145; NID:9562124; PID:9562125
##cross-references EMBL:U16145; NID:9562124; PID:9562125
FICATION #superfamily protein-tyrosine kinase tec; pleckstrin repeat homology; protein kinase homology; SH2 homology; SH3 homology
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##molecule_type genomic RNA
##residues 1-3011 ##label OKA
##cross-references EMBL:D10749; NID:g221586; PID:d1002057; PID:g221587
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                    #authors Haire, R.N.; Litman, G.W.
#journal Mamm. Genome (1995) 6:476-480
#title The murine form of TXK, a novel TEC kinase expressed in thymus maps to chromosome 5.
#cross-references MUID:96059336
#accession 149133
                                                                                                                                                                                                                                              #formal_name Mus musculus #common_name house mouse 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 12-Feb-1999
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polyprotein precursor - hepatitis C virus
#formal_name hepatitis C virus
20.Feb-1995 #sequence_revision 20-Feb-1995 #text_change
18 Sep-1999 S40770;
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#domain SH2 homology #label SH2\
#domain protein kinase homology #label KIN\
#region protein kinase AP-binding motif
#length 527 #molecular-weight 61108 #checksum 785
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Pred. No. 2.96e+00;
7; Mismatches 8; Indels
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                                                                   242 LRYPIGLLGSCLPATSGFSYEKWEIDP 268
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                                                                                           24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Best Local Similarity 44.4%;
Matches 12; Conservative
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Txk - mouse
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269-527
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Search completed: Wed Sep 1 16:14:10 1999 Job time: 19 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 1 16:12:32 1999; MasPar time 4.84 Seconds 455.488 Million cell updates/sec Run on:

Tabular output not generated.

>PCT-US99-13024-2 (1-78) from PCTUS9913024.pep (5 of 12) 551 1 MEKFWAEFGGGXVQTPFLSE......GLHLRVFDPSTGALVDSKSY 78 Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Searched:

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 38.840; Variance 62.332; scale 0.623 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	6.06e-47	9.436-04	1.92e-01	1.92e-01	1.92e-01	2.75e-01	2.75e-01	5.61e-01	7.96e-01	7.96e-01	1.13e+00	1.59e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00	3.14e+00						
	Description	HYPOTHETICAL 7.3 KD PR	NON-STRUCTURAL POLYPRO	LATE EMBRYOGENESIS ABU	NON-STRUCTURAL POLYPRO	NON-STRUCTURAL POLYPRO	HYPOTHETICAL 76.2 KD P	CFA/I FIMBRIAL SUBUNIT	HYPOTHETICAL 67.2 KD P	HYPOTHETICAL 51.4 KD P	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	HYPOTHETICAL 19.0 KD P	RECEPTOR-TYPE ADENYLAT	NUCLEAR POLYADENYLATED	PUTATIVE FAMILY 31 GLU	IMPORTIN BETA-3 SUBUNI	VITELLOGENIN PRECURSOR	GENOME POLYPROTEIN [CO	VITAMIN D-BINDING PROT	VITAMIN D-BINDING PROT	70 KD CRYSTAL PROTEIN	HYPOTHETICAL 108.4 KD	PUTATIVE PEPTIDASE IN
SUMMARIES	Ωī	Y15A_BPT4	POLN_HEVMY	EMB8_PICGL	POLN_HEVBU	POLN_HEVPA	Y4II_RHISN	CFAC_ECOLI	YX45_MYCTU	YM60_YEAST	TXK_HUMAN	TXK_MOUSE	YCB2_PSEDE	CY42_TRYBB	NAB3_YEAST	YB79_YEAST	IMB3_HUMAN	VIT_ONCMY	POLG_HCV1	VTDB_MOUSE	VTDB_HUMAN	CR72_BACTK	YJ31_YEAST	YQHT_BACSU
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	Length	65	1693	457	1693	1693	703	869	611	449	527	527	171	572	803	954	1097	1659	3011	472	474	633	935	353
% Query	Match	54.4	18.1	15.6	15.6	15.6	15.4	15.4	15.1	14.9	14.9	14.7	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.3	14.3	14.3	14.3	14.2
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VTDB_RABIT CK71_BACTK SSYS_XEAST POLG HCVH RL14_THEMA RL14_THEMA RCC_RCC_RCC_RCC_RCC_RCC_RCC_RCC_RCC_RCC	ALIGNMENTS PRT;	EATED) ST SEQUENCE UPI ST ANNOTATION (EIN IN GP34-GP) NO RNA STAGE; 7	SWISS-PROT	Score 300; DB 1 Pred. No. 6.06e- 3; Mismatches	ISVRYKISIAGSC	PRT; 16 (OUENCE UP	YPROTEIN (CONTAINS: RN. ICASE). (STRAIN MYANMAR) (HEV) ITIVE-STRAND VIRUSES, 1	IIDA F	MAJOR
2.2.2 4.76 1.2.2 6.33 1.2.1 1.2.	STANDARD;	1995 (REL. 31, CREAT 1995 (REL. 31, LAST 1995 (REL. 31, LAST 173 (REL. 31, LAST 173 AD PROTEIN 234.1. 34.1.	N.A. V-1994) TO THE PROTEIN. AA; 7334 MW;	54.4%; Similarity 82.1%; 46; Conservative	WTRICPNAILSESN :: GQGYVQTPFLSESN	SULT 2 POLN_HEVMY STANDARD; 004610; 01-OCT-1993 (REL. 27, CREATED) 11-OCT-1998 (REL. 37, LAST SEC	L POLYPROTEIN ; HELICASE]. IRUS (STRAIN M A POSITIVE-STR	N.A. 7573. IDA T., MA M.Z. AINN K.;	95-109(1993). E VIRUS IS THE
22	1 5A_BPT4 9509;	01-FEB-1995 (REL 01-FEB-1995 (REL 01-FEB-1995 (REL HYPOTHERICAL 7.3 115A OR 34.1. BACTERIOPHAGE TA VIRUSES; DSDNA V.	[1] SEQUENCE FROM N.A. KUTTER E.M.; SUBMITTED (NOV-1994) HYPOTHETICAL PROTEIN SEQUENCE 65 AA; 7	Match Local	1 MEKFMAEI : 1 MEKFMAEF	POLN_HEVMY 004610; 01-0CT-1993 (1 01-0CT-1993 (1 15-DEC-1999 (1	NON-STRUCTURA (EC 2.7.7.48) HEPATITIS E V. VIRUSES; SSRNI CALICIVIRUS.	SEQUENCE FROM N.A. MEDLINE, 93227573. AXE T.T., UCHIDA T. RIKHISA T., WINN K	Myanmar."; VIRUS GENES 7:
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EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
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                                                                                                                                POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
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                                                                                                                                                                                            Length 1693;
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Pred. No. 9.43e-04;
22; Mismatches 24; Indels
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SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE UPF0017 FAMILY.
                                                                                                          ............
IRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                        (POTENTIAL).
FFCB786D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51019 MW; AE7CB4CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
LATE EMBRYGGENESIS ABUNDANT PROTEIN EMB8.
                                                                                                                                                                                                                                                                                                                                                               457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REL. 24, CREATED)
(REL. 24, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                       982 ATP
185215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L47118; G1350545; -. PROSITE; PS01133; UPF0017; 1.
                                                                                                                                                                                         Query Match 18.1%;
Best Local Similarity 26.9%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PICEA GLAUCA (WHITE SPRUCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.6%;
Best Local Similarity 34.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                    EMBL; D10330; G221705;
                                                                                                                                                      NP_BIND 975 9
SEQUENCE 1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       632 FAPGVSP 638
                                                                                                                                                                                                                                                                                                       FDPSTGA 71
                                                                                                                                            ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                             EMB8_PICGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLN_HEVBU
P29324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS E VIRUS (STRAIN PAKISTAN) (HEV).
; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                       NO DNA STAGE; CALICIVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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"Characterization of a prototype strain of hepatitis E virus.";

PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992)

-I- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE ACENT OF ENTERICALLY

TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48); HELICASE].
HEPATITIS E VIRUS (STRAIN BURMA) (HEV).
WHOUSES: SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; CALICIVIRIDA CALICIVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (REL. 28, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NON-STRUCTURAL POLIFPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE (RC 2.7.7.48); HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length viral genome.";
viroLoGY 185:120-131(1991).
-1- HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A40778; MNWWHE.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis E virus (HEV): molecular cloning and sequencing of tull-length viral genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                 TAM A.W., SMITH M.M., GUERRA M.E., HUANG C.-C., BRADLEY D.W., FRY K.E., REYES G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86; DB 1; Length 1693;
Pred. No. 1.92e-01;
22; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL).
IW; C560BE14 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975 982 ATE
1693 AA; 185191 MW;
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M73218; G330024; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 92115700.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 92024067.
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65 FDPSTGA 71
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869 AA

PRT;

PCT-US99-13024-2-05.rsp

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"The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli."; MICROB. PATHOG. 6:297-309(1989).
                                        01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
CFA/I FIMERIAL SUBUNIT C PRECURSOR (COLONISATION FACTOR ANTIGEN
SUBUNIT C).
                                                                                                                              PLASMID NTP513.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                 HAMERS A.M., PEL H.J., WILLSHAW G.A., KUSTERS J.G.,
VAN DER ZEIJST B.A.M., GAASTRA W.;
                                      CREATED)
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                            STRAIN-ENTEROTOXIGENIC; MEDLINE; 89330163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 869 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-H37RV;
                                                                                                                ESCHERICHIA COLI.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE
                                                                                                                                                        ESCHERICHIA.
                                     01-MAY-1992
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YX45_MYCTU
Q10830;
             CFAC_ECOLI
P25733;
                윱
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                                                                                                                            572 FRTSFVDGAVLETNGPERHNLSFDASQSTMAAGPFSLTYAASAAGLEVRYVAAGLDHRAV 631
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-:- SIMILARITY: NONE OBVIOUS.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL
EMBL; M80581; G329998; -.
POLYPROTEIN; TRANSFERASE; RNA-DIRECTED RNA POLYMERASE; HELICASE;
                                                                                                                                                                                                                                                                                                                                                            PLASMID SYM PNGR234A.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of symbiosis between Rhizobium and legumes."; NATURE 387:394-401(1997) .
                                                                                                    3;
                                                                         Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 85; DB 1; Length 703;
Pred. No. 2.75e-01;
17; Mismatches 28; Indels
                                                                                                  22; Mismatches 25; Indels
                                    (POTENTIAL).
FBCA2483 CRC32;
                                                                                     Pred. No. 1.92e-01;
                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEDUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NOPOTHETICAL 76.2 KD PROTEIN YAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2BA53CE CRC32;
                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEMBRANE.
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POTENTIAL.
POTENTIAL.
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                                                                         Score 86;
                                    982 ATP
185149 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 PC
664 PC
76183 MW;
                                                                                                                                                                                                                                                                                                                                                (STRAIN NGR234).
                                                                        h
Similarity 25.4%;
17; Conservative
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Best Local Similarity 27.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; PROTEOBACTERIA
RHIZOBIACEAE; RHIZOBIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN;
TRANSMEM 23 43
                                    975 98
1693 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
357
432
644
703 AA;
                                                                                     Local Similarity
                                                                                                                                                                            632 FAPGVSP 638
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FDPSTGA 71
                                                                                                                                                                                                                                                                                                                                                RHIZOBIUM SP.
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                         ATP-BINDING.
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Y4II_RHISN
P55492;
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                                    NP_BIND
SEQUENCE
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TRANSMEM
SEQUENCE
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TRANSMEM
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                                                                                                  Matches
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-!- SIMILARITY: BELONGS TO THE N-ACYL-D-AMINO-ACID DEACYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 34, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 34, LAST ANNOTATION UPDATE)
MYCOTAGETICAL 67.2 KD PROFINI CY274.45C.
MYCOBACTERIUM TUBERCULOSIS.
MYCOBACTERIUM TUBERCULOSIS.
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIUM.
SEQUENCE FROM N.A.
MEDLINE; 92329981.
JORDI B.J.A.W., WILLSHAW G.A., VAN DER ZEIJST B.A.M., GAASTRA W.;
"The complete nucleotide sequence of region 1 of the CFA/I fimbrial
Operon of human enterotoxigenic Escherichia coli.";
DNA SEQ. 2:257-263(1992).
-I-FUNCTION: MAY SERVE AS ANCHOR FOR THE FIMBRIAE IN THE OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CFA/I FIMBRIAL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M55661; G145510; -.
ANTIGEN; SIGNAL; FIMBRIA; OUTER MEMBRANE; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97830 MW; 7AF76347 CRC32;
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llarity 32.4%;
Conservative
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SAPIENS (HUMAN).
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BINDING
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 YMMGFSLGASIMTNYLGEESDRTKIECAISVSNPFDLYNSAYF-INSTPMGSRFYSPAL 284
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
ω
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
DEDWAN K., BROWN D., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.,
WALSH S.V.;
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
HYPOTHETICAL S1, LAST ANNOTATION UPDATE)
HYPOTHETICAL S1, AND PROTEIN IN RAR1-SCJ1 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 1; Length 449;
Pred. No. 7.96e-01;
18; Mismatches 22; Indels
                                                                                                                                                         Score 83; DB 1; Length 611;
Pred. No. 5.61e-01;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                EMBL: Z74697; E249958; -.
EMBL: Z74024; E248895; -.
HYPOTHETICAL PROTEIN; HYDROLASE.
SQUENCE 611 AA; 67205 WW; 9DF140EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 AA; 51437 MW; FE884F32 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TXK_HUMAN STANDARD; PRT; 527 AA. P426H; 014220; REL. 32, CREATED) 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112).
                                                                                                                                                                                                                                                                            449 AA
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                       319 VRFQHLPVPFELYSDGIDLPVFE 341
                                                                                                                                                                                                                             44 VKFQDNPVGSQTFSAGLHLRVFD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01133; UPF0017; 1.
PFAM; PF00561; abhydrolase; 1.
HYPOTHETICAL PROTEIN.
                                                                                                                                                           Query Match 15.1%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 14.9%;
Best Local Similarity 27.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z49809; G854462;
                                                                                                                                                                                                                                                                          YM60_YEAST
Q03649;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                    HAIRE R.N., OHTA Y., LEWIS J.E., FU S.M., KROISEL P.M., LITMAN G.W.; "TXK a novel human tyrosine Kinase expressed in T cells shares sequence identity with Tec family kinases and maps to 4p12."; HUM. MOL. GENET. 3:897-901(1994).
                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE BTK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
SH3 DOMAIN; PHOSPHORYLATION.
EUKĀRYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;, EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13356; G161364; JOINED.
193369; G1161364; JOINED.
193370; G1161364; JOINED.
193372; G1161364; JOINED.
1934372; G1161364; JOINED.
1934373; G1161364; JOINED.
1934374; G1161364; JOINED.
193376; G1161364; JOINED.
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HSSP; Q06187; 1AWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L27071; G684986; -.
EMBL; U34379; G1161364; -
EMBL; U34367; G1161364; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G1161364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00017; SH2; 1.
PFAM; PF00018; SH3; 1.
                                                                                           TISSUE-BLOOD;
MEDLINE; 95038742.
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE
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         SOLUTION SOL
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SEQUENCE FROM N.A.
STRIN-C57BL/6J; TISSUE-THYMUS;
MEDLINE; 96059536.
HAIRE R.N., LITMAN G.W.;
"The murine form of TXK, a novel TEC kinase expressed in thymus maps
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAST CELLS.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: TO OTHEIN PROTEIN TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE BTK SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 95130578.

HU Q., DAVIDSON D., SCHWARTZBERG P.L., MACCHIARINI F.,
LENARDO M.J., BLUESTONE J.A., MATIS L.A.;
Identification of R1k, a novel protein tyrosine kinase with
predominant expression in the T cell lineage.";
J. BIOL. CHEM. 270:1928-1934(1995).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- TISSUE SPECIFICITY: EXPRESSED IN EARLY THYMOCYTES, T CELLS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
STRAIN-FVB/N: TISSUE-THYMUS;
SOMMERS_C.L., HUANG K., GRINBERG A., CHARLICK D.A., KOZAK C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CSTBL/6; TISSUE-LIVER;
HIGASHITSUJI H., NONOGUCHI K., ARII S., FURUTANI M., KANEKO Y.,
NAKAYAMA H., FUJITA J.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                       Score 82; DB 1; Length 527; Pred. No. 7.96e-01; 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
45 H -> R (IN REF. 2),
61239 MW; 8DF019E3 CRC32;
                                                                                                                                                                                                                   242 LRYPVGLMGSCLPATAGFSYEKWEIDP 268
                                                                                                                                                                                                                                                       24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQI
15-JUL-1998 (REL. 36, LAST ANN
                                                                                       / Match 14.9%;
Local Similarity 44.4%;
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U16145; G562125; -. EMBL; U19607; G643065; -.
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TXK OR RLK.
MUS MUSCULUS (MOUSE).
   45
527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYMPHOCYTE KINASE).
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                                                                                                                                                                                                                                                                                                                                                                               LT 11
TXK_MOUSE
P42682;
CONFLICT
                                                                                           Query Match
                                                                                                                                                            Matches
   SO
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                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMERON B., GUILHOT C., BLANCHE F., CAUCHOIS L., ROUYEZ M.-C., RIGAULT S., LEYY-SCHIL S., CROUZET J.; Genetic and sequence analyses of a Pseudomonas denitrificans DNA fragment containing two cob genes."; J. BACTERIOL. 173:6058-6065(1991).

-! SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
                                                                                                                                                                  PFAM; PF00017; SH2; 1.
PFAM; PF000018; SH3; 1.
PFAM; PF000069; pkinase; 1.
HSSP; Q06187; LAWW.
TRANSFERASE; TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 527;
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01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 19.0 KD PROTEIN IN COBS 5'REGION (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LS -> SF (IN REF. 3).
Y -> D (IN REF. 3).
A -> T (IN REF. 3).
R -> S (IN REF. 3).
S 5B39DA78 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81; DB 1; Len
Pred. No. 1.13e+00;
7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 AA
                                     MGD; MGI:102960; TXK.,
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                   POLY-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LRYPIGLLGSCLPATSGFSYEKWEIDP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 VRYKISIAGSCPLSTAGPSYVKFQDNP 50
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PROSITE; PS50076; DNAJ_2; 1.
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                                                                                                                                                                                                                                                                             SH3 DOMAIN; PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    larity 44.4%;
Conservative
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                   G623443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00226; DnaJ; 1.
HSSP; P08622; 1XBL.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                     200
200
200
300
D43963; G604884;
L35268; G623443;
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272
497
527 AA;
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CONFLICT
CONFLICT
SEQUENCE
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BINDING
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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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                                                                                                                                                                 SWANSON M.S.
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P38138;
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SEQUENCE
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   SOURCE STATE STATE SOURCE COURT SERVICE SOURCE SOUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 EYNKGYNFFSGLSDSEVARYQKEAITGHRPTWTVGVN-KNAKNGPTQSQTRSGSAGAQAR 82
                                                                                         EUKARYOTA; EUGLENOZOA; KINETOPLASTIDA; TRYPANOSOMATIDAE; TRYPANOSOMA
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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PFAM, PF00211; quanylate_cyc; 1.
HSSP: Q02846; 1AML.
LYASE; CAMP SYNTHESIS; TRANSMEMBRANE; RECEPTOR; GLYCOPROTEIN.
                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PYRCPHORPHATE-LYASE) (ADENYLYL CYCLASE) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 LSTAERSQFDVTPLGGVPLRGVSEPVEVYQLNAVPGRSF-AELRLDRVLD 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80; DB 1; Length 572; Pred. No. 1.59e+00;
Score 80; DB 1; Length 171;
Pred. No. 1.59e+00;
11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
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CE3202BF CRC32;
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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Best Local Similarity 30.0%;
Query Match 14.5%;
Best Local Similarity 37.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TRYPANOSOMA BRUCEI BRUCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                       STANDARD;
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152
572 AA;
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VFDP 67
                                                                                                                                            MRDP 86
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Q99396;
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P38996;
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DOMAIN
TRANSMEM
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                                                                                                                                                            SEQUENCE FROM N.A.
WILSON S.M., OBERDORF A.M., DATAR K.V., SWEDLOW J.R., PADDY M.R.,
                          NAB3 OR YPL190C.
SECHARONYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCCTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (REL. 30, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PUTATIVE FAMILY 31 GLUCOSIDASE IN PCS60-ABD1 INTERGENIC REGION
(EC. 3.2.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.
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Pred. No. 1.59e+00;
10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 802;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
RIEGER M., MUELLER-AUER S., SCHAEFER M.;
SCHMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SUBCELLLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
                                                                                                                                                                                                                                              SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 QGY-VQTPF-LSESNSVRYKISIAGSCPLSTAGPSYVKFQDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 QGYGSQPPIPMNQSYG-RYQTSIPPPPPQQQIPQGYGRYQAGP
NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLN.
FB180EDB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954 AA
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POLY-ASP.
POLY-ASP.
POLY-ASP.
POLY-GLU.
POLY-GLU.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%;
larity 32.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U05314; G476220; -. EMBL; Z73546; E246917; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S48529; S48529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; L0001228; NAB3.
PFAM; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723
765
769
802 AA;
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nes 14; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RBR229C OR YBR1526.
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PCT-US99-13024-2-05.rsp

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-!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                             EMBL; Z36098; G536626; -.
PIR; S46105; S46105.
PROSITE: PS00129; GLYCOSYL_HYDROL_F31_1; 1.
PROSITE: PS00707; GLYCOSYL_HYDROL_F31_2; FALSE_NEG.
PFAM: PF01055; Glycosyl_hydrl5; 1.
PFOTHETICAL PROTEIN: HYDROLASE: GLYCOSIDASE.
ACT_SITE 537
SCOURCE 954 AA: 110265 MW; 9710BA62 CRC32;
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136 KFQEEANRTSIPQFHFLKQKQTVNSFWSKISSFLSLSNSTADTFHLRNGDVSVEIFAEPF 195

g ò g Search completed: Wed Sep 1 16:12:47 1999 Job time: 15 secs.

Query Match
14.5%; Score 80; DB 1; Length 954;
Best Local Similarity 21.5%; Pred. No. 1.59e+00;
Matches 14; Conservative 20; Mismatches 29; Indels 2; Gaps